

GenCore version 5.1.6  
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4 nucleic - nucleic search, using sw model

on: February 5, 2004, 22:17:43 ; Search time 576 Seconds  
(without alignments)  
10240.056 Million cell updates/sec

File: US-09-989-279-228  
Project score: 2185  
Sequence: 1 gtttccttcctcgccaaa.....aaagacaaaagtcaaaaca 2185

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1659446

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : N Geneseq 19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	2185	21	Human PRO1111 nucl
2	2185	100.0	2185	21	Membrane-bound pro
3	2185	100.0	2185	22	Human cDNA sequenc
4	2185	100.0	2185	22	Human PRO1111 (UNQ
5	2185	100.0	2185	25	cDNA encoding huma
6	2185	100.0	2185	25	Human cDNA encodin
7	2185	100.0	2185	25	DNA encoding novel
8	2185	100.0	2185	25	Novel human secret

9	2185	100.0	2185	25	ABX80774	Human secreted/tra
10	2185	100.0	2185	25	ABX81157	Novel human secret
11	2185	100.0	2185	25	ABX90247	Human secreted/tra
12	2185	100.0	2185	25	ABX77858	Human PRO polynuci
13	2185	100.0	2185	25	ABX79454	Human secreted/tr
14	2185	100.0	2185	25	ABX64093	cDNA encoding huma
15	2185	100.0	2185	25	ABX17057	Human PRO polynuci
16	1982	90.7	2324	22	AAS28823	Human immunoglobul
17	1911	87.5	1962	22	RAU16345	Human sbgPRO331a g
18	1910	87.4	2360	20	AAK90848	cDNA clone CC359.4
19	1826	83.6	2341	21	AAA93620	Human SLIT protein
20	1778	81.4	2159	22	ABA06571	Human cDNA SEQ ID
21	1778	81.4	2159	24	ABV83908	Human polynucleoti
22	1440	65.9	2607	21	AAAG3621	Human SLIT protein
23	1351	61.8	1805	21	AAC77300	Human OREF ORF2855
24	1178	53.9	1356	21	AAAG3631	Human SLIT protein
25	758	34.7	1168	22	ABA06744	Human cDNA SEQ ID
26	758	34.7	1168	22	AAS28872	Human immunoglobul
27	758	34.7	1168	24	ABV84081	Human polynucleoti
28	259	11.9	274	20	AAV88338	EST clone FX353.
29	193	8.8	257	20	AAV89165	EST clone CC359.
30	60	2.7	60	24	ABN40900	Human spliced tran
31	50	2.3	50	21	AAC58254	Human PRO1111 hybr
32	50	2.3	50	21	AAZ65183	Probe specific for
33	50	2.3	50	22	AAF44340	Human PRO1111 hybr
34	50	2.3	50	25	ABX80286	Novel human secret
35	50	2.3	50	25	ABX80790	Human secreted/tra
36	50	2.3	50	25	ABX81173	Novel human secret
37	50	2.3	50	25	ABX90263	Human secreted/tra
38	50	2.3	50	25	ABX77874	Human PRO probe #2
39	50	2.3	50	25	ABX79470	Human secreted/tr
40	50	2.3	50	25	ABX64109	Human PRO DNA prob
41	50	2.3	50	25	ABX17073	Human PRO probe #2
42	31	1.4	31	21	AAC58323	Human PRO1111 hybr
43	31	1.4	31	22	AAF44427	Human PRO1111 hybr
44	31	1.4	31	25	ABX80436	Human secreted or
45	31	1.4	31	25	ABX80940	Human secreted/tra
46	31	1.4	31	25	ABX81323	Human secreted or
47	31	1.4	31	25	ABX90413	Human secreted/tra
48	31	1.4	31	25	ABX78024	Human PRO probe #5
49	31	1.4	31	25	ABX79620	Human secreted/tr
50	31	1.4	31	25	ABX64259	Human PRO DNA prob
51	31	1.4	31	25	ABX17223	Human PRO probe #5
52	29	1.3	39	21	AAAG3644	Human mature SECK
53	29	1.3	757	21	AAAG3881	Human secreted exp
54	29	1.3	973	21	AAZ98019	Human secreted pro
55	29	1.3	973	22	ADL11632	Human secreted pro
56	29	1.3	973	24	ABK69728	Human secreted pro
57	29	1.3	973	25	ACC50741	Human secreted pro
58	29	1.3	984	21	AAZ98088	Human secreted pro
59	29	1.3	984	22	ADL11701	Human secreted pro
60	29	1.3	984	24	ABK69797	Human secreted pro
61	29	1.3	984	25	ACC50742	Human secreted pro
62	29	1.3	1002	25	ACC50471	Human secreted pro
63	29	1.3	1869	24	ABK34766	Human cDNA for nov
64	29	1.3	2083	24	ABX03572	Human nervous svst
65	29	1.3	2090	24	AAS62318	cDNA sequence #105
66	29	1.3	2316	25	ABK70472	DNA encoding human
67	29	1.3	2337	24	ABK62093	Human cDNA encodin
68	29	1.3	2450	24	ABX03571	DNA encoding human
69	29	1.3	2493	22	AAD21287	Human leucine-rich
70	29	1.3	2756	24	ABX03577	DNA encoding human
71	29	1.3	3027	24	ABK62087	Human cDNA encodin
72	27	1.2	27	21	AAAG3653	Human SECK 3352358
73	27	1.2	29	20	AAK90858	Oligonucleotide pr
74	26	1.2	26	21	AAK90858	Human PRO1111 reve
75	26	1.2	26	22	AAF44426	Human secreted or
76	26	1.2	26	25	ABX80435	Human secreted/tra
77	26	1.2	26	25	ABX80939	Human secreted or
78	26	1.2	26	25	ABX81322	Human secreted/tra
79	26	1.2	26	25	ABX90412	Human PRO PCR prim
80	26	1.2	26	25	ABX78023	Human secreted/tra
81	26	1.2	26	25	ABX79619	Human secreted/tra

Human PRO DNA PCR  
Human PRO PCR prim  
Drosophila melanog  
Human SECC 3352358  
Human SECC 3352358  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
DNA encoding Dros  
Human PRO1111 forw  
Human PRO1111 forw  
Human mature SECC  
Human mature SECC  
Human mature SECC  
Human mature SECC  
Human PRO1111 forw  
Human secreted or  
Human secreted or  
Human secreted or  
Human secreted or  
Human PRO PCR prim  
Human secreted/tr  
Human secreted/tr  
Human PRO DNA PCR  
Human PRO PCR prim  
Drosophila melanog  
Human breast cauce  
Human neuroblastom  
Human cDNA clone ( G-protein coupled-  
Human olfactory re  
Human GPCR-14 cDN  
Human polynucleoti  
Human novel polynu  
Drosophila melanog  
Drosophila melanog  
Human cDNA sequenc  
Human polynucleoti  
Human secreted pro  
Nucleotide sequenc  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
DNA transcription  
Drosophila melanog  
Nucleotide sequenc  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Human small induci  
Drosophila melanog  
Human nervous syst  
Human immune/haema  
Drosophila melanog  
Total base sequenc  
Human immune/haema  
Human secreted pro  
Human secreted pro  
Human secreted pro  
Human excretory re

RESULT 1  
AAC58383  
ID AAC58383 standard; cDNA; 2185 BP.  
XX AAC58383;  
AC AAC58383;  
XX 29-JAN-2001 (first entry)  
DT Human PRO1111 nucleotide sequence SEQ ID NO:45.  
DE Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW neoplastic; neuroprotective; antineoplastic; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
KW neuronal disorder; glioma; astrocytic disorder; astrocytic malignancy;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocoele disorder;  
KW inflammatory disorder; immunologic disorder; ss.  
XX Homo sapiens.  
OS WO200053755-A2.  
XX 14-SEP-2000.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 26-JUL-1999; 99US-0145698.  
XX 30-NOV-1999; 99WO-US28313.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
Watanabe CK, Wood WI;  
WPI; 2000-572270/53.  
P-PSDB; AAB24073.  
Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
treatment, diagnosis and prevention of cancer -  
Claim 50; Fig 33; 286pp; English.  
The present invention describes an isolated antibody that binds to  
one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO335,  
PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
PRO1187, PRO1231, PRO23, PRO39, PRO334, PRO1317, PRO1710, PRO2094,  
PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
growth. The PRO polypeptides and nucleotides are useful in the  
treatment, diagnosis and prevention of cancer. The antibodies and other  
anti-tumour compounds may be used to treat various conditions, including  
those characterised by overexpression and/or activation of the amplified  
PRO genes. Exemplary conditions include benign or malignant tumours  
(e.g., renal, liver, kidney, pancreatic, lung, vulva, thyroid, hepatic  
colorectal, prostate, glioblastomas, and various head and neck tumours),  
carcinomas, sarcomas, glioblastomas, and other disorders such as neuronal,  
leukaemias and lymphoid malignancies, other disorders such as neuronal,  
glioma, astrocytic, hypothalamic and other glandular, macrophagal,  
epithelial, stromal and blastocoele disorders, and inflammatory,  
angiogenic and immunologic disorders. AAC58383 to AAC58366 represent PCR  
primers and hybridisation probes used in the isolation of the human PRO  
sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
PRO polynucleotide and protein sequences given in the exemplification of  
the present invention.



X Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Query Match 100.0%; Score 2185; DB 21; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 b 1 GTTCTCTTCCGAGCCAAATCCAGGGGATGGTGAATTAATGAACGTGGCACACCATGA 60

61 AGCTCTTGGGAGGTAATCTGTCACACACACCTGGAAATGCCATCTGCTCCGTTTCG 120  
 b 61 AGCTCTTGGGAGGTAATCTGTCACACACACCTGGAAATGCCATCTGCTCCGTTTCG 120

121 TCTACCTCAGCGGCAAGTGTGGATTTCTGTGTGACGCCATGCTCTCCGCTCAGCGG 180  
 b 121 TCTACCTCAGCGGCAAGTGTGGATTTCTGTGTGACGCCATGCTCTCCGCTCAGCGG 180

181 GSCCCAGAACTGCCCTCCGTTTGTCTGTCAGTAAACGATTCAGCAAGGTGTGCA 240  
 b 181 GSCCCAGAACTGCCCTCCGTTTGTCTGTCAGTAAACGATTCAGCAAGGTGTGCA 240

241 CGCGCGGGGCTCTCCGAGGTCCCGCAGGGTATTCCTTCGAACACCCGGTACCTCAAC 300  
 b 241 CGCGCGGGGCTCTCCGAGGTCCCGCAGGGTATTCCTTCGAACACCCGGTACCTCAAC 300

301 TATGTGAGAAACATCTCAGATGATCCAGGCGACACCTTCGCGCACCTCCACACCTGG 360  
 b 301 TATGTGAGAAACATCTCAGATGATCCAGGCGACACCTTCGCGCACCTCCACACCTGG 360

361 AGTCTCTGAGTTGGGAGGAGTCCATCCGCGCAGATTCAGGTGGGGCTTCACAGGCC 420  
 b 361 AGTCTCTGAGTTGGGAGGAGTCCATCCGCGCAGATTCAGGTGGGGCTTCACAGGCC 420

421 TGCGCAGCTTCAACACCTTGGAGCTTTTCGACAACTGGCTGACATCTCCCTAGCGGG 480  
 b 421 TGCGCAGCTTCAACACCTTGGAGCTTTTCGACAACTGGCTGACATCTCCCTAGCGGG 480

481 CTTTGAATACCTGTCCAGCTCGGGAGCTCTGGCTTCGCAACACCCATCGAAAGCA 540  
 b 481 CTTTGAATACCTGTCCAGCTCGGGAGCTCTGGCTTCGCAACACCCATCGAAAGCA 540

541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGAATGGGGAGCTCA 600  
 b 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGAATGGGGAGCTCA 600

601 AGAAGCTGGAGTATCTCTGAGGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGA 660  
 b 601 AGAAGCTGGAGTATCTCTGAGGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGA 660

661 ACTTGGGCTGTGCAATTAAGACATGCCAATCTCAACCCCTGGTGGGCTGGAGG 720  
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721 AGTGGAGATGTGAGGAAACCATCTCCCTGAGATCAGGCTGGCTCTTCCATGGCCTGA 780  
 b 721 AGTGGAGATGTGAGGAAACCATCTCCCTGAGATCAGGCTGGCTCTTCCATGGCCTGA 780

781 GCTCCCTCAAGAAGCTCTGGGTCACTGATCTCAGGTTCAGCTGATTGAGCGGAATGTT 840  
 b 781 GCTCCCTCAAGAAGCTCTGGGTCACTGATCTCAGGTTCAGCTGATTGAGCGGAATGTT 840

841 TTGACGGGCTGGCTTCACTTTGTGAACTCAACTGGGCCCAATAAATCTCTCTTTTCG 900  
 b 841 TTGACGGGCTGGCTTCACTTTGTGAACTCAACTGGGCCCAATAAATCTCTCTTTTCG 900

901 CCAATGACCTTTTACCGGCTGAGTACTGAGTGGAGTTGATCTACACACACACCTTT 960  
 b 901 CCAATGACCTTTTACCGGCTGAGTACTGAGTGGAGTTGATCTACACACACACCTTT 960

961 GGAACGTGATGTGACATTTCTGTGGTACGCTGGTGGCTTCGAGGTATATACCCACA 1020  
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 Db 1021 ATTCCACCTGTGTGGCGCTGTCTCATGTCTCCATGCACATGCGAGGCGCTACCTCGTGG 1080

1081 AGTGGACAGGCGCTCTTCCAGTGTCTGCCCCCTTATCATGTGACGACACCTCGAGACC 1140  
 Qy 1081 AGTGGACAGGCGCTCTTCCAGTGTCTGCCCCCTTATCATGTGACGACACCTCGAGACC 1140

1141 TCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGTGGACTCCCCCTATGTCTCTCG 1200  
 Db 1141 TCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGTGGACTCCCCCTATGTCTCTCG 1200

1201 TGAAGTGTGTGTCGCCAATGCGACAGTGTCTCAGCAAGCTCCCGCCACCCAGAGTCT 1260  
 Qy 1201 TGAAGTGTGTGTCGCCAATGCGACAGTGTCTCAGCAAGCTCCCGCCACCCAGAGTCT 1260

1261 CTGTCTCTCAACAGCGGACCTTTGAACTTTTCCACAGTGTCTTTTCAGACACTGGGGTGT 1320  
 Db 1261 CTGTCTCTCAACAGCGGACCTTTGAACTTTTCCACAGTGTCTTTTCAGACACTGGGGTGT 1320

1321 ACACATGCTGTGTGACCAATGTGTGAGGCAACTCCAAAGCTCCGCTCGGCTACCTCAATGTA 1380  
 Qy 1321 ACACATGCTGTGTGACCAATGTGTGAGGCAACTCCAAAGCTCCGCTCGGCTACCTCAATGTA 1380

1381 GCACGCTGAGCTTAACTCCTCCAACTACAGCTTTTTCACACAGTAAACAGTGGAGACA 1440  
 Db 1381 GCACGCTGAGCTTAACTCCTCCAACTACAGCTTTTTCACACAGTAAACAGTGGAGACA 1440

1441 CGGAGATCTGGCTGAGGACACAAACCGGAAAGTACAGCTGTGCTTACACAGTCCACTG 1500  
 Qy 1441 CGGAGATCTGGCTGAGGACACAAACCGGAAAGTACAGCTGTGCTTACACAGTCCACTG 1500

1501 GTTACAGCGCGGATATACCACTCTTACCAAGCTGTCTTACAGCTACCCCTGTGCCCCA 1560  
 Db 1501 GTTACAGCGCGGATATACCACTCTTACCAAGCTGTCTTACAGCTACCCCTGTGCCCCA 1560

1561 AGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAAGTACAGCTGGATGAAG 1620  
 Qy 1561 AGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAAGTACAGCTGGATGAAG 1620

1621 TCATGAGACACCAAGATCATCTGCTGTGCTGTGTCAGTGTCTGCTAGCTGGCG 1680  
 Db 1621 TCATGAGACACCAAGATCATCTGCTGTGCTGTGTCAGTGTCTGCTAGCTGGCG 1680

1681 CCATGTTGATGTCTTCTATAAACTTCTGTAAGCGGACACAGCAGCGAGTACAGTCAAG 1740  
 Qy 1681 CCATGTTGATGTCTTCTATAAACTTCTGTAAGCGGACACAGCAGCGAGTACAGTCAAG 1740

1741 CGCGCGGACTGTTGAGATATCCAGGTGGAACGAGACATCCAGAGCAACATCCGCGAG 1800  
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1801 CAGCAGCAGCAGCTCCGCTGGTGTATCAGGTGAGGGGCGAGTAGTGTGCGCCACAATTC 1860  
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1861 ATGACCATATTAATCAACACCTCAAAACAGCACAATGGGCGCCACTGGAACAGAAAAA 1920  
 Db 1861 ATGACCATATTAATCAACACCTCAAAACAGCACAATGGGCGCCACTGGAACAGAAAAA 1920

1921 GCCTGGGAACTCTGTGCAACCCAGAGTCAACACTATCTCTGACCTTATATATTCAG 1980  
 Qy 1921 GCCTGGGAACTCTGTGCAACCCAGAGTCAACACTATCTCTGACCTTATATATTCAG 1980

1981 CCAATACCAAGGACAGGTACAGAAACTCAAAATGACTCTCCCTCCCCCAAAAAATTTA 2040  
 Db 1981 CCAATACCAAGGACAGGTACAGAAACTCAAAATGACTCTCCCTCCCCCAAAAAATTTA 2040

2041 TAAATGCAATAGATGCGACAAAGAGAGCACTTTTGTACAGGTGGGAGAGCTTT 2100  
 Qy 2041 TAAATGCAATAGATGCGACAAAGAGAGCACTTTTGTACAGGTGGGAGAGCTTT 2100

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OY 2101 TCTGTATATGCTTATATATTAAGTCTATGGCTGTTAAAAAACAAGATTATATAA 2160
      |||||
DB 2101 TCTGTATATGCTTATATATTAAGTCTATGGCTGTTAAAAAACAAGATTATATAA 2160
      |||||
OY 2161 AATTAAAGACAAAAGTCAAAACA 2185
      |||||
DB 2161 AATTAAAGACAAAAGTCAAAACA 2185
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RESULT 2
AAZ65033
ID AAZ65033 standard; cDNA; 2185 BP.
XX AC AAZ65033;
XX DT 05-APR-2000 (first entry)
XX DE Membrane-bound protein PRO1111 encoding cDNA.
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX OS Homo sapiens.
XX PN WO9963088-A2.
XX PD 09-DEC-1999.
XX PF 02-JUN-1999; 99WO-US12252.
XX PR 02-JUN-1998; 98US-0087607.
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PR 03-JUN-1998; 98US-0087759.
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PR 17-JUN-1998; 98US-0088876.
PR 17-JUN-1998; 98US-0089090.
PR 17-JUN-1998; 98US-0089105.
PR 17-JUN-1998; 98US-0089440.
PR 17-JUN-1998; 98US-0089512.
PR 17-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089601.
PR 17-JUN-1998; 98US-0089607.
PR 17-JUN-1998; 98US-0089608.
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PR 17-JUN-1998; 98US-0089948.
PR 17-JUN-1998; 98US-0089952.
PR 17-JUN-1998; 98US-0090246.
PR 17-JUN-1998; 98US-0090252.
PR 17-JUN-1998; 98US-0090254.
PR 17-JUN-1998; 98US-0090349.
PR 17-JUN-1998; 98US-0090355.
PR 17-JUN-1998; 98US-0090429.
PR 17-JUN-1998; 98US-0090431.
PR 17-JUN-1998; 98US-0090435.
PR 17-JUN-1998; 98US-0090444.
PR 17-JUN-1998; 98US-0090445.
PR 17-JUN-1998; 98US-0090461.
PR 17-JUN-1998; 98US-0090472.
PR 17-JUN-1998; 98US-0090535.
PR 17-JUN-1998; 98US-0090538.
PR 17-JUN-1998; 98US-0090540.
PR 17-JUN-1998; 98US-0090557.
PR 17-JUN-1998; 98US-0090676.
PR 17-JUN-1998; 98US-0090678.
PR 17-JUN-1998; 98US-0090688.
PR 17-JUN-1998; 98US-0090690.
PR 17-JUN-1998; 98US-0090691.
PR 17-JUN-1998; 98US-0090694.
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PR 17-JUN-1998; 98US-0090862.
PR 17-JUN-1998; 98US-0090863.
PR 17-JUN-1998; 98US-0091358.
PR 17-JUN-1998; 98US-0091360.
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PR 17-JUN-1998; 98US-0091486.
PR 17-JUN-1998; 98US-0091519.
PR 17-JUN-1998; 98US-0091626.
PR 17-JUN-1998; 98US-0091633.
PR 17-JUN-1998; 98US-0091646.
PR 17-JUN-1998; 98US-0091673.
PR 17-JUN-1998; 98US-0091978.
PR 17-JUN-1998; 98US-0091982.
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PR 17-JUN-1998; 98US-0092472.
PR 17-JUN-1998; 98US-0093339.
PR 17-JUN-1998; 98US-0094651.
PR 17-JUN-1998; 98US-0095282.
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PR 17-JUN-1998; 98US-0095301.
PR 17-JUN-1998; 98US-0095302.
PR 17-JUN-1998; 98US-0095318.
PR 17-JUN-1998; 98US-0095321.
PR 17-JUN-1998; 98US-0095325.
PR 17-JUN-1998; 98US-0095316.
PR 17-JUN-1998; 98US-0095929.
PR 17-JUN-1998; 98US-0096012.
PR 17-JUN-1998; 98US-0096143.
PR 17-JUN-1998; 98US-0096146.
PR 17-JUN-1998; 98US-0096329.
PR 17-JUN-1998; 98US-0096757.
PR 17-JUN-1998; 98US-0096766.
PR 17-JUN-1998; 98US-0096768.
PR 17-JUN-1998; 98US-0096773.
PR 17-JUN-1998; 98US-0096791.
PR 17-JUN-1998; 98US-0096867.
PR 17-JUN-1998; 98US-0096891.
PR 17-JUN-1998; 98US-0096894.
PR 17-JUN-1998; 98US-0096895.
PR 17-JUN-1998; 98US-0096897.
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R 18-AUG-1998; 98US-0096949.  
R 18-AUG-1998; 98US-0096950.  
R 18-AUG-1998; 98US-0096959.  
R 18-AUG-1998; 98US-0096960.  
R 18-AUG-1998; 98US-0097022.  
R 18-AUG-1998; 98US-0097141.  
R 20-AUG-1998; 98US-0097218.  
R 24-AUG-1998; 98US-0097661.  
R 24-AUG-1998; 98US-0097951.  
R 26-AUG-1998; 98US-0097952.  
R 26-AUG-1998; 98US-0097954.  
R 26-AUG-1998; 98US-0097955.  
R 26-AUG-1998; 98US-0097971.  
R 26-AUG-1998; 98US-0097974.  
R 26-AUG-1998; 98US-0097978.  
R 26-AUG-1998; 98US-0097979.  
R 26-AUG-1998; 98US-0097986.  
R 26-AUG-1998; 98US-0098014.  
R 31-AUG-1998; 98US-0098525.  
R 16-SEP-1998; 98US-0100634.  
R 12-JAN-1999; 99US-0115565.

(GETH ) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
Wood WI, Yuan J;

WPI; 2000-072883/06.  
P-PSDB; AAY66694.

Membrane-bound proteins and related nucleotide sequences -

Claim 2; Fig 156; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 21; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 GTTCTCTTTCCAGGCAAAATCCAGGGGATGGTGAATTAAGACGTGCCACACATGA 60  
b 1 GTTCTCTTTCCAGGCAAAATCCAGGGGATGGTGAATTAAGACGTGCCACACATGA 60  
Y 61 AGCTCTTTGGCGAGGTAATGTGCAACAACACCTGGAAATGCCATCTGCTCCCGTTGG 120  
b 61 AGCTCTTTGGCGAGGTAATGTGCAACAACACCTGGAAATGCCATCTGCTCCCGTTGG 120  
Y 121 TCTACCTTCAGGCGCAAGTGTGATTTCTGTGTGACGCCATCGTCTGCGGCTTCAGCGG 180  
b 121 TCTACCTTCAGGCGCAAGTGTGATTTCTGTGTGACGCCATCGTCTGCGGCTTCAGCGG 180  
Y 181 GGGCCCGAGAACTGCCCTCCGTTTGTCTGTGCAAGTAACAGTTCACGAAGTGTGTGCA 240  
b 181 GGGCCCGAGAACTGCCCTCCGTTTGTCTGTGCAAGTAACAGTTCACGAAGTGTGTGCA 240  
Y 241 CCGCCCGGGGCTCTCGAGGTCGCGAGGTAATTCCTTCGACACCCCGGTACTCAACC 300

Db 241 CGCGCGGGGCTCTCTCGAGGTCGCGAGGTAATTCCTCGAACACCCGGTACTCAACC 300  
QY 301 TCATGGAGAACACATCCAGATCATCCAGCGGACACCTTCCGCGACCTCCACCACTGG 360  
Db 301 TCATGGAGAACACATCCAGATCATCCAGCGGACACCTTCCGCGACCTCCACCACTGG 360  
QY 361 AGGTCTCTGAGGTTGGGACGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420  
Db 361 AGGTCTCTGAGGTTGGGACGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420  
QY 421 TGGCGAGCTCAACACCCCTGGAGCTGTTGCACTGGCTGGACAGTCACTCCCTAGCGGG 480  
Db 421 TGGCGAGCTCAACACCCCTGGAGCTGTTGCACTGGCTGGACAGTCACTCCCTAGCGGG 480  
QY 481 CTTTGAATACCTGTCCAAAGCTCGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540  
Db 481 CTTTGAATACCTGTCCAAAGCTCGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540  
QY 541 TCCCTCTTACGCTTCAACCGGGTGCCTCCTCATGCGCTGGACAGTTCGGGGAGCTCA 600  
Db 541 TCCCTCTTACGCTTCAACCGGGTGCCTCCTCATGCGCTGGACAGTTCGGGGAGCTCA 600  
QY 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGGGGGCTTTCAACCTCAAGTATCTGA 660  
Db 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGGGGGCTTTCAACCTCAAGTATCTGA 660  
QY 661 ACTTGGGCAATGTCCAAACATTAAGACATGCCCAATCTCACCCCCTGTGTGGGCTGGAGG 720  
Db 661 ACTTGGGCAATGTCCAAACATTAAGACATGCCCAATCTCACCCCCTGTGTGGGCTGGAGG 720  
QY 721 AGCTGGAGATGTGAGGGAACCACTTCCCTGAGATCAGGCTCGCTCTTCCATGGCTCA 780  
Db 721 AGCTGGAGATGTGAGGGAACCACTTCCCTGAGATCAGGCTCGCTCTTCCATGGCTCA 780  
QY 781 GCTCCCTCAAGAGCTCTGGTTCATGAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840  
Db 781 GCTCCCTCAAGAGCTCTGGTTCATGAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840  
QY 841 TTGACGGGCTGGCTTCACTTGTGGAATCACTTGGCCCAATACCTTCTCTTTTC 900  
Db 841 TTGACGGGCTGGCTTCACTTGTGGAATCACTTGGCCCAATACCTTCTCTTTTC 900  
QY 901 CCATGACCTCTTTTACCCGCTGAGTACCTTGTGTGAGTTCATCTACACCAACCTT 960  
Db 901 CCATGACCTCTTTTACCCGCTGAGTACCTTGTGTGAGTTCATCTACACCAACCTT 960  
QY 961 GGAATGTGATGTGACATCTCTGCTGAGCTGTGGCTTGGAGTATATACCAACA 1020  
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QY 1081 AGTGGACCAAGGCTCTCTTCCAGTGTCTGCGCCCTTTCATGTGAGCGACCTCGAGCC 1140  
Db 1081 AGTGGACCAAGGCTCTCTTCCAGTGTCTGCGCCCTTTCATGTGAGCGACCTCGAGCC 1140  
QY 1141 TCACATTTCTGAGGTTGGGACGAACTTAAGTGTGGAATCTCCCTCTATGTCTCTCG 1200  
Db 1141 TCACATTTCTGAGGTTGGGACGAACTTAAGTGTGGAATCTCCCTCTATGTCTCTCG 1200  
QY 1201 TGAAGTGTGTGCTGCCCAATGGGACAGTCTCAGCCACGCTCCGCGCACCAAGATCT 1260  
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QY 1261 CTGTCTCAAGCGAGGCACTTGAACTTTTCCCACTGCTGCTTTCAGACACTGGGGTGT 1320  
Db 1261 CTGTCTCAAGCGAGGCACTTGAACTTTTCCCACTGCTGCTTTCAGACACTGGGGTGT 1320  
QY 1321 ACACATGATGTGTGACCAATGTTGACAGGCAACTTCCAAACGCTCGGCTTCAATGTGA 1380  
Db 1321 ACACATGATGTGTGACCAATGTTGACAGGCAACTTCCAAACGCTCGGCTTCAATGTGA 1380



3Q Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
 Query Match 100.0%; Score 2185; DB 22; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GTTCTCCTTTCCGAGCCAAATCCAGCCGATGGTGAATATGAAAGTGGCCACACCTGA 60  
 1 GTTCTCCTTTCCGAGCCAAATCCAGCCGATGGTGAATATGAAAGTGGCCACACCTGA 60  
 61 AGCTCTTGTGCGAGTAAGTGTGACACACACACCTGGAAATGCACTCTCCCGTTCG 120  
 61 AGCTCTTGTGCGAGTAAGTGTGACACACACACCTGGAAATGCACTCTCCCGTTCG 120  
 121 TCTACCTCAAGCGCAAGTGTGATTTGTGTGAGCAATCGTGTGCGGCTCAGCGG 180  
 121 TCTACCTCAAGCGCAAGTGTGATTTGTGTGAGCAATCGTGTGCGGCTCAGCGG 180  
 181 GGCCCCAGAACTGCCCTCCGTTGCTGTCGAGTAACAGATTTCAGCAAGTGGTGTGA 240  
 181 GGCCCCAGAACTGCCCTCCGTTGCTGTCGAGTAACAGATTTCAGCAAGTGGTGTGA 240  
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 421 TGGCGAGCTTCACACCTCGAGCTGTTCGACAACTGCTGACAGTCACTCCCTAGGGG 480  
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 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTTCAGGGGCTTTCAACCTCAAGTATCTGA 660  
 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTTCAGGGGCTTTCAACCTCAAGTATCTGA 660  
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 661 ACTTGGGCATGTGCAACATTAAGACATGCCAAATCTCAACCCCTTGGTGGGCTGGAGG 720  
 721 AGCTGGAGATGTGAGGAACTCTCCCTGAGTACAGGCTGGCTTCCTCCATGCCCTGA 780  
 721 AGCTGGAGATGTGAGGAACTCTCCCTGAGTACAGGCTGGCTTCCTCCATGCCCTGA 780  
 781 GCTCCCTCAAGAAAGCTCTGGGTCAATGAATCAAGCTCAGCTGATTTGAGCGGAAATGCTT 840  
 781 GCTCCCTCAAGAAAGCTCTGGGTCAATGAATCAAGCTCAGCTGATTTGAGCGGAAATGCTT 840  
 841 TTGACGGGCTGGCTTCCCTGAGTACAGGCTGGCTTCCTCCATGCCCTTCCTTTTCG 900  
 841 TTGACGGGCTGGCTTCCCTGAGTACAGGCTGGCTTCCTCCATGCCCTTCCTTTTCG 900  
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 901 CCCATGACCTCTTTTACCCGCTGAGTACCTGGTGGGTTGATCTACACCAACACCTT 960  
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 961 GGAAGCTGTGATGTGACATTTCTGTGCTAGCTGGTGTTCGAGATATATATACCAACA 1020

QY 1021 ATTCACTGCTGTGGCGCTGTGATGCTCCCATGCAATGCCAGGCGCTACTCTGTGG 1080  
 DB 1021 ATTCACTGCTGTGGCGCTGTGATGCTCCCATGCAATGCCAGGCGCTACTCTGTGG 1080  
 QY 1081 AGGTGGACCAAGGCTCTCCATGCTGTGCTCCCTTTCATGGAAGCGACCTCGAGAC 1140  
 DB 1081 AGGTGGACCAAGGCTCTCCATGCTGTGCTCCCTTTCATGGAAGCGACCTCGAGAC 1140  
 QY 1141 TCAACATTTCTGAGGTCGGATGCGAGAACTTAAGTGTGCGACTCCCTCTATGCTCCG 1200  
 DB 1141 TCAACATTTCTGAGGTCGGATGCGAGAACTTAAGTGTGCGACTCCCTCTATGCTCCG 1200  
 QY 1201 TGAAGTGGTTCGCTGCCCAATGGGACAGTGTGAGCAAGCTTCGCGCACCCAGGATCT 1260  
 DB 1201 TGAAGTGGTTCGCTGCCCAATGGGACAGTGTGAGCAAGCTTCGCGCACCCAGGATCT 1260  
 QY 1261 CTGTCTCTCAACGACGCGACCTTGAACCTTTCCACGCTGTCTTTCAGACACTGGGGTGT 1320  
 DB 1261 CTGTCTCTCAACGACGCGACCTTGAACCTTTCCACGCTGTCTTTCAGACACTGGGGTGT 1320  
 QY 1321 ACATATGATGCTGACCAATGTTGAGGCAACTCCAGGCTCGGCTTACCTCAATGTGA 1380  
 DB 1321 ACATATGATGCTGACCAATGTTGAGGCAACTCCAGGCTCGGCTTACCTCAATGTGA 1380  
 QY 1381 GCAGGCTGAGCTTAACACCTTCCAACTACAGCTTCTTCCACAGTAACAGTGGAGACCA 1440  
 DB 1381 GCAGGCTGAGCTTAACACCTTCCAACTACAGCTTCTTCCACAGTAACAGTGGAGACCA 1440  
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 DB 1441 CGGAGATCTCGCTGAGGACCAACCGGAAAGTAAAGCTGTCTTACCACTGCTTCCACTG 1500  
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 DB 1561 AGCAGGTGGAGTACCGCGGACAGACCACTGCAAGATGCAAGACCGCTGAGTGAAG 1620  
 QY 1621 TCATGAAGACCAAGATGATCATTTGGCTGTCTTGGCAGTGTCTTGGCTGTCTTGGCTGT 1680  
 DB 1621 TCATGAAGACCAAGATGATCATTTGGCTGTCTTGGCAGTGTCTTGGCTGTCTTGGCTGT 1680  
 QY 1681 CCATGTTGATGTTCTTCTATAAACTTCTGTAAGCGGACCAAGACCGGAGTACAGTCA 1740  
 DB 1681 CCATGTTGATGTTCTTCTATAAACTTCTGTAAGCGGACCAAGACCGGAGTACAGTCA 1740  
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 DB 1741 CCGCCCGGACTGTGTGAGTAAATCCAGGTGGAAGCAATCCAGCAAGCAATCCGAG 1800  
 QY 1801 CAGCAACAGCAGCTTCCGCTCGGCTGATCAGGTGAGGCGGAGTGTGCTGCCCAATTC 1860  
 DB 1801 CAGCAACAGCAGCTTCCGCTCGGCTGATCAGGTGAGGCGGAGTGTGCTGCCCAATTC 1860  
 QY 1861 ATGACCAATTAATCAACACCTCAAAACAGCAATGGGCGGCTGAGCAGAAACA 1920  
 DB 1861 ATGACCAATTAATCAACACCTCAAAACAGCAATGGGCGGCTGAGCAGAAACA 1920  
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 DB 1921 GCCTGGGAGTCTCTGCGACCCCAAGTCACTATCTCTGAACTTATATATTCAGA 1980  
 QY 1981 CCATACCAAGGACAAAGTACAGGAACTCAAAATATGACTCCCTCCCTCCCAAACTTA 2040  
 DB 1981 CCATACCAAGGACAAAGTACAGGAACTCAAAATATGACTCCCTCCCTCCCAAACTTA 2040  
 QY 2041 TAAATGCAATAGAAATGCAACAAAGACAGCACTTTTGTACAGAGTGGGAGACTTT 2100  
 DB 2041 TAAATGCAATAGAAATGCAACAAAGACAGCACTTTTGTACAGAGTGGGAGACTTT 2100

QY 2101 TTCTTGATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAACAAGATTATATTA 2160  
 Db 2101 TTCTTGATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAACAAGATTATATTA 2160  
 QY 2161 AATTAAACACAAAAGTCAAAACA 2185  
 Db 2161 AATTAAACACAAAAGTCAAAACA 2185

RESULT 4  
 ID AAF44179  
 XX AAF44179 standard; cDNA; 2185 BP.  
 AC AAF44179;  
 XX

DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1111 (UNQ554) nucleotide sequence SEQ ID NO:228.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytostatic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 CS Homo sapiens.  
 XX

PN WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX

PF 30-MAR-2000; 2000WO-US08439.  
 XX

PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0148222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0153663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US06219.  
 PR 06-JAN-2000; 2000WO-US0376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.

XX (GETH ) GENENTECH INC.

XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI: 2001-032160/04.  
 DR P-PSDB; AAB65217.

XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -

PS Claim 2; Fig 156; 935pp; English.

XX

CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX  
 SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 22; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCTCTCTTCCGAGCCAAATCCCGAGCGGATGGTGAATATGACGTCGCACACCATGA 60  
 Db 1 GTCTCTCTTCCGAGCCAAATCCCGAGCGGATGGTGAATATGACGTCGCACACCATGA 60  
 QY 61 AGCTCTTGTGGCAGGTAACTGTGCACACACACACCTGGAATGCCATCTCTCCCGTTGG 120  
 Db 61 AGCTCTTGTGGCAGGTAACTGTGCACACACACACCTGGAATGCCATCTCTCCCGTTGG 120  
 QY 121 TCTACTCTACGGCGCAAGTGTGGATTCCTGTGTGAGCCATCGCTGTCGCCCTCAGCGG 180  
 Db 121 TCTACTCTACGGCGCAAGTGTGGATTCCTGTGTGAGCCATCGCTGTCGCCCTCAGCGG 180  
 QY 181 GGCCCCAGAACTGCCCTCCGTTCTGTGAGTAACTGACGTTGAGCAAGTGTGTGCA 240  
 Db 181 GGCCCCAGAACTGCCCTCCGTTCTGTGAGTAACTGACGTTGAGCAAGTGTGTGCA 240  
 QY 241 CGCGCGGGGGCTCTCCGAGTCCCGAGGGTATTCCTCGAACAACCCGGTACCTCAACC 300  
 Db 241 CGCGCGGGGGCTCTCCGAGTCCCGAGGGTATTCCTCGAACAACCCGGTACCTCAACC 300  
 QY 301 TCATGAGAACAACTCCAGATGATCCAGGCGGACACCTCCGCGACCTCCACACCTGG 360  
 Db 301 TCATGAGAACAACTCCAGATGATCCAGGCGGACACCTCCGCGACCTCCACACCTGG 360  
 QY 361 AGTCTCTGCAAGTGTGGCAGGAACTCCATCCGCGCAGATTGAGTGGGGGCTTCAACGGCC 420  
 Db 361 AGTCTCTGCAAGTGTGGCAGGAACTCCATCCGCGCAGATTGAGTGGGGGCTTCAACGGCC 420  
 QY 421 TGGCCAGCTCAACACCTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG 480  
 Db 421 TGGCCAGCTCAACACCTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG 480  
 QY 481 CCTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACAAACCCCAATCAAGCA 540  
 Db 481 CCTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACAAACCCCAATCAAGCA 540  
 QY 541 TCCCTCTTACGCTTCAACCGGGTCCCTCTCTCATCGGCTGGAATTGGGGAGCTCA 600  
 Db 541 TCCCTCTTACGCTTCAACCGGGTCCCTCTCTCATCGGCTGGAATTGGGGAGCTCA 600  
 QY 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTGGAGGGCTGTTCAACTCAAGTATCTGA 660  
 Db 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTGGAGGGCTGTTCAACTCAAGTATCTGA 660  
 QY 661 ACTTGGGATGTGAAACATTAAGACATGCGCAATCTCACCCCTGGTGGGCTGGAGG 720  
 Db 661 ACTTGGGATGTGAAACATTAAGACATGCGCAATCTCACCCCTGGTGGGCTGGAGG 720  
 QY 721 AGCTGGAGATGTGAGGAACCACTTCCCTGAGATCAGGCTGGGCTCTTCCATGGCCTGA 780  
 Db 721 AGCTGGAGATGTGAGGAACCACTTCCCTGAGATCAGGCTGGGCTCTTCCATGGCCTGA 780



781 GCTCCCTCAGAGCTCTGGGTCTAGACTCAGAGTCAAGCTGATGAGCGGATGCTT 840  
781 GCTCCCTCAGAGCTCTGGGTCTAGACTCAGAGTCAAGCTGATGAGCGGATGCTT 840  
841 TTGACGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAATAAATCTCTCTTTTC 900  
841 TTGACGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAATAAATCTCTCTTTTC 900  
901 CCATGACCTCTTTACCCCGCTGAGTACCTGGTGGAGTTGATCTACACCAACCCCTT 960  
901 CCATGACCTCTTTACCCCGCTGAGTACCTGGTGGAGTTGATCTACACCAACCCCTT 960  
961 GGAACCTGTGATGTGACATCTCTGTGCTAGCTAGCTGGTGGCTTCGAGAGTATATACCACCA 1020  
961 GGAACCTGTGATGTGACATCTCTGTGCTAGCTAGCTGGTGGCTTCGAGAGTATATACCACCA 1020  
1021 ATTCCACCTGTGTGGCCGCTGTCAATGCTCCCATGACATGCGAGGCGCTACTCTGFGG 1080  
1021 ATTCCACCTGTGTGGCCGCTGTCAATGCTCCCATGACATGCGAGGCGCTACTCTGFGG 1080  
1081 AGGTGACACGAGGCTCTTCCAGTGTCTGCGCCCTTCAATCATGAGACGCACTCGAGACC 1140  
1081 AGGTGACACGAGGCTCTTCCAGTGTCTGCGCCCTTCAATCATGAGACGCACTCGAGACC 1140  
1141 TCAACATTTCTGAGGCTCGAGTGGCAGAACTTAAGTGTGCGACTCCCTCTATGCTCTCG 1200  
1141 TCAACATTTCTGAGGCTCGAGTGGCAGAACTTAAGTGTGCGACTCCCTCTATGCTCTCG 1200  
1201 TGAAGTGTGTGCGCCCATGGAAGCTGCTCAGCGAGCCCTCCCGCCACCCAGGATCT 1260  
1201 TGAAGTGTGTGCGCCCATGGAAGCTGCTCAGCGAGCCCTCCCGCCACCCAGGATCT 1260  
1261 CTGTCTCTCAACGAGGCACTTGAATTTTCCAGTGTCTGCTTTTTCAGACACTGGGGTGT 1320  
1261 CTGTCTCTCAACGAGGCACTTGAATTTTCCAGTGTCTGCTTTTTCAGACACTGGGGTGT 1320  
1321 ACATGCTGTGTGACCAATTTGCGGCACTTCCAACTGCGGCTGAGCTCAATGTGA 1380  
1321 ACATGCTGTGTGACCAATTTGCGGCACTTCCAACTGCGGCTGAGCTCAATGTGA 1380  
1381 GCACGCTGAGCTTAACCTTCCAACTGAGCTTCTTACACAGTAACTAGTGAGACCA 1440  
1381 GCACGCTGAGCTTAACCTTCCAACTGAGCTTCTTACACAGTAACTAGTGAGACCA 1440  
1441 CGGAGATCTCGCTGAGGACCAACGCGGAAGTACAGCTTCTTACCACTGCTCACTG 1500  
1441 CGGAGATCTCGCTGAGGACCAACGCGGAAGTACAGCTTCTTACCACTGCTCACTG 1500  
1501 GTTACAGCGCGCATATACCTCTTACACGCTGCTTATTCAGACTACCGTGTGCCA 1560  
1501 GTTACAGCGCGCATATACCTCTTACACGCTGCTTATTCAGACTACCGTGTGCCA 1560  
1561 AGCAGTGGCAGTACCCGCGACAGACCACTGACAGATGACAGACCCAGCTGGATGAAG 1620  
1561 AGCAGTGGCAGTACCCGCGACAGACCACTGACAGATGACAGACCCAGCTGGATGAAG 1620  
1621 TATGAAGACCAAGATCATCTATGCTGCTTTTGTGGCAGTGACTCTGCTAGCTGCGG 1680  
1621 TATGAAGACCAAGATCATCTATGCTGCTTTTGTGGCAGTGACTCTGCTAGCTGCGG 1680  
1681 CCAATGTTGATGCTTCTATATAAATTCGTAAGCGGCACAGCAGCGGAGTACAGTCAAG 1740  
1681 CCAATGTTGATGCTTCTATATAAATTCGTAAGCGGCACAGCAGCGGAGTACAGTCAAG 1740  
1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGAGAGACATCCACAGCAATCCCGGAG 1800  
1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGAGAGACATCCACAGCAATCCCGGAG 1800  
1801 CAGCACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGCACTAGTGTGCCCAATTC 1860  
1801 CAGCACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGCACTAGTGTGCCCAATTC 1860  
1861 ATGACCATTAATTAACAACACTTACAAACCGACATCGGGGCCCACTGGACAGAAAACA 1920

1861 ATGACCATTAATTAACAACACTTACAAACCGACATCGGGGCCCACTGGACAGAAAACA 1920  
1921 GCCTGGGGAATCTCTGCAACCCACAGTCAACCACTATCTCTGAACTTATATAATTCAGA 1980  
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1981 CCATACCAAGGACAGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAACTTA 2040  
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2161 AATTTAAAGCAAAAAGTCAAAAACA 2185  
2161 AATTTAAAGCAAAAAGTCAAAAACA 2185

RESULT 5  
ACA03821

ID ACA03821 standard; cDNA; 2185 BP.

XX ACA03821;

XX AC

XX DT 23-MAY-2003 (first entry)

XX DE cDNA encoding human PRO polypeptide #219.

XX KW Human, PRO polypeptide; secreted and transmembrane protein;

XX KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

XX KW differentiation; chondrocyte; tumour; genetic disorder;

XX KW cytoskeletal; gene; ss.

XX OS Homo sapiens.

XX PN US2003036180-A1.

XX PD 20-FEB-2003.

XX PP 09-MAY-2002; 2002US-0143114.

XX PP 31-MAR-1997; 97WO-US05230.

XX PP 12-JUN-1998; 98WO-US12456.

XX PP 14-JUL-1998; 98WO-US14552.

XX PP 28-AUG-1998; 98WO-US17888.

XX PP 10-SEP-1998; 98WO-US18824.

XX PP 14-SEP-1998; 98WO-US19093.

XX PP 14-SEP-1998; 98WO-US19177.

XX PP 16-SEP-1998; 98WO-US19330.

XX PP 17-SEP-1998; 98WO-US19437.

XX PP 07-OCT-1998; 98WO-US21141.

XX PP 29-OCT-1998; 98WO-US22392.

XX PP 20-NOV-1998; 98WO-US24855.

XX PP 01-DEC-1998; 98WO-US25108.

XX PP 05-JAN-1999; 99WO-US00106.

XX PP 08-MAR-1999; 99WO-US05028.

XX PP 10-MAR-1999; 99WO-US05190.

XX PP 20-APR-1999; 99WO-US08615.

XX PP 14-MAY-1999; 99WO-US10733.

XX PP 02-JUN-1999; 99WO-US12252.

XX PP 01-SEP-1999; 99WO-US20111.

XX PP 08-SEP-1999; 99WO-US20594.

XX PP 13-SEP-1999; 99WO-US20944.

XX PP 15-SEP-1999; 99WO-US21090.

XX PP 15-SEP-1999; 99WO-US21547.



PR 05-OCT-1999; 99WO-US23089.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 22-DEC-1999; 99WO-US30720.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 05-JAN-2000; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 10-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US09439.  
 PR 17-MAY-2000; 2000WO-US11705.  
 PR 22-MAY-2000; 2000WO-US114042.  
 PR 30-MAY-2000; 2000WO-US114941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30673.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US15692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
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 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

XX (GETH ) GENENTECH INC.  
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood MI, Zhang Z;  
 XX WPI; 2003-332040/31.  
 DR P-PSDB; ABU66788.  
 XX New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping as chromosome markers, in  
 PT tissue typing, and in chromosome identification  
 XX Claim 2; Fig 437; 660pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdsIDentry.html.  
 XX

SQ Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 25; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTCTCTTTTCGAGCCAAATCCAGGCGATGGTGAATTATGAACGTGCCACACCATGA 60  
 DB 1 GTTCTCTTTTCGAGCCAAATCCAGGCGATGGTGAATTATGAACGTGCCACACCATGA 60  
 QY 61 AGCTCTTGTGGCAGGTAATGTGCACACACACCTGGAAATGCCATCTGCTCCGGTTCG 120  
 DB 61 AGCTCTTGTGGCAGGTAATGTGCACACACACCTGGAAATGCCATCTGCTCCGGTTCG 120  
 QY 121 TCTACTCTACGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGCGCCCTCAGCG 180  
 DB 121 TCTACTCTACGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGCGCCCTCAGCG 180  
 QY 181 GGGCCCGAGAACTGCCCTTCGGTTTGTCTGTCAGTAACCACTTCCAGAGTGGTGTGCA 240  
 DB 181 GGGCCCGAGAACTGCCCTTCGGTTTGTCTGTCAGTAACCACTTCCAGAGTGGTGTGCA 240  
 QY 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGCTATTCCCTCGAACACCGGTACCTCAACC 300  
 DB 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGCTATTCCCTCGAACACCGGTACCTCAACC 300  
 QY 301 TCATGGAGAAACAATCCAGATGATCCAGGCCGACACTTCCCGCCACTCCACCACTGG 360  
 DB 301 TCATGGAGAAACAATCCAGATGATCCAGGCCGACACTTCCCGCCACTCCACCACTGG 360  
 QY 361 AGGTCTCTCAGTTGGGCGAGGAACCTCCATCCGGCAGATTGAGTGGGGGCTTCAACGGCC 420  
 DB 361 AGGTCTCTCAGTTGGGCGAGGAACCTCCATCCGGCAGATTGAGTGGGGGCTTCAACGGCC 420  
 QY 421 TGGCCAGGCTCAACACCTCGAGCTGTTCGACACTGCTGACAGTCACTCCTAGCGGGG 480

421 TGGCCAGCCTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGTCATCCCTAGCGGG 480  
481 CTTTGAATACCTCTCAAGCTGGGAGCTCTGGCTTCGACAAACCCCATCGAAGCA 540  
481 CTTTGAATACCTCTCAAGCTGGGAGCTCTGGCTTCGACAAACCCCATCGAAGCA 540  
541 TCCCTCTTAGCCCTTCAACCGGGTGCCTCCCTCATFGGCTTGGAATTGGGGGAGCTCA 600  
541 TCCCTCTTAGCCCTTCAACCGGGTGCCTCCCTCATFGGCTTGGAATTGGGGGAGCTCA 600  
601 AGAAGCTGAGTATATCTCTGAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660  
601 AGAAGCTGAGTATATCTCTGAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660  
661 ACTTGGGCTATGCAACATTAAGAGCATGCCAATCTACCCCTCTGGTGGGCTGGAG 720  
661 ACTTGGGCTATGCAACATTAAGAGCATGCCAATCTACCCCTCTGGTGGGCTGGAG 720  
721 AGCTGGAGATGTCAGGGAAACCTCTCCCTCAGATCAGGCTGCTCTCTCCATGGCCTGA 780  
721 AGCTGGAGATGTCAGGGAAACCTCTCCCTCAGATCAGGCTGCTCTCTCCATGGCCTGA 780  
781 GCTCCCTCAAGAGCTCTGGGTATGAATCTACAGGTGAGCTGATTTGAGCGGAATGCTT 840  
781 GCTCCCTCAAGAGCTCTGGGTATGAATCTACAGGTGAGCTGATTTGAGCGGAATGCTT 840  
841 TTGACGGGCTGGCTTCACTTGTGGAACTGAACTTGGGCCACATTAACCTCTCTCTTTC 900  
841 TTGACGGGCTGGCTTCACTTGTGGAACTGAACTTGGGCCACATTAACCTCTCTCTTTC 900  
901 CCATGACCTCTTACCCCTCTGAGTACCTGCTGGAGTTGATCTTACACCAACACCTTT 960  
901 CCATGACCTCTTACCCCTCTGAGTACCTGCTGGAGTTGATCTTACACCAACACCTTT 960  
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961 GGAATGTGATTTGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
1021 ATTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
1021 ATTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
1081 AGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
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1321 ACATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
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1381 GCACGGCTGAGCTTAAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 1440  
1441 CGGAGATCTCGCTGAGGACACACCGGAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
1441 CGGAGATCTCGCTGAGGACACACCGGAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
1501 GTTACACGCGGCTATACCACTCTACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
1501 GTTACACGCGGCTATACCACTCTACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

QY 1561 AGCAGTGGCAGTACCCGCGACAGACACCACTGCAAGATGACAGCAGCCTTGATGAAG 1620  
Db 1561 AGCAGTGGCAGTACCCGCGACAGACACCACTGCAAGATGACAGCAGCCTTGATGAAG 1620  
QY 1621 TCATGAAGACCAACAGATCATCATTTGGCTGCTTTGTGGCAGTGAATCTGCTAGCTGCG 1680  
Db 1621 TCATGAAGACCAACAGATCATCATTTGGCTGCTTTGTGGCAGTGAATCTGCTAGCTGCG 1680  
QY 1681 CCATGTTGATTTGCTTCTATAAATCTTCTAAGCGGACACAGCAGCGGAGTACAGTCAACAG 1740  
Db 1681 CCATGTTGATTTGCTTCTATAAATCTTCTAAGCGGACACAGCAGCGGAGTACAGTCAACAG 1740  
QY 1741 CCGCCCGGAGTGTGAGTAAATCCAGGTGACGAGACATCCAGAGCAACATCCCGCAG 1800  
Db 1741 CCGCCCGGAGTGTGAGTAAATCCAGGTGACGAGACATCCAGAGCAACATCCCGCAG 1800  
QY 1801 CAGCAACAGCAGCTCCGTCGCGGTATCAGGTGAGGGGCGAGTAGTGTGCTGCCACAATTC 1860  
Db 1801 CAGCAACAGCAGCTCCGTCGCGGTATCAGGTGAGGGGCGAGTAGTGTGCTGCCACAATTC 1860  
QY 1861 ATGACCATATTAATCAACACCTTACAAACACAGCAGCATGGGGCCCATCTGGACAGAAACA 1920  
Db 1861 ATGACCATATTAATCAACACCTTACAAACACAGCAGCATGGGGCCCATCTGGACAGAAACA 1920  
QY 1921 GCCTGGGGAACTCTTGCACCCGACAGTGCACCTATCTCTGAACCTTATATTAATTCAGA 1980  
Db 1921 GCCTGGGGAACTCTTGCACCCGACAGTGCACCTATCTCTGAACCTTATATTAATTCAGA 1980  
QY 1981 CCCATACCAAGGCAAGGTACAGGAACTCAATATGACTCCCTCCCTCCCTCCCTCCCTCCCT 2040  
Db 1981 CCCATACCAAGGCAAGGTACAGGAACTCAATATGACTCCCTCCCTCCCTCCCTCCCTCCCT 2040  
QY 2041 TAAATGCAATGAGTACACACAAAGCAGCAACTTTGTACAGAGTGGGAGAGACTTT 2100  
Db 2041 TAAATGCAATGAGTACACACAAAGCAGCAACTTTGTACAGAGTGGGAGAGACTTT 2100  
QY 2101 TTCTGTATATGCTTATATTAATTAAGTCTATGGCTGTTTAAATAAAGACAGATTATATA 2160  
Db 2101 TTCTGTATATGCTTATATTAATTAAGTCTATGGCTGTTTAAATAAAGACAGATTATATA 2160  
QY 2161 AATTAAAGCAAAAAGTCAAAACA 2185  
Db 2161 AATTAAAGCAAAAAGTCAAAACA 2185

## RESULT 6

ACH04242  
ID ACA04242 standard; cDNA; 2185 BP.

XX ACA04242;

XX AC

XX 27-MAY-2003 (first entry)

XX Human cDNA encoding a secreted/transmembrane protein, SEQ ID 437.

XX Human; ss; gene; secreted protein; transmembrane protein; PRO;

XX inflammatory disease; organ failure; atherosclerosis; cardiac injury;

XX infertility; birth defects; premature aging; AIDS; biosensor;

XX acquired immunodeficiency syndrome; cancer; diabetic complication;

XX biosensor; tumour.

XX Homo sapiens.

XX OS

XX US2003032155-A1.

XX 13-FEB-2003.

XX 03-MAY-2002; 2002US-0137865.

XX 31-MAR-1997; 97WO-US05230.

XX 12-JUN-1998; 98WO-US12456.

XX 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 16-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21144.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 29-OCT-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 98WO-US00106.  
 PR 08-MAR-1999; 98WO-US05028.  
 PR 10-MAR-1999; 98WO-US05190.  
 PR 20-APR-1999; 98WO-US06615.  
 PR 14-MAY-1999; 98WO-US10733.  
 PR 02-JUN-1999; 98WO-US12252.  
 PR 01-SEP-1999; 98WO-US20111.  
 PR 08-SEP-1999; 98WO-US20594.  
 PR 13-SEP-1999; 98WO-US20944.  
 PR 15-SEP-1999; 98WO-US21090.  
 PR 15-SEP-1999; 98WO-US21547.  
 PR 05-OCT-1999; 98WO-US23089.  
 PR 29-NOV-1999; 98WO-US28214.  
 PR 30-NOV-1999; 98WO-US28313.  
 PR 30-NOV-1999; 98WO-US28409.  
 PR 01-DEC-1999; 98WO-US28301.  
 PR 01-DEC-1999; 98WO-US28634.  
 PR 02-DEC-1999; 98WO-US28551.  
 PR 02-DEC-1999; 98WO-US28564.  
 PR 02-DEC-1999; 98WO-US28565.  
 PR 16-DEC-1999; 98WO-US30095.  
 PR 20-DEC-1999; 98WO-US30911.  
 PR 20-DEC-1999; 98WO-US30999.  
 PR 22-DEC-1999; 98WO-US30720.  
 PR 30-DEC-1999; 98WO-US31243.  
 PR 30-DEC-1999; 98WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US01565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05745.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US11705.  
 PR 22-MAY-2000; 2000WO-US11402.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
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 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US18692.  
 PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796496.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.  
 P-PSDB; AB067064.

New secreted and transmembrane nucleic acids and polypeptides,  
 designated as PRO, useful for treating inflammation, organ failure,  
 atherosclerosis, cardiac injury, infertility, birth defects, premature  
 aging, AIDS, or cancer

Claim 2; Fig 437; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is  
 at least 80% identical to, or the full-length coding sequence of, any of  
 the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 (one of 275 secreted or transmembrane proteins). The nucleic acid  
 further comprises the full-length coding sequence of the DNA deposited  
 under American Type Culture Collection (ATCC) accession number in a list  
 given in the specification. Also included are vectors and host  
 cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 antibodies, PRO extracellular domains and mature sequences, methods  
 of detecting PRO proteins, methods for stimulating the release of  
 TNF-alpha (tumour necrosis factor alpha) from human blood,  
 and the proliferation of differentiation of chondrocyte cells, the  
 proliferation of, or gene expression in pericyte cells, the release or  
 proteoglycans from cartilage, proliferation of inner ear utricular  
 supporting cells, the proliferation of T-lymphocyte cells, the release  
 of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 proliferation of endothelial cells, a method for modulating the uptake  
 of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 a method for inhibiting the binding of A-peptide to factor VIIA,  
 or the differentiation of adipocyte cells, a method for detecting the  
 presence of a tumour in a mammal and an oligonucleotide probe derived  
 from any of the nucleotide sequences cited above. The nucleic acids and  
 polypeptides are useful for treating inflammatory diseases, organ  
 failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 diabetic complications. The nucleic acids are useful as hybridisation  
 probes, in chromosome and gene mapping, and in generating antisense RNA  
 or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 biosensors or bioreactors. Both are useful in tissue typing.  
 The present sequence encodes a PRO protein of the invention.

Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

SQ

Query Match		100.0%	Score 2185;	DB 25;	Length 2185;		
Best Local Similarity		100.0%	Pred. No. 0;				
Matches 2185; Conservative		0;	Mismatches	0;	Indels	0;	Gaps
Y	1	GTCTCTCTTCCGAGCCAAATCCGAGGCGATGCTGAATATGCAAGTCGACACACATGA	60				
b	1	GTCTCTCTTCCGAGCCAAATCCGAGGCGATGCTGAATATGCAAGTCGACACACATGA	60				
Y	61	AGCTCTTGTGCGCAGGTAATGTGACACACACACACACACCTTGGAAATGCCATCTCTGCTCCGCTTCG	120				
b	61	AGCTCTTGTGCGCAGGTAATGTGACACACACACACACACCTTGGAAATGCCATCTCTGCTCCGCTTCG	120				
Y	121	TCTACCTCAGCGGCGAAGTGTGATTCGTGTGTCAGCCATTCCTGCTGCGCTCAGCGG	180				
b	121	TCTACCTCAGCGGCGAAGTGTGATTCGTGTGTCAGCCATTCCTGCTGCGCTCAGCGG	180				
Y	181	GGCCCCAGAACTGCCCTCGCTTGTGCTGTGAGTAACAGATTCCAGAGGTGGTGTGCA	240				
b	181	GGCCCCAGAACTGCCCTCGCTTGTGCTGTGAGTAACAGATTCCAGAGGTGGTGTGCA	240				
Y	241	CGCGCGGCGCTCTCCGAGGTCGCGAGGTAATTCCTTCGAACACCCGCTTACCTCAACC	300				
b	241	CGCGCGGCGCTCTCCGAGGTCGCGAGGTAATTCCTTCGAACACCCGCTTACCTCAACC	300				
Y	301	TCAATGAGAACAAATCCAGATGATCCAGGCGACACCTTCGCGACCTCCACACCTGG	360				
b	301	TCAATGAGAACAAATCCAGATGATCCAGGCGACACCTTCGCGACCTCCACACCTGG	360				
Y	361	AGTTCCTGCAAGTTGGGAGGAATCCATCCGCGAGATTCAGGTGGGGGCTTCAACGGCC	420				
b	361	AGTTCCTGCAAGTTGGGAGGAATCCATCCGCGAGATTCAGGTGGGGGCTTCAACGGCC	420				
Y	421	TGCGCAGCTCAGACCTCGAGCTGTTCGACAACTGCTGACAGTCACTCCCTAGCGGG	480				
b	421	TGCGCAGCTCAGACCTCGAGCTGTTCGACAACTGCTGACAGTCACTCCCTAGCGGG	480				
Y	481	CTTTTGAATACCTGTCCAGCTCGGAGCTCTGCTTCGCAACACCCCAATCGAAGCA	540				
b	481	CTTTTGAATACCTGTCCAGCTCGGAGCTCTGCTTCGCAACACCCCAATCGAAGCA	540				
Y	541	TGCGCTTACGCTTCAACCGGCGCTCTCTCTGATCAGGCTGAGTTCGAGGAGCTCA	600				
b	541	TGCGCTTACGCTTCAACCGGCGCTCTCTCTGATCAGGCTGAGTTCGAGGAGCTCA	600				
Y	601	AGAAGCTGAGTATATCTGAGGAGCTTTTTCAGGGGCTTTCAACCTCAAGTATCTGA	660				
b	601	AGAAGCTGAGTATATCTGAGGAGCTTTTTCAGGGGCTTTCAACCTCAAGTATCTGA	660				
Y	661	ACTTGGGCATGTCACATTAAGACATGCCCCAATCTCAACCCCTGCTGGGCTGGAGG	720				
b	661	ACTTGGGCATGTCACATTAAGACATGCCCCAATCTCAACCCCTGCTGGGCTGGAGG	720				
Y	721	AGCTGGAGATGTCAGGAACTCTCCCTGAGATCAGGCTGCTCTTCCATGGCCTGA	780				
b	721	AGCTGGAGATGTCAGGAACTCTCCCTGAGATCAGGCTGCTCTTCCATGGCCTGA	780				
Y	781	GCTCCCTCAAGAACTCTGCTGATCAATCAAGGTCAAGCTGATGAGCGGAATGCTT	840				
b	781	GCTCCCTCAAGAACTCTGCTGATCAATCAAGGTCAAGCTGATGAGCGGAATGCTT	840				
Y	841	TTGACGGGCTGGCTTCACTTGTGAGTCACTTGGCGGACATTAACCTCTCTTTTCG	900				
b	841	TTGACGGGCTGGCTTCACTTGTGAGTCACTTGGCGGACATTAACCTCTCTTTTCG	900				
Y	901	CCCATGACCTCTTACCCCGCTGAGTACCTGCTGGAGTTGATCTACACCAACCCCTT	960				
b	901	CCCATGACCTCTTACCCCGCTGAGTACCTGCTGGAGTTGATCTACACCAACCCCTT	960				
Y	961	GGAAGCTGATGTCATCTGTGGTGTGCTGTGGCTGTGAGTATATACCCACA	1020				
b	961	GGAAGCTGATGTCATCTGTGGTGTGCTGTGGCTGTGAGTATATACCCACA	1020				
Y	1021	ATTCCACCTGCTGTGGCGCTGTCTATGCTCTCCCATGCAATGCGAGGCGCTACCTCGTGG	1080				

Db	1021	ATTCCACCTGCTGTGGCGCTGTCTATGCTCTCCCATGCAATGCGAGGCGCTACCTCGTGG	1080
Qy	1081	AGTGGACACAGGCTCTCTTCCAGTGTCTGCCCCCTTCATCATGTGACGACACCTCGAGACC	1140
Db	1081	AGTGGACACAGGCTCTCTTCCAGTGTCTGCCCCCTTCATCATGTGACGACACCTCGAGACC	1140
Qy	1141	TCAACATTTCTGAGGTCGAGTGGAGAACTTAAAGTGTGGAATCCCTTATGTCTCTCG	1200
Db	1141	TCAACATTTCTGAGGTCGAGTGGAGAACTTAAAGTGTGGAATCCCTTATGTCTCTCG	1200
Qy	1201	TGAAGTGTGCTGCTGCCCAATGGGACAGTGTCTAGCCACGCTCCGCCACCCCAAGATCT	1260
Db	1201	TGAAGTGTGCTGCTGCCCAATGGGACAGTGTCTAGCCACGCTCCGCCACCCCAAGATCT	1260
Qy	1261	CTGTCTCTCAAAGCGGACCTTTGAACTTTTCCACGCTGCTTTTTCAGACACTGGGGTGT	1320
Db	1261	CTGTCTCTCAAAGCGGACCTTTGAACTTTTCCACGCTGCTTTTTCAGACACTGGGGTGT	1320
Qy	1321	ACACATGCTGCTGAGCAATGTTGCAAGGCAACTTCCAAACGCTCGGCTACCTCAATGTGA	1380
Db	1321	ACACATGCTGCTGAGCAATGTTGCAAGGCAACTTCCAAACGCTCGGCTACCTCAATGTGA	1380
Qy	1381	GCACGCTGAGCTTAAACACCTCCAACTACAGCTTCTTCAACACAGTAAACAGTGGAGACA	1440
Db	1381	GCACGCTGAGCTTAAACACCTCCAACTACAGCTTCTTCAACACAGTAAACAGTGGAGACA	1440
Qy	1441	CGAGATCTGCTGAGGACACAAACGGAAGTACAAAGCTTCTTCCACACGCTCCACATG	1500
Db	1441	CGAGATCTGCTGAGGACACAAACGGAAGTACAAAGCTTCTTCCACACGCTCCACATG	1500
Qy	1501	GTTCACAGCCGCGATATACCACTTACCAACGCTGCTCAATTCAGACTACCCGCTGCCA	1560
Db	1501	GTTCACAGCCGCGATATACCACTTACCAACGCTGCTCAATTCAGACTACCCGCTGCCA	1560
Qy	1561	AGCAGTGGCAGTACCCGCGACAGACACCACTGACAGTACAGACGCTGGATGAG	1620
Db	1561	AGCAGTGGCAGTACCCGCGACAGACACCACTGACAGTACAGACGCTGGATGAG	1620
Qy	1621	TCATGAAGACACCAAGATCATCATTTGGCTGCTTTTGGCAGTGAATCTGCTAGCTGCCG	1680
Db	1621	TCATGAAGACACCAAGATCATCATTTGGCTGCTTTTGGCAGTGAATCTGCTAGCTGCCG	1680
Qy	1681	CCATGTTGATGTTCTTATAAATCTTAAAGCGGACCCAGCAGCGGAGTACAGTACAG	1740
Db	1681	CCATGTTGATGTTCTTATAAATCTTAAAGCGGACCCAGCAGCGGAGTACAGTACAG	1740
Qy	1741	CCGCCGAGCTGTTGAGTAACTCCAGTGGAGACACATCCAGCAGCAACATCCGAG	1800
Db	1741	CCGCCGAGCTGTTGAGTAACTCCAGTGGAGACACATCCAGCAGCAACATCCGAG	1800
Qy	1801	CAGCAACAGCAGCTCCGCTCGGCTGATCAGGTGAGGGGCGAGTGTGCTGCCCAATTC	1860
Db	1801	CAGCAACAGCAGCTCCGCTCGGCTGATCAGGTGAGGGGCGAGTGTGCTGCCCAATTC	1860
Qy	1861	ATGACCATATTAATCAACCTACCAACAGCAGCATGGGCGCCACTGCGAGAGAAACA	1920
Db	1861	ATGACCATATTAATCAACCTACCAACAGCAGCATGGGCGCCACTGCGAGAGAAACA	1920
Qy	1921	GCCTGGGAACTCTCTGCAACCCCAAGTCACTATCTCTGAACTTATATAATTCAG	1980
Db	1921	GCCTGGGAACTCTCTGCAACCCCAAGTCACTATCTCTGAACTTATATAATTCAG	1980
Qy	1981	CCCATACCAAGGACAGGTACAGGAACTCAATATGATCTCCCTCCCCCAAAACCTTA	2040
Db	1981	CCCATACCAAGGACAGGTACAGGAACTCAATATGATCTCCCTCCCCCAAAACCTTA	2040
Qy	2041	TAAATGCAATAGATGACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT	2100
Db	2041	TAAATGCAATAGATGACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT	2100
Qy	2101	TTCTGTGATATGCTTATATTAATTAAGTCTATGGCTGGTAAAAAACAAGATTAATTA	2160

Db 2101 TTCCTGTATGCTTATATATTAATTAAGTCTATGGCTGGTGAATAAAAAACAGATTATATTA 2160

Qy 2161 AATTTAAAGACAAAGATCAAAACA 2185  
2162 |||||  
Db 2161 AATTTAAAGACAAAGATCAAAACA 2185

RESULT 7

AX89359  
ID ABX9359 standard; cDNA; 2185 BP.

XX  
AC ABX89359;

XX  
DT 13-MAY-2003 (first entry)

XX  
DE DNA encoding novel secreted and transmembrane protein PRO1111.

XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumor; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.

XX  
OS Homo sapiens.

XX  
PN US2003017563-A1.

XX  
PX 23-JAN-2003.

XX  
PF 07-MAY-2002; 2002US-0140808.

XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17886.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 16-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US00106.  
PR 08-MAR-1999; 98WO-US05028.  
PR 10-MAR-1999; 98WO-US05190.  
PR 20-APR-1999; 98WO-US08615.  
PR 14-MAY-1999; 98WO-US10733.  
PR 02-JUN-1999; 98WO-US12252.  
PR 01-SEP-1999; 98WO-US20111.  
PR 08-SEP-1999; 98WO-US20594.  
PR 13-SEP-1999; 98WO-US20844.  
PR 15-SEP-1999; 98WO-US21090.  
PR 15-SEP-1999; 98WO-US21547.  
PR 29-OCT-1999; 98WO-US23089.  
PR 29-NOV-1999; 98WO-US28214.  
PR 30-NOV-1999; 98WO-US28313.  
PR 30-NOV-1999; 98WO-US28409.  
PR 01-DEC-1999; 98WO-US28301.  
PR 01-DEC-1999; 98WO-US28634.  
PR 02-DEC-1999; 98WO-US28551.  
PR 02-DEC-1999; 98WO-US28564.  
PR 02-DEC-1999; 98WO-US28565.  
PR 16-DEC-1999; 98WO-US30095.  
PR 20-DEC-1999; 98WO-US30911.

PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0865028.  
PR 25-MAY-2001; 2001US-0865034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0026072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao M;  
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14.  
P-PSDB; ABUS9869.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346

T and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
T are therapeutically useful for enhancing immune response and in cancer  
T treatments -  
X S Claim 2; Fig 437; 659pp; English.  
X C The invention describes an isolated human PRO polypeptide. The PRO  
C polypeptides are useful in detecting PRO polypeptides in a sample, in  
C linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
C in modulating at least one biological activity of a cell expressing a PRO  
C polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
C useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
C stimulate adrenal cortical capillary endothelial growth, and PRO536,  
C PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
C PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
C useful for treating conditions or disorders where angiogenesis would be  
C beneficial, e.g. wound healing and antagonist of this polypeptide are  
C useful for treating cancerous tumours. PRO812 inhibits vascular  
C endothelial growth factor (VEGF) stimulated proliferation of endothelial  
C cells and is thus useful for inhibiting endothelial cell growth in  
C mammals which would be beneficial in inhibiting tumour growth. PRO826,  
C PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
C stimulated T-lymphocytes and are therapeutically useful for enhancing  
C immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
C retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
C rod photoreceptor cells) and therefore are useful for treating retinal  
C disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813  
C and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
C and therefore are useful for treating kidney disorders associated with  
C decreased mesangial cell function such as Berger disease or Crohn's  
C nephropathies associated with dermatitis, herpeticiformis or Crohn's  
C disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
C proliferation and/or redifferentiation of chondrocytes in culture and  
C are thus useful for treating sports injuries, and arthritis. This  
C sequence encodes a novel human PRO protein.

X Q Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;  
Query Match 100.0%; Score 2185; DB 25; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 GTTCTCTTCCAGGCAAAATCCAGGGGATGGTGAATTATGACGTGCGCACCATGA 60  
b 1 GTTCTCTTCCAGGCAAAATCCAGGGGATGGTGAATTATGACGTGCGCACCATGA 60  
Y 61 AGCTCTTGTGCGAGTAACCTGTCACACACACACCTGGAATGCCATCTGCTCCCGTTG 120  
b 61 AGCTCTTGTGCGAGTAACCTGTCACACACACACCTGGAATGCCATCTGCTCCCGTTG 120  
Y 121 TCTACCTCAAGCGCGCAAGTGTGATTTCTGTGTCAGCCATGCTGCTCCCGTTG 180  
b 121 TCTACCTCAAGCGCGCAAGTGTGATTTCTGTGTCAGCCATGCTGCTCCCGTTG 180  
Y 181 GCGCCAGAGTAACCTGCTGTCAGAGTAACCTGTCAGAGTAACCTGTCAGAGTAAC 240  
b 181 GCGCCAGAGTAACCTGCTGTCAGAGTAACCTGTCAGAGTAACCTGTCAGAGTAAC 240  
Y 241 CGGCGCGCGGCTCTCCAGGCTCCGCGAGGATTTCCCTCGAACACCGGTACCTCAACC 300  
b 241 CGGCGCGCGGCTCTCCAGGCTCCGCGAGGATTTCCCTCGAACACCGGTACCTCAACC 300  
Y 301 TCATGGAGAACATATCCAGATATCCAGGCGAGACCTTCGCGACCTCCAGACCTGG 360  
b 301 TCATGGAGAACATATCCAGATATCCAGGCGAGACCTTCGCGACCTCCAGACCTGG 360  
Y 361 AGTTCCTGCAAGTTGGGAGGAACTCCATCCGCGAGATTTGAGGTGGGGGCTTCAACGGCC 420  
b 361 AGTTCCTGCAAGTTGGGAGGAACTCCATCCGCGAGATTTGAGGTGGGGGCTTCAACGGCC 420  
Y 421 TGGCCAGCTCAACACCTCGAGCTGTTCACAACTGGCTGACAGTCATCTCCCTAGCGGG 480  
b 421 TGGCCAGCTCAACACCTCGAGCTGTTCACAACTGGCTGACAGTCATCTCCCTAGCGGG 480

QY 481 CTTTGAATACCTGTCRAAGCTGCGGAGCTCTGCTTCGCAACCAACCCATCGAAAGCA 540  
DB 481 CTTTGAATACCTGTCRAAGCTGCGGAGCTCTGCTTCGCAACCAACCCATCGAAAGCA 540  
QY 541 TCCCTCTTACGCTTCAACCGGCTTCCCTCATGCGCTGAGCTTGGGGAGCTCA 600  
DB 541 TCCCTCTTACGCTTCAACCGGCTTCCCTCATGCGCTGAGCTTGGGGAGCTCA 600  
QY 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA 660  
DB 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCACCTCAAGTATCTGA 660  
QY 661 ACTTGGGCTGTGACATTAAGACATGCGGCTTCAACCTCAACCTTGGGGCTGGAGG 720  
DB 661 ACTTGGGCTGTGACATTAAGACATGCGGCTTCAACCTCAACCTTGGGGCTGGAGG 720  
QY 721 AGCTGAGAGTGTGAGGAACTTCCCTGAGATCAGGCTGGCTCTTCCATGAGCTGA 780  
DB 721 AGCTGAGAGTGTGAGGAACTTCCCTGAGATCAGGCTGGCTCTTCCATGAGCTGA 780  
QY 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGAGTCAAGCTGAGCGGAATGCTT 840  
DB 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGAGTCAAGCTGAGCGGAATGCTT 840  
QY 841 TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCACTAATACCTCTCTTCTTTCG 900  
DB 841 TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCACTAATACCTCTCTTCTTTCG 900  
QY 901 CCATGACCTCTTTACCCGCTGAGTACTCTGGTGGAGTGTGATCAGACCAACCTT 960  
DB 901 CCATGACCTCTTTACCCGCTGAGTACTCTGGTGGAGTGTGATCAGACCAACCTT 960  
QY 961 GGAACCTGTGATGTGACATTTCTGTGCTAGCTGAGCTGGCTTGGAGTATATACCCACCA 1020  
DB 961 GGAACCTGTGATGTGACATTTCTGTGCTAGCTGAGCTGGCTTGGAGTATATACCCACCA 1020  
QY 1021 ATTCCACCTGCTGTGCGCTGTGATCTCCATGCAATGAGAGCGCTACCTGCTGG 1080  
DB 1021 ATTCCACCTGCTGTGCGCTGTGATCTCCATGCAATGAGAGCGCTACCTGCTGG 1080  
QY 1081 AGTGACAGGCTCTCTTCCAGTGTCTGCGCTTCACTCATGAGCGCACCTCGAGAC 1140  
DB 1081 AGTGACAGGCTCTCTTCCAGTGTCTGCGCTTCACTCATGAGCGCACCTCGAGAC 1140  
QY 1141 TCAACATTTCTGAGGGTGGATGCGAGAACTTAAAGTGTGCGACTCCCTATGCTCTCG 1200  
DB 1141 TCAACATTTCTGAGGGTGGATGCGAGAACTTAAAGTGTGCGACTCCCTATGCTCTCG 1200  
QY 1201 TGAAGTGTGCTGCCAATGAGGAGTGTCTGAGCGAGCTCCCGCCAGCAAGATCT 1260  
DB 1201 TGAAGTGTGCTGCCAATGAGGAGTGTCTGAGCGAGCTCCCGCCAGCAAGATCT 1260  
QY 1261 CTGCTCTCAACGAGCGCACTTGAACCTTTTCCACCTGCTGCTTTTTCAGACACTGGGGTGT 1320  
DB 1261 CTGCTCTCAACGAGCGCACTTGAACCTTTTCCACCTGCTGCTTTTTCAGACACTGGGGTGT 1320  
QY 1321 ACATGCTGATGAGCAATGTTGAGGCAATCTTCAACCGCTCGGCTTACCTCAATGTGA 1380  
DB 1321 ACATGCTGATGAGCAATGTTGAGGCAATCTTCAACCGCTCGGCTTACCTCAATGTGA 1380  
QY 1381 GCGGCTGAGCTTAAACCTTCCAACTGAGCTTTCACCAAGTAAAGTGGAGCA 1440  
DB 1381 GCGGCTGAGCTTAAACCTTCCAACTGAGCTTTCACCAAGTAAAGTGGAGCA 1440  
QY 1441 CGGAGATCTCGCTGAGGACACCAACCGGAAAGTAAAGCTGTCTTCTACAGCTCCACTG 1500  
DB 1441 CGGAGATCTCGCTGAGGACACCAACCGGAAAGTAAAGCTGTCTTCTACAGCTCCACTG 1500  
QY 1501 GTTACGAGCGGATATACCACTTACCAAGCTGCTTACAGACTTACCTGCTGCCCA 1560  
DB 1501 GTTACGAGCGGATATACCACTTACCAAGCTGCTTACAGACTTACCTGCTGCCCA 1560





10-JUN-1998; 98US-088742P.  
 10-JUN-1998; 98US-088810P.  
 10-JUN-1998; 98US-088824P.  
 10-JUN-1998; 98US-088828P.  
 11-JUN-1998; 98US-088858P.  
 11-JUN-1998; 98US-088861P.  
 11-JUN-1998; 98US-088876P.  
 12-JUN-1998; 98US-089105P.  
 16-JUN-1998; 98US-089440P.  
 16-JUN-1998; 98US-089512P.  
 16-JUN-1998; 98US-089514P.  
 17-JUN-1998; 98US-089532P.  
 17-JUN-1998; 98US-089538P.  
 17-JUN-1998; 98US-089598P.  
 17-JUN-1998; 98US-089599P.  
 17-JUN-1998; 98US-089600P.  
 17-JUN-1998; 98US-089653P.  
 18-JUN-1998; 98US-089801P.  
 18-JUN-1998; 98US-089907P.  
 18-JUN-1998; 98US-089908P.  
 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM, Wood WI, Zhang Z;

WPI; 2003-247083/24.  
 P-PSDB; ABUS9111.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Claim 2; Fig 158; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide.

Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 25; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;			Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	DB	QY	DB	QY	DB
1	1	GTCTCTCTTCCGAGCCAAATCCAGGCGATGGTGAATATGAAGTGCACACCATGA	60		
1	1	GTCTCTCTTCCGAGCCAAATCCAGGCGATGGTGAATATGAAGTGCACACCATGA	60		
61	61	AGCTCTTGTGGCAGGTAACTGTGCACCAACACACCTTGGAAATCCATCTCTCCGTTGG	120		
61	61	AGCTCTTGTGGCAGGTAACTGTGCACCAACACACCTTGGAAATCCATCTCTCCGTTGG	120		
121	121	TCTACCTCAGGCGCAAGTGTGATCTGTGTGAGGCGATCGCTGCTGCGGCTCAGCG	180		
121	121	TCTACCTCAGGCGCAAGTGTGATCTGTGTGAGGCGATCGCTGCTGCGGCTCAGCG	180		
181	181	GGCCCCAGAACTGCCCTTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240		
181	181	GGCCCCAGAACTGCCCTTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240		
241	241	CGCGCGGGGCTCTCCGAGTCCCGAGGTTTCCCTCGAAGGCTTCCCTCGAAGGCTT	300		
241	241	CGCGCGGGGCTCTCCGAGTCCCGAGGTTTCCCTCGAAGGCTTCCCTCGAAGGCTT	300		
301	301	TCATGGAGAACCAATCCAGATGATCCAGCCGACACTTCCGCACTTCCACACCTGG	360		
301	301	TCATGGAGAACCAATCCAGATGATCCAGCCGACACTTCCGCACTTCCACACCTGG	360		
361	361	AGGTCTCTGAGTCTGGGAGGAACTCCATCCGCGAGATGAGGTGGGGGCTTCAAGGCC	420		
361	361	AGGTCTCTGAGTCTGGGAGGAACTCCATCCGCGAGATGAGGTGGGGGCTTCAAGGCC	420		
421	421	TGGCCAGCTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480		
421	421	TGGCCAGCTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480		
481	481	CTTTGATATCTCTCAAGTCTGGGAGCTCTGGCTTCGCAACAACTCCATCGAAAGCA	540		
481	481	CTTTGATATCTCTCAAGTCTGGGAGCTCTGGCTTCGCAACAACTCCATCGAAAGCA	540		
541	541	TCCCTCTTACGCTTCAACCGGCTGCGCTCCCTCATGCGCTGGACTTGGGGAGCTCA	600		
541	541	TCCCTCTTACGCTTCAACCGGCTGCGCTCCCTCATGCGCTGGACTTGGGGAGCTCA	600		
601	601	AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660		
601	601	AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660		
661	661	ACTTGGGAGTGTCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGGCTGGAG	720		
661	661	ACTTGGGAGTGTCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGGCTGGAG	720		
721	721	AGCTGGAGTGTCAAGGAACTCCCTGAGATCAGGCTGGCTCTCTCCATGGGCTGA	780		
721	721	AGCTGGAGTGTCAAGGAACTCCCTGAGATCAGGCTGGCTCTCTCCATGGGCTGA	780		
781	781	GCTCCCTCAAGAGCTCTGGGTCAATGAACCTCAGGTCAGCTGATGAGGGAATGCTT	840		
781	781	GCTCCCTCAAGAGCTCTGGGTCAATGAACCTCAGGTCAGCTGATGAGGGAATGCTT	840		
841	841	TGAGGGGCTGGCTTCACTGTGGAATCACTTGGGCGGCAATAACTCTCTCTTTCG	900		
841	841	TGAGGGGCTGGCTTCACTGTGGAATCACTTGGGCGGCAATAACTCTCTCTTTCG	900		
901	901	CCCATGACTCTTTTACCCCGCTGAGGTACCTGTGGAGTTGCAATACCAACACCTT	960		
901	901	CCCATGACTCTTTTACCCCGCTGAGGTACCTGTGGAGTTGCAATACCAACACCTT	960		
961	961	GGAACTGTGATGTGACATCTCTGTGGCTAGCTGTGGCTGGCTGGAGTATATCCACCA	1020		
961	961	GGAACTGTGATGTGACATCTCTGTGGCTAGCTGTGGCTGGCTGGAGTATATCCACCA	1020		
1021	1021	ATTCCACCTGCTGGGCGCTGCTCATCTCCCATGCACATCGAGGCGGCTTACCTGTGG	1080		

Db 1021 ATTCCACCTGCTGTGCGCGCTGTCACTGCTCCCATGCAATGCGAGCGCGCTACCTCCTGG 1080  
 QY 1081 AGGTGACACAGGCTCTTCCAGTGTCTGCGCCCTTTCATCATGACGACCACTCTGGAGACC 1140  
 Db 1081 AGGTGACACAGGCTCTTCCAGTGTCTGCGCCCTTTCATCATGACGACCACTCTGGAGACC 1140  
 QY 1141 TCACATTTCTGAGGTGCGATGCGAGAACTTAAAGTGTGCGACTCCCTATGCTCTCG 1200  
 Db 1141 TCACATTTCTGAGGTGCGATGCGAGAACTTAAAGTGTGCGACTCCCTATGCTCTCG 1200  
 QY 1201 TGAAGTGTGCTGCGCAATGCGACAGTCTCAGCACGCTCCCGCCACCCAGGATCT 1260  
 Db 1201 TGAAGTGTGCTGCGCAATGCGACAGTCTCAGCACGCTCCCGCCACCCAGGATCT 1260  
 QY 1261 CTGTCTCTCAACGACGCGACCTTTGAATTTTCCACGCTGCTGTTTTAGACACACTGCGGTGT 1320  
 Db 1261 CTGTCTCTCAACGACGCGACCTTTGAATTTTCCACGCTGCTGTTTTAGACACACTGCGGTGT 1320  
 QY 1321 ACATGTCATGTCAGCAATGTCAGGCAATCTCAACGCTGCGCTACCTCAATGTGA 1380  
 Db 1321 ACATGTCATGTCAGCAATGTCAGGCAATCTCAACGCTGCGCTACCTCAATGTGA 1380  
 QY 1381 GCACGCTGAGCTTAACTCACTCACTCAGCTTTCTTCCACAGTAACTAGTGGAGACCA 1440  
 Db 1381 GCACGCTGAGCTTAACTCACTCACTCAGCTTTCTTCCACAGTAACTAGTGGAGACCA 1440  
 QY 1441 CGGAGATCTGCTGAGGACACAAACGCGAAAGTCAAGCTGTTCTTACCACTGCTCCACTG 1500  
 Db 1441 CGGAGATCTGCTGAGGACACAAACGCGAAAGTCAAGCTGTTCTTACCACTGCTCCACTG 1500  
 QY 1501 GTTACACGCGGATATACACCTCTTACCACTGCTTCACTCAGACTACCTGCTGCGCA 1560  
 Db 1501 GTTACACGCGGATATACACCTCTTACCACTGCTTCACTCAGACTACCTGCTGCGCA 1560  
 QY 1561 AGCAGTGTGAGTACCGCGACAGACCACTGACAAAGATGACAGACGAGTGGATGAAG 1620  
 Db 1561 AGCAGTGTGAGTACCGCGACAGACCACTGACAAAGATGACAGACGAGTGGATGAAG 1620  
 QY 1621 TCATGAGACCCACAGATATCATTTGGCTGCTTTGTCAGTGACTCTGCTAGTGGCG 1680  
 Db 1621 TCATGAGACCCACAGATATCATTTGGCTGCTTTGTCAGTGACTCTGCTAGTGGCG 1680  
 QY 1681 CCATGTTGATGTTCTTATACTTAACTTCGTAAGCGCACAGCGAGTACAGTCAAG 1740  
 Db 1681 CCATGTTGATGTTCTTATACTTAACTTCGTAAGCGCACAGCGAGTACAGTCAAG 1740  
 QY 1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGAAGAGACATCCACGACGAGTCCCGAG 1800  
 Db 1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGAAGAGACATCCACGACGAGTCCCGAG 1800  
 QY 1801 CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGSCAGTGTGCTGCCCAATTC 1860  
 Db 1801 CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGSCAGTGTGCTGCCCAATTC 1860  
 QY 1861 ATGACCATATTACTACACACTTCAAAACGAGACATGCGGCGCCACTGGACAGAAACA 1920  
 Db 1861 ATGACCATATTACTACACACTTCAAAACGAGACATGCGGCGCCACTGGACAGAAACA 1920  
 QY 1921 GCTGCGGGAATCTCTGCAACCCACAGTCCACCTATCTCTGAACCTTATATATTCAGA 1980  
 Db 1921 GCTGCGGGAATCTCTGCAACCCACAGTCCACCTATCTCTGAACCTTATATATTCAGA 1980  
 QY 1981 CCATACCAAGGACAGGTACAGGAACTCAAAATGATGCTCCCTCCCGCAAAACTTA 2040  
 Db 1981 CCATACCAAGGACAGGTACAGGAACTCAAAATGATGCTCCCTCCCGCAAAACTTA 2040  
 QY 2041 TAAATGCAATAGATGACACAGACAGCAACTTTTGTACAGAGTGGGAGACCTTT 2100  
 Db 2041 TAAATGCAATAGATGACACAGACAGCAACTTTTGTACAGAGTGGGAGACCTTT 2100  
 QY 2101 TTCCTGTATATGCTTATATTAATTAAGTCTATGGCTGGTTTAAAAAACAAGATTATTA 2160  
 Db 2101 TTCCTGTATATGCTTATATTAATTAAGTCTATGGCTGGTTTAAAAAACAAGATTATTA 2160

QY 2161 AATTAAAGCAAAAAGTCAAAACA 2185  
 Db 2161 AATTAAAGCAAAAAGTCAAAACA 2185

RESULT 9  
 ABX80774  
 ID ABX80774 standard; cdNA; 2185 BP.  
 XX AC ABX80774;  
 XX 22-APR-2003 (first entry)  
 XX Human secreted/transmembrane protein cDNA, #93.

Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
 antibody-dependent enzyme mediated prodrug therapy; cytostatic.

OS Homo sapiens.  
 XX US2003027162-A1.  
 PN 06-FEB-2003.  
 PD 15-NOV-2001; 2001US-0997428.  
 PF 05-NOV-1997; 97WO-US200069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US21108.  
 PR 03-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US12252.  
 PR 02-JUN-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 10-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-049787P.



Db 61 AGCTCTTGTGGCAGGTAACCTGTGCAACCAACACCTGGAAATGCCATCTCTGCTCCGGTTGC 120  
 Qy 121 TCTACCTCAGCGCGCAAGTGTGATTTCTCTGTGTGACAGCATCTCTCTCGCGCTCAGCGG 180  
 Db 121 TCTACCTCAGCGCGCAAGTGTGATTTCTCTGTGTGACAGCATCTCTCTCGCGCTCAGCGG 180  
 Qy 181 GGCCCCAGAACTGCCCCCTCCGTTTGTCTGTGAGTAAACAGTTTCAAGAGTGTGTGTGCA 240  
 Db 181 GGCCCCAGAACTGCCCCCTCCGTTTGTCTGTGAGTAAACAGTTTCAAGAGTGTGTGTGCA 240  
 Qy 241 CGCGCGCGGGCTCTCCGAGGTCGCGAGGTAATTCCTCGAAACACCGGTACCTCAACC 300  
 Db 241 CGCGCGCGGGCTCTCCGAGGTCGCGAGGTAATTCCTCGAAACACCGGTACCTCAACC 300  
 Qy 301 TCATGGAGAACAAATPCAGATGATCCAGCGGACACCTTTCGGCCACCTCCACACCTCTGG 360  
 Db 301 TCATGGAGAACAAATPCAGATGATCCAGCGGACACCTTTCGGCCACCTCCACACCTCTGG 360  
 Qy 361 AGTCTCTGAGTTGGGACGAACTCCATCCGACAGATTGAGTGTGGGGCTTTCAACGGCC 420  
 Db 361 AGTCTCTGAGTTGGGACGAACTCCATCCGACAGATTGAGTGTGGGGCTTTCAACGGCC 420  
 Qy 421 TGGCCAGCCTCAACACCTCGAGCTGTTCGACAACTGCTGACAGTCAATCCCTAGCGGG 480  
 Db 421 TGGCCAGCCTCAACACCTCGAGCTGTTCGACAACTGCTGACAGTCAATCCCTAGCGGG 480  
 Qy 481 CTTTGAATACCTGTCCAGCTGCGGAGCTCTGCTTCGAAACACCCATCGAAGCA 540  
 Db 481 CTTTGAATACCTGTCCAGCTGCGGAGCTCTGCTTCGAAACACCCATCGAAGCA 540  
 Qy 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGACTTGGGGAGCTCA 600  
 Db 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGACTTGGGGAGCTCA 600  
 Qy 601 AGAAGCTGAGATATCTCTGAGGAGCTTTTGGGGGCTGTTCACCTCAAGTATCTGA 660  
 Db 601 AGAAGCTGAGATATCTCTGAGGAGCTTTTGGGGGCTGTTCACCTCAAGTATCTGA 660  
 Qy 661 ACTTGGGCAATGTCAACATTAAGACATGCCCAATCTCAACCTGTGGGGCTGGAGG 720  
 Db 661 ACTTGGGCAATGTCAACATTAAGACATGCCCAATCTCAACCTGTGGGGCTGGAGG 720  
 Qy 721 AGTGGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTCTTCCATGGCCTGA 780  
 Db 721 AGTGGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTCTTCCATGGCCTGA 780  
 Qy 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGAGTCAAGCTGAGGCTGAGGCTGAGG 840  
 Db 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGAGTCAAGCTGAGGCTGAGGCTGAGG 840  
 Qy 841 TTGAACGGCTGGCTTCACTTGTGGAACTCAACTTGGCCACAAATACCTCTCTTCTTTC 900  
 Db 841 TTGAACGGCTGGCTTCACTTGTGGAACTCAACTTGGCCACAAATACCTCTCTTCTTTC 900  
 Qy 901 CCATGACCTCTTACCGCTGAGTACTCTGGTGGAGTGTGATCTACACCAACCTT 960  
 Db 901 CCATGACCTCTTACCGCTGAGTACTCTGGTGGAGTGTGATCTACACCAACCTT 960  
 Qy 961 GGAACCTGTGATGTGACATCTCTGAGTCTGAGCTGTGGCTTGGAGTATATACCCCA 1020  
 Db 961 GGAACCTGTGATGTGACATCTCTGAGTCTGAGCTGTGGCTTGGAGTATATACCCCA 1020  
 Qy 1021 ATTCCACCTCTGTGCGCGTGTATCTCCATGCAATGAGGCGCTTACCTCTGTGG 1080  
 Db 1021 ATTCCACCTCTGTGCGCGTGTATCTCCATGCAATGAGGCGCTTACCTCTGTGG 1080  
 Qy 1081 AGGTGACACAGGCTCTCTTCCAGTGTCTGCGCCCTTATCATGACGACCTCGAGACC 1140  
 Db 1081 AGGTGACACAGGCTCTCTTCCAGTGTCTGCGCCCTTATCATGACGACCTCGAGACC 1140  
 Qy 1141 TCAACATTTCTGAGGTCGAGTGGCAGAACTTAAGTGTGCGACTCCCTCTATGTCCTCG 1200  
 Db 1141 TCAACATTTCTGAGGTCGAGTGGCAGAACTTAAGTGTGCGACTCCCTCTATGTCCTCG 1200

RESULT 10  
 ABX81157  
 ID ABX81157 standard; DNA; 2185 BP.

Qy 1201 TGAAGTGTGTGCTGCCCAATGGGACAGTGTCTCAGCAACGCTCCCGCCACCCAAAGATCT 1260  
 Db 1201 TGAAGTGTGTGCTGCCCAATGGGACAGTGTCTCAGCAACGCTCCCGCCACCCAAAGATCT 1260  
 Qy 1261 CTGTCTCTCAACGAGCGCACTTGAACCTTTCCACAGTGTCTTCCACAGTGTGTGAGG 1320  
 Db 1261 CTGTCTCTCAACGAGCGCACTTGAACCTTTCCACAGTGTCTTCCACAGTGTGTGAGG 1320  
 Qy 1321 ACACATGTGATGTGTGACCAATGTTCAGGCAACTCCAAAGCTTCGGCTTACCTCAATGTGA 1380  
 Db 1321 ACACATGTGATGTGTGACCAATGTTCAGGCAACTCCAAAGCTTCGGCTTACCTCAATGTGA 1380  
 Qy 1381 GCAAGCTGAGCTTAAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 1440  
 Db 1381 GCAAGCTGAGCTTAAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 1440  
 Qy 1441 CGGAGATCTCGCTGAGGACACCAACGCGAAAGTACAAGCTTCTTCTTACCAGCTCCACTG 1500  
 Db 1441 CGGAGATCTCGCTGAGGACACCAACGCGAAAGTACAAGCTTCTTCTTACCAGCTCCACTG 1500  
 Qy 1501 GTTACAGCGCGCATATACCACTCTACCAAGTGTCTATTCAGACTACCTGTGTGCCA 1560  
 Db 1501 GTTACAGCGCGCATATACCACTCTACCAAGTGTCTATTCAGACTACCTGTGTGCCA 1560  
 Qy 1561 AGCAGTGTGAGTACCCGCGACAGACACCACTGCAAGATGCAAGCTTCTTCTTACCAGCTCCACTG 1620  
 Db 1561 AGCAGTGTGAGTACCCGCGACAGACACCACTGCAAGATGCAAGCTTCTTCTTACCAGCTCCACTG 1620  
 Qy 1621 TCAATGAAGACCAACCAAGATCAATGGCTGTCTTGTGGCTGTCTTGTAGTGTGG 1680  
 Db 1621 TCAATGAAGACCAACCAAGATCAATGGCTGTCTTGTGGCTGTCTTGTAGTGTGG 1680  
 Qy 1681 CCAATGTGATGTCTTCTTATAAATCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1740  
 Db 1681 CCAATGTGATGTCTTCTTATAAATCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1740  
 Qy 1741 CCGCCCGGACTGTGTGAGATAATCCAGTGTGAGGAAAGATCCAGCAAGCAATCCCGAG 1800  
 Db 1741 CCGCCCGGACTGTGTGAGATAATCCAGTGTGAGGAAAGATCCAGCAAGCAATCCCGAG 1800  
 Qy 1801 CAGCAACAGCTCGCTCGGTGTATCAGGTGAGGGGCGAGTGTCTGCCCAATTC 1860  
 Db 1801 CAGCAACAGCTCGCTCGGTGTATCAGGTGAGGGGCGAGTGTCTGCCCAATTC 1860  
 Qy 1861 ATGACCATTAATTAACACCACTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 1920  
 Db 1861 ATGACCATTAATTAACACCACTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 1920  
 Qy 1921 GCTTGGGAACTCTCTGCAACCCACAGTCAACCTATCTCTGAACTTATATATTCAGA 1980  
 Db 1921 GCTTGGGAACTCTCTGCAACCCACAGTCAACCTATCTCTGAACTTATATATTCAGA 1980  
 Qy 1981 CCAATACCAAGCAAGTATCAGGAACTCAATATGACTTCCCTTCCCTTCCCTTCCCTTCCCT 2040  
 Db 1981 CCAATACCAAGCAAGTATCAGGAACTCAATATGACTTCCCTTCCCTTCCCTTCCCTTCCCT 2040  
 Qy 2041 TAAATATGCAATGATGACACAAAGACAGCACTTTTGTACAGTGTGGGAGAGACTTT 2100  
 Db 2041 TAAATATGCAATGATGACACAAAGACAGCACTTTTGTACAGTGTGGGAGAGACTTT 2100  
 Qy 2101 TTCTTCTATATCTTATATTAAGTCTATGCTGTGCTTAAAGAAACAGATTTATATTA 2160  
 Db 2101 TTCTTCTATATCTTATATTAAGTCTATGCTGTGCTTAAAGAAACAGATTTATATTA 2160  
 Qy 2161 AATTTAAGACAAAGTCAAAACA 2185  
 Db 2161 AATTTAAGACAAAGTCAAAACA 2185

X	C	ABX81157;	PR	24-NOV-1997;	97US-066770P.
X	X	22-APR-2003 (first entry)	PR	25-FEB-1998;	98US-075945P.
X	X	Novel human secreted or transmembrane protein PRO1344 DNA.	PR	20-MAR-1998;	98US-078910P.
X	X	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;	PR	28-APR-1998;	98US-083322P.
X	X	cardiac insufficiency disorder; cancer; tumour; immune response;	PR	07-MAY-1998;	98US-084600P.
X	X	adrenal cortical capillary endothelial growth; c-fos induction;	PR	02-JUN-1998;	98US-087106P.
X	X	vascular endothelial growth factor inhibition; VEGF inhibition;	PR	02-JUN-1998;	98US-087607P.
X	X	endothelial cell growth inhibitor; T-lymphocytes stimulation;	PR	02-JUN-1998;	98US-087609P.
X	X	retinal neurons cell survival; rod photoreceptor cell survival;	PR	03-JUN-1998;	98US-087827P.
X	X	retinal disorder; retinitis pigmentosa; kidney disorder;	PR	04-JUN-1998;	98US-088021P.
X	X	mammalian kidney mesangial cell proliferation; Berger disease;	PR	04-JUN-1998;	98US-088025P.
X	X	dermatitis; herpesiformis; Crohn's disease; chondrocyte proliferation;	PR	04-JUN-1998;	98US-088028P.
X	X	chondrocyte redifferentiation; sports injury; arthritis; gene; ds.	PR	04-JUN-1998;	98US-088030P.
X	S	Homo sapiens.	PR	04-JUN-1998;	98US-088033P.
X	X	US2003027985-A1.	PR	04-JUN-1998;	98US-088326P.
X	X	06-FEB-2003.	PR	05-JUN-1998;	98US-088167P.
X	X	14-NOV-2001; 2001US-0990562.	PR	05-JUN-1998;	98US-088202P.
X	X	05-NOV-1997; 97WO-US20069.	PR	05-JUN-1998;	98US-088212P.
X	R	16-SEP-1998; 98WO-US19330.	PR	05-JUN-1998;	98US-088217P.
X	R	17-SEP-1998; 98WO-US19437.	PR	09-JUN-1998;	98US-088555P.
X	R	07-OCT-1998; 98WO-US21141.	PR	10-JUN-1998;	98US-088734P.
X	R	01-DEC-1998; 98WO-US25108.	PR	10-JUN-1998;	98US-088738P.
X	R	05-JAN-1999; 99WO-US00106.	PR	10-JUN-1998;	98US-088742P.
X	R	08-MAR-1999; 99WO-US05028.	PR	10-JUN-1998;	98US-088810P.
X	R	02-JUN-1999; 99WO-US12252.	PR	10-JUN-1998;	98US-088824P.
X	R	15-SEP-1999; 99WO-US21090.	PR	11-JUN-1998;	98US-088826P.
X	R	15-SEP-1999; 99WO-US21547.	PR	11-JUN-1998;	98US-088858P.
X	R	30-NOV-1999; 99WO-US28313.	PR	11-JUN-1998;	98US-088861P.
X	R	01-DEC-1999; 99WO-US28301.	PR	12-JUN-1998;	98US-088876P.
X	R	01-DEC-1999; 99WO-US28634.	PR	12-JUN-1998;	98US-0889105P.
X	R	16-DEC-1999; 99WO-US30095.	PR	16-JUN-1998;	98US-089440P.
X	R	20-DEC-1999; 99WO-US30911.	PR	16-JUN-1998;	98US-089512P.
X	R	05-JAN-2000; 2000WO-US00219.	PR	17-JUN-1998;	98US-089514P.
X	R	06-JAN-2000; 2000WO-US00376.	PR	17-JUN-1998;	98US-089532P.
X	R	11-FEB-2000; 2000WO-US03565.	PR	17-JUN-1998;	98US-089538P.
X	R	18-FEB-2000; 2000WO-US04341.	PR	17-JUN-1998;	98US-089599P.
X	R	22-FEB-2000; 2000WO-US04414.	PR	17-JUN-1998;	98US-089600P.
X	R	24-FEB-2000; 2000WO-US04914.	PR	17-JUN-1998;	98US-089653P.
X	R	24-FEB-2000; 2000WO-US05004.	PR	18-JUN-1998;	98US-089801P.
X	R	02-MAR-2000; 2000WO-US05841.	PR	18-JUN-1998;	98US-089907P.
X	R	10-MAR-2000; 2000WO-US06319.	PR	18-JUN-1998;	98US-089908P.
X	R	15-MAR-2000; 2000WO-US06884.	PR	19-JUN-1998;	98US-089947P.
X	R	20-MAR-2000; 2000WO-US07377.	PR	19-JUN-1998;	98US-089948P.
X	R	30-MAR-2000; 2000WO-US08439.	PR	19-JUN-1998;	98US-089952P.
X	R	15-MAY-2000; 2000WO-US13358.	PR	22-JUN-1998;	98US-090246P.
X	R	17-MAY-2000; 2000WO-US13705.	PR	22-JUN-1998;	98US-090252P.
X	R	22-MAY-2000; 2000WO-US14042.	PR	22-JUN-1998;	98US-090254P.
X	R	30-MAY-2000; 2000WO-US14941.	PR	23-JUN-1998;	98US-090349P.
X	R	02-JUN-2000; 2000WO-US15284.	PR	23-JUN-1998;	98US-090355P.
X	R	28-JUL-2000; 2000WO-US20710.	PR	23-JUN-1998;	98US-090429P.
X	R	11-AUG-2000; 2000WO-US22031.	PR	24-JUN-1998;	98US-090431P.
X	R	23-AUG-2000; 2000WO-US23522.	PR	24-JUN-1998;	98US-090435P.
X	R	24-AUG-2000; 2000WO-US23328.	PR	24-JUN-1998;	98US-090444P.
X	R	08-NOV-2000; 2000WO-US30952.	PR	24-JUN-1998;	98US-090445P.
X	R	01-DEC-2000; 2000WO-US32678.	PR	24-JUN-1998;	98US-090472P.
X	R	28-FEB-2001; 2001WO-US06520.	PR	24-JUN-1998;	98US-090555P.
X	R	01-JUN-2001; 2001WO-US17800.	PR	24-JUN-1998;	98US-090540P.
X	R	20-JUN-2001; 2001WO-US19692.	PR	24-JUN-1998;	98US-090542P.
X	R	29-JUN-2001; 2001WO-US21066.	PR	24-JUN-1998;	98US-090557P.
X	R	09-JUL-2001; 2001WO-US21735.	PR	25-JUN-1998;	98US-090676P.
X	R	16-JUN-1997; 97US-0457872.	PR	25-JUN-1998;	98US-090678P.
X	R	17-OCT-1997; 97US-062250P.	PR	25-JUN-1998;	98US-090690P.
X	R	12-NOV-1997; 97US-065186P.	PR	25-JUN-1998;	98US-090695P.
X	R	13-NOV-1997; 97US-065311P.	PR	25-JUN-1998;	98US-090696P.
X	R		PR	26-JUN-1998;	98US-090862P.
X	R		PR	26-JUN-1998;	98US-090863P.
X	R		PR	01-JUL-1998;	98US-091360P.
X	R		PR	01-JUL-1998;	98US-091544P.



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1441 CGAGATCTCGCTGAGGACACAAACCGAAAGTAAAGCTGTCTTACCACTGCACTG 1500
1441 CGAGATCTCGCTGAGGACACAAACCGAAAGTAAAGCTGTCTTACCACTGCACTG 1500
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2101 TTCTTGTATATGCTTATATTAAGTCTATGGCTGTTTAAAGGACAGATTAATTA 2160
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2161 AATTTAAGACAAAAGTCAAAACA 2185

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RESULT 11

EX90247  
D ABX90247 standard; cDNA; 2185 BP.

X C ABX90247;

X T 01-MAY-2003 (first entry)

X E Human secreted/transmembrane protein cDNA, #93.

X M Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
X W pharmaceutical; diagnostic; therapeutic; gene therapy.

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XX OS Homo sapiens.
XX XX US2002160384-A1.
XX XX 31-OCT-2002.
XX XX 14-NOV-2001; 2001US-0992598.
XX XX 05-NOV-1997; 97WO-US200069.
XX PR 16-SEP-1998; 98WO-US19330.
XX PR 17-SEP-1998; 98WO-US19437.
XX PR 07-OCT-1998; 98WO-US21141.
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 05-JAN-1999; 99WO-US00106.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 01-DEC-1999; 99WO-US28634.
XX PR 16-DEC-1999; 99WO-US30095.
XX PR 20-DEC-1999; 99WO-US30911.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PR 11-FEB-2000; 2000WO-US03565.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 24-FEB-2000; 2000WO-US04914.
XX PR 24-FEB-2000; 2000WO-US05004.
XX PR 02-MAR-2000; 2000WO-US05841.
XX PR 15-MAR-2000; 2000WO-US06319.
XX PR 15-MAR-2000; 2000WO-US06884.
XX PR 20-MAR-2000; 2000WO-US07377.
XX PR 30-MAR-2000; 2000WO-US08439.
XX PR 15-MAY-2000; 2000WO-US13358.
XX PR 17-MAY-2000; 2000WO-US13705.
XX PR 22-MAY-2000; 2000WO-US14042.
XX PR 30-MAY-2000; 2000WO-US14941.
XX PR 02-JUN-2000; 2000WO-US15264.
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XX PR 11-AUG-2000; 2000WO-US22031.
XX PR 23-AUG-2000; 2000WO-US23322.
XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 08-NOV-2000; 2000WO-US30952.
XX PR 01-DEC-2000; 2000WO-US32678.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 01-JUN-2001; 2001WO-US17800.
XX PR 20-JUN-2001; 2001WO-US19692.
XX PR 29-JUN-2001; 2001WO-US21066.
XX PR 09-JUL-2001; 2001WO-US21735.
XX PR 16-JUN-1997; 97US-049787P.
XX PR 17-OCT-1997; 97US-062250P.
XX PR 12-NOV-1997; 97US-065186P.
XX PR 13-NOV-1997; 97US-065311P.
XX PR 24-NOV-1997; 97US-066770P.
XX PR 25-FEB-1998; 98US-075945P.
XX PR 20-MAR-1998; 98US-078910P.
XX PR 28-APR-1998; 98US-083322P.
XX PR 07-MAY-1998; 98US-084600P.
XX PR 28-MAY-1998; 98US-087106P.
XX PR 02-JUN-1998; 98US-087607P.
XX PR 02-JUN-1998; 98US-087609P.
XX PR 02-JUN-1998; 98US-087759P.
XX PR 04-JUN-1998; 98US-088021P.
XX PR 04-JUN-1998; 98US-088025P.
XX PR 04-JUN-1998; 98US-088026P.
XX PR 04-JUN-1998; 98US-088028P.
XX PR 04-JUN-1998; 98US-088029P.
XX PR 04-JUN-1998; 98US-088030P.
XX PR 04-JUN-1998; 98US-088033P.

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PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Garritsen ME, Goddard A, Godowski PU;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI: 2003-258106/28.  
 DR P-PSDB; ABU60541.

XX New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, or in generating probes -

XX Claim 2; Fig 156; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell, expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful in gene therapy, in chromosome  
 CC identification, as chromosome markers, or in generating probes. The PRO  
 CC polypeptides are useful as molecular markers for protein  
 CC electrophoresis, and the isolated nucleic acids may be used for  
 CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
 CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 CC in diagnostic assays for PRO, and in affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The sequences presented in  
 CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
 CC probes detecting the PRO polynucleotides of the invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

XX Query Match 100.0%; Score 2185; DB 25; Length 2185;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTCGAGCCAAATCCCGAGGATGGTGAATTATGAACGTCACACCATGA 60

Db 1 GTTCTCTTCGAGCCAAATCCCGAGGATGGTGAATTATGAACGTCACACCATGA 60  
 QY 61 AGCTCTTTGGCAGGTAACTGTGACCAACCACTGGAATGCCATCTGTCTCCGTTGG 120  
 Db 61 AGCTCTTTGGCAGGTAACTGTGACCAACCACTGGAATGCCATCTGTCTCCGTTGG 120  
 QY 121 TCTACCTCAGCGGCAAGTGTGGATTCTGTGTGACGACCATGCTCTCCGCTCAGCGG 180  
 Db 121 TCTACCTCAGCGGCAAGTGTGGATTCTGTGTGACGACCATGCTCTCCGCTCAGCGG 180  
 QY 181 GGCCCCAGAACTCCGCTTCCTGCTGTCAGTAACTGTCAGCAAGGTGGTGTGA 240  
 Db 181 GGCCCCAGAACTCCGCTTCCTGCTGTCAGTAACTGTCAGCAAGGTGGTGTGA 240  
 QY 241 CGCGCCGGGGCTCTCCGAGGTCCCGAGGATATCCCTCGAAACACCCGGTACCTCAACC 300  
 Db 241 CGCGCCGGGGCTCTCCGAGGTCCCGAGGATATCCCTCGAAACACCCGGTACCTCAACC 300  
 QY 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACACCTGG 360  
 Db 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACACCTGG 360  
 QY 361 AGGTCTCGAGTTGGGCGAGAACTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCC 420  
 Db 361 AGGTCTCGAGTTGGGCGAGAACTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCC 420  
 QY 421 TGGCCAGACCTCAACACCTCGAGAGCTGTTCCGAACTGGCTGACAGTCACTCCTACGCGGG 480  
 Db 421 TGGCCAGACCTCAACACCTCGAGAGCTGTTCCGAACTGGCTGACAGTCACTCCTACGCGGG 480  
 QY 481 CTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACCAACCCCATCGAAGCA 540  
 Db 481 CTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACCAACCCCATCGAAGCA 540  
 QY 541 TCCCTCTTACGCTTCAACCGGTCGCTCCCTCATCGGCTGACATTTGGGCGGAGCTCA 600  
 Db 541 TCCCTCTTACGCTTCAACCGGTCGCTCCCTCATCGGCTGACATTTGGGCGGAGCTCA 600  
 QY 601 AGAGCTGAGTATATCTCTGAGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660  
 Db 601 AGAGCTGAGTATATCTCTGAGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660  
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 Db 661 ACTTGGGCACTGTGCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGCTGGAGG 720  
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 Db 721 AGCTGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGCCCTGA 780  
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 Db 781 GCTCCCTCAGGAGCTCTGGGTCATGAATCAGAGTCAAGTCAAGTCAAGGGAATGCTT 840  
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 Db 841 TTGAGCGGCTGCTCTTCACTTGTGGAATCAACTTGGGCCCAATAAACCCTCTCTTTTC 900  
 QY 901 CCCATGACCTCTTTACCGGCTGAGGTACCTGCTGGAGTTCATCTACACCAACCCCTT 960  
 Db 901 CCCATGACCTCTTTACCGGCTGAGGTACCTGCTGGAGTTCATCTACACCAACCCCTT 960  
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 Db 961 GGAACTGTGATGTGACATTTCTGCTGCTAGCTGCTGCTTTCGAGAGTATATACCCACCA 1020  
 QY 1021 ATTCCACCTGCTGTGGCGCTGTGATGCTCCCATGCAATCGAGGCGGCTTACCTCTGGG 1080  
 Db 1021 ATTCCACCTGCTGTGGCGCTGTGATGCTCCCATGCAATCGAGGCGGCTTACCTCTGGG 1080  
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1501 GTTACACAGCGGCACTATACCACTTACCAAGCTGTCTTCTTCCAGACTACCGGTGTCCTCA 1560  
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2101 TTTCTGTATGCTTATATTAAGTGTATGCTGTGTTAAAAAACAAGATTAATTA 2160  
2161 AATTTAAGACAAAAGTCAAAACA 2185  
2161 AATTTAAGACAAAAGTCAAAACA 2185

RESULT 12  
ABX77858  
ID ABX77858 standard; cDNA; 2185 BP.  
XX  
AC ABX77858;  
XX  
DT 14-APR-2003 (first entry)  
XX  
Human PRO polynucleotide #64.  
XX  
Human; PRO; gene; ss: cytosolic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADERT;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027163-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997666.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06684.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
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PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
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PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-DEC-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.

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PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
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DB 61 AGCTCTTGTGGCAGTAACTGTGCACCAACACACACTGCAATGCCATCTGCTCCGTTG 120
QY 121 TCTACTCAGCGCGCAAGTGGATTCTGTGTGAGCATGCTGTGCGGCTCAGCG 180
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DT 17-APR-2003 (first entry)

XX Human secreted/transmembrane protein cDNA, #93.  
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 KW pharmacological; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
 XX Homo sapiens.  
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 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen WE, Goddard A, Godowski P;  
 PI Grimaldi JC, Gurney RJ, Kijavini J, Napier MA, Pan J, Paoni NP;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

WPI: 2003-155950/15.

P-PSDB; ABUS8963.

PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Claim 2; Fig 156; 647pp; English.

CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention.

CC Note: The sequence data for this patent is also available in electronic

% format from USPTO at seqdata.uspto.gov/sequence.html.

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%X Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;
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%Z Best Local Similarity 100.0%; Pred. No. 0;
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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961 GGAACGTGATGTGACATTCGTGGGTAGCTGCTGGTCTCGAGAGTATATACCCACCA 1020

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%Y 1021 ATTCCACCTGCTGTCGCGCTGTCATGCTCCCATGACATGCGAGGCGCTACTCGTGG 1080
%Z 1021 ATTCCACCTGCTGTCGCGCTGTCATGCTCCCATGACATGCGAGGCGCTACTCGTGG 1080
%Y 1081 AGTGGACACGAGGCTCTCCAGTCTCTCCGCTTTCATCATGAGGACCACTCGAGACC 1140
%Z 1081 AGTGGACACGAGGCTCTCTCCAGTCTCTCCGCTTTCATCATGAGGACCACTCGAGACC 1140
1141 TCAACATTTCTGAGGGTTCGATGCGAGAACTTAAGTGTGCGACTTCCCTATGCTCTCG 1200
1141 TCAACATTTCTGAGGGTTCGATGCGAGAACTTAAGTGTGCGACTTCCCTATGCTCTCG 1200
1201 TGAAGTGTGCTGCCCAATGGGACAGTGTGAGCGCACTCCAGCGCTCCCGCCACCAAGATCT 1260
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1261 CTGTCTCTCAACGAGCGGCACTTGAACCTTTTCCACGCTGCTTTCAGACACTGGGGTGT 1320
1261 CTGTCTCTCAACGAGCGGCACTTGAACCTTTTCCACGCTGCTTTCAGACACTGGGGTGT 1320
1321 ACACATGATGCTGACCAATGTTGCGAGGCACTCCAGCGCTCGGCTACTCTCAATGTGA 1380
1321 ACACATGATGCTGACCAATGTTGCGAGGCACTCCAGCGCTCGGCTACTCTCAATGTGA 1380
1381 GCACGGCTGAGCTTTAAACCTCCAACTACAGCTTCTTCCACAGTAACAGTGGAGACCA 1440
1381 GCACGGCTGAGCTTTAAACCTCCAACTACAGCTTCTTCCACAGTAACAGTGGAGACCA 1440
1441 CGGAGATCTCGCTGAGGACACACACGCGAAGTACAGCGCTGTTCTTCCACAGTCCACTG 1500
1441 CGGAGATCTCGCTGAGGACACACACGCGAAGTACAGCGCTGTTCTTCCACAGTCCACTG 1500
1501 GTTACCGAGCGGCAATATACCACTTACCACTTACCACTGCTTTCAGACTACCCGTTGCCA 1560
1501 GTTACCGAGCGGCAATATACCACTTACCACTTACCACTGCTTTCAGACTACCCGTTGCCA 1560
1561 AGCAGGTGGAGTATCCCGGAGACACACCTGACAGATGCGAGACCGAGCTGGATGAG 1620
1561 AGCAGGTGGAGTATCCCGGAGACACACCTGACAGATGCGAGACCGAGCTGGATGAG 1620
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1741 CGCGCGGAGCTGTTGAGTATCCAGGTGCGAGAGACATCCCGAGCAACATCCGCGAG 1800
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1921 GCCTGGGAACTCTCTGCAACCCCACTGACCTATCTCTGAACCTTATATATTCAGA 1980
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1981 CCCATACCAAGGACAAAGTACAGGAACTCAAAATATGACTCCCTCCCAAAACTTAA 2040
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Db 2101 TTCTGTATATGCTATATATTAAGTCTATGCGCTGTTAAAAAACAAGATTTATATAA 2160  
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Db 2161 AATTTAAACAAAAAGTCAAAACA 2185

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AC ABX64093;  
XX  
XX 26-FEB-2003 (first entry)  
XX cDNA encoding human PRO1111 polypeptide.  
DE Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gens; ss.  
XX Homo sapiens.  
OS  
PN US2002103125-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 20-NOV-2001; 2001US-0989731.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US0106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04514.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
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PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088367P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 18-JUN-1998; 98US-088810P.  
PR 18-JUN-1998; 98US-088824P.  
PR 18-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
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PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH LTD.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
Zhang Z;

WFI; 2003-102117/09.  
P-PSDB; ABU13923.

Novel secreted and transmembrane polypeptide for modulating biological  
activity of cell expressing the polypeptide, identifying agonists or  
antagonists of polypeptide, and as molecular weight markers -

Claim 2; Fig 156; 649pp; English.

The present invention relates to the isolation of novel human PRO  
polypeptides, and the polynucleotide sequences encoding them. The



PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at [seqdata.uspto.gov/psipsDIDEntry.html](http://seqdata.uspto.gov/psipsDIDEntry.html).

Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 25; Length 2185;  
 Best Local Similarity 100.0%; P-Ed. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GTCTCTCTCCGAGCCAAATCCGAGCGATGGTGAATATGAACGTGCCACCATGA 60  
 b 1 GTCTCTCTCCGAGCCAAATCCGAGCGATGGTGAATATGAACGTGCCACCATGA 60  
 Y 61 AGCTCTTGTGGCAGGTAACTGTGCACACACACCTGGAAATGCCATCTCTCCCGTCG 120  
 b 61 AGCTCTTGTGGCAGGTAACTGTGCACACACACCTGGAAATGCCATCTCTCCCGTCG 120  
 Y 121 TCTACCTCAGCGGCAAGTGTGAATCTGTGTGAGCCATTCCTGTGCTCCGCTCAGCG 180  
 b 121 TCTACCTCAGCGGCAAGTGTGAATCTGTGTGAGCCATTCCTGTGCTCCGCTCAGCG 180  
 Y 181 GGCCCGCAGAACTCCCTCCCTTGTCTGTGAGTAAACAGTTCAGCAAGGTGTGTGA 240  
 b 181 GGCCCGCAGAACTCCCTCCCTTGTCTGTGAGTAAACAGTTCAGCAAGGTGTGTGA 240  
 Y 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGATTCCTCTCGAACAACCGGTACCTCAACC 300  
 b 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGATTCCTCTCGAACAACCGGTACCTCAACC 300  
 Y 301 TCAATGAGAACACATCCAGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGAT 360  
 b 301 TCAATGAGAACACATCCAGATCCAGGATCCAGGATCCAGGATCCAGGATCCAGGAT 360  
 Y 361 AGTCTCTGAGTGGGAGCAACTCCATCCGAGGATTCAGGTGGGGGCTTCAACGGCC 420  
 b 361 AGTCTCTGAGTGGGAGCAACTCCATCCGAGGATTCAGGTGGGGGCTTCAACGGCC 420  
 Y 421 TGGCGAGCTCAACAGCTGGAGCTTGTGACNACTGGGCTGAGTCACTCCCTAGCGGG 480  
 b 421 TGGCGAGCTCAACAGCTGGAGCTTGTGACNACTGGGCTGAGTCACTCCCTAGCGGG 480  
 Y 481 CTTTGAATACCTGTCCAACTCCGAGCTTGTGGCTTCGCAACACCCCAATCGAAGCA 540  
 b 481 CTTTGAATACCTGTCCAACTCCGAGCTTGTGGCTTCGCAACACCCCAATCGAAGCA 540  
 Y 541 TCCCTCTTACGGCTTCAACCGGGTGCCTTCTCATGCGCTGAGCTTGGGGGAGCTCA 600  
 b 541 TCCCTCTTACGGCTTCAACCGGGTGCCTTCTCATGCGCTGAGCTTGGGGGAGCTCA 600  
 Y 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTGTGAGGGGCTTCAACCTCAAGTATCTGA 660  
 b 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTGTGAGGGGCTTGTCAACCTCAAGTATCTGA 660  
 Y 661 ACTTGGGCATGTGCAACATTAAGACATGCCCAATCTCAACCCCTGTGGGCTGGAGG 720  
 b 661 ACTTGGGCATGTGCAACATTAAGACATGCCCAATCTCAACCCCTGTGGGCTGGAGG 720

721 AGCTGGAGATGTCCAGGAAACCACTTCCCTGAGATCAGGCTCGCTCTTCCATGSCCTGA 780  
 Db AGCTGGAGATGTCCAGGAAACCACTTCCCTGAGATCAGGCTCGCTCTTCCATGSCCTGA 780  
 Y 781 GCTCCCTCAAGAGCTCTGGGTGATGAATCTCAGAGTCAAGCTGAGCTGATGAGCGGATGTT 840  
 Db GCTCCCTCAAGAGCTCTGGGTGATGAATCTCAGAGTCAAGCTGAGCTGATGAGCGGATGTT 840  
 Y 841 TTGACGGGCTGGCTTCACTGTGGAACTCAACTTGGGCCCAATAAACCCTCTCTTTTTCG 900  
 Db TTGACGGGCTGGCTTCACTGTGGAACTCAACTTGGGCCCAATAAACCCTCTCTTTTTCG 900  
 Y 901 CCATGACCTCTTTTACCCGCTGAGGTACTCTGTGAGTGTGATCTACACCAACCTTT 960  
 Db CCATGACCTCTTTTACCCGCTGAGGTACTCTGTGAGTGTGATCTACACCAACCTTT 960  
 Y 961 GGAACGTGATGTGACATCTGTGGCTAGCTGTGGTGGCTTGGAGGTATATACCCACCA 1020  
 Db GGAACGTGATGTGACATCTGTGGCTAGCTGTGGTGGCTTGGAGGTATATACCCACCA 1020  
 Y 1021 ATTCCACCTGTGTGGCGCTGTCACTGCTCCATGACATGAGGCGCTACCTCTGTGG 1080  
 Db ATTCCACCTGTGTGGCGCTGTCACTGCTCCATGACATGAGGCGCTACCTCTGTGG 1080  
 Y 1081 AGTGGACAGGCTCTCTTCCAGTGTCTGCCCTTTCATCATGAGCAGCCTCGAGACC 1140  
 Db AGTGGACAGGCTCTCTTCCAGTGTCTGCCCTTTCATCATGAGCAGCCTCGAGACC 1140  
 Y 1141 TCAACATTTCTGAGGTCGGATGGCAGAACTTAAAGTGTGGACTCCCCCTATGTCTCGG 1200  
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 Y 1201 TGAAGTGTGTGCCCAATGGAGGAGTCTCAGCCAGCTCCCGCCACCAAGATCT 1260  
 Db TGAAGTGTGTGTGCCCAATGGAGGAGTCTCAGCCAGCTCCCGCCACCAAGATCT 1260  
 Y 1261 CTGTCTCTCAACGAGCAGCTTGAACCTTTTCCACGCTGTCTTTTTCAGACACTGGGGTGT 1320  
 Db CTGTCTCTCAACGAGCAGCTTGAACCTTTTCCACGCTGTCTTTTTCAGACACTGGGGTGT 1320  
 Y 1321 ACATGTCATGTGACCAATGTGGAGGAACTCCAGCTCCGCTCGGCTACCTCAATGTA 1380  
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 Y 1381 GCACGGCTGAGCTTAAACCTCCACTCAGCTTCTTCAACACAGTAAACAGTGGAGACCA 1440  
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 Y 1441 CGGAGTCTCGCTGAGGACACAAACGAGGAGTACAGCTGTCTTCTTCTACCACTGCTG 1500  
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 Y 1501 GTTACAGCGCGCATATACCACTTACCACTGCTCTTCACTCAGACTACCTGTGCGCA 1560  
 Db GTTACAGCGCGCATATATCACTTACCACTGCTCTTCACTCAGACTACCTGTGCGCA 1560  
 Y 1561 AGCAGTGGCAGTACCGGAGACACCACTGACAAAGTACAGCTGAGCTTGGATGAAG 1620  
 Db AGCAGTGGCAGTACCGGAGACACCACTGACAAAGTACAGCTGAGCTTGGATGAAG 1620  
 Y 1621 TCATGAGACCAACAGATCATCTTGGCTGTCTTGTGGCAGTGTCTGTCTGTCTGTCTG 1680  
 Db TCATGAGACCAACAGATCATCTTGGCTGTCTTGTGGCAGTGTCTGTCTGTCTGTCTG 1680  
 Y 1681 CCATGTTGATGTCTTCTATAAATTCGTAAGCGGCAACAGAGGAGTACAGTCAACAG 1740  
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 Y 1741 CCAGCGGAGCTGTGAGATATCCAGGTGGAGGAGTATCCAGCAGCAGCAGCAGCAGCAG 1800  
 Db CCAGCGGAGCTGTGAGATATCCAGGTGGAGGAGTATCCAGCAGCAGCAGCAGCAGCAG 1800  
 Y 1801 CAGCAACAGCAGCTCGCTCGGTGTATCAGGTGAGGGGGCAGTGTGTGTGTGTGTGTGT 1860

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Db      1801  CAGCAACAGCAGCTCCGTCGGGTGTATCAGGTGAGGGGCGAGTAGTCTGCCCAATTC 1860
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Db      1861  ATGACCATATTAACATAACACCTACAAACCCAGACACATGGGGCCCACTGGACAGAAAACA 1920
Qy      1921  GCCTGGGAACCTCTGCACCCACAGTCACACATCTCTGAACCTTATATTAATTCAGA 1980
Db      1921  GCCTGGGAACCTCTGCACCCACAGTCACACATCTCTGAACCTTATATTAATTCAGA 1980
Qy      1981  CCATACCAAGACAAAGGTACAGGAACCTCAAAATATGACTCCCTCCCAAAAACTTA 2040
Db      1981  CCATACCAAGACAAAGGTACAGGAACCTCAAAATATGACTCCCTCCCAAAAACTTA 2040
Qy      2041  TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT 2100
Db      2041  TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT 2100
Qy      2101  TTCCTGTATATGCTTATATATTAATTAAGTCTATGGCTGGTTAAATAAAACAGATATATTA 2160
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Db      2161  AATTTAAAGACAAAAGTCAAAAACA 2185

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RESULT 15

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ABX17057
ID      ABX17057 standard; cDNA; 2185 BP.
AC      ABX17057;
XX      Human PRO polynucleotide #64.
DT      04-FEB-2003 (first entry)
DE      Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW      toxin; radioabel; cell death; gene mapping; chromosome mapping;
KW      protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;
KW      antibacterial.
XX      Homo sapiens.
XX      US2602123463-A1.
PD      05-SEP-2002.
XX      19-NOV-2001; 2001US-0989732.
XX      05-NOV-1997; 97WO-US20069.
XX      16-SEP-1998; 98WO-US19330.
XX      17-SEP-1998; 98WO-US19437.
XX      07-OCT-1998; 98WO-US21141.
XX      01-DEC-1998; 98WO-US25108.
XX      05-JAN-1999; 99WO-US00106.
XX      08-MAR-1999; 99WO-US05028.
XX      02-JUN-1999; 99WO-US12252.
XX      15-SEP-1999; 99WO-US21547.
XX      30-NOV-1999; 99WO-US28313.
XX      01-DEC-1999; 99WO-US28301.
XX      16-DEC-1999; 99WO-US28634.
XX      20-DEC-1999; 99WO-US30095.
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XX      11-FEB-2000; 2000WO-US00376.
XX      18-FEB-2000; 2000WO-US03565.
XX      22-FEB-2000; 2000WO-US04341.
XX      24-FEB-2000; 2000WO-US04414.
XX      24-FEB-2000; 2000WO-US04914.
XX      24-FEB-2000; 2000WO-US05004.

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PR      02-MAR-2000; 2000WO-US05841.
PR      10-MAR-2000; 2000WO-US06319.
PR      15-MAR-2000; 2000WO-US06884.
PR      20-MAR-2000; 2000WO-US07377.
PR      30-MAR-2000; 2000WO-US08439.
PR      15-MAY-2000; 2000WO-US13358.
PR      17-MAY-2000; 2000WO-US13705.
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PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15264.
PR      28-JUL-2000; 2000WO-US20710.
PR      11-AUG-2000; 2000WO-US22031.
PR      23-AUG-2000; 2000WO-US23522.
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PR      01-DEC-2000; 2000WO-US32678.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
PR      16-JUN-1997; 97US-049787P.
PR      17-OCT-1997; 97US-062505P.
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PR      24-NOV-1997; 97US-066770P.
PR      25-FEB-1998; 98US-075945P.
PR      20-MAR-1998; 98US-078910P.
PR      28-APR-1998; 98US-083322P.
PR      07-MAY-1998; 98US-084600P.
PR      28-MAY-1998; 98US-087106P.
PR      02-JUN-1998; 98US-087607P.
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PR      02-JUN-1998; 98US-087759P.
PR      03-JUN-1998; 98US-087827P.
PR      04-JUN-1998; 98US-088021P.
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PR      05-JUN-1998; 98US-088212P.
PR      05-JUN-1998; 98US-088217P.
PR      09-JUN-1998; 98US-088655P.
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PR      10-JUN-1998; 98US-088826P.
PR      11-JUN-1998; 98US-088858P.
PR      11-JUN-1998; 98US-088861P.
PR      11-JUN-1998; 98US-088876P.
PR      12-JUN-1998; 98US-089105P.
PR      16-JUN-1998; 98US-089440P.
PR      16-JUN-1998; 98US-089512P.
PR      16-JUN-1998; 98US-089514P.
PR      17-JUN-1998; 98US-089532P.
PR      17-JUN-1998; 98US-089538P.
PR      17-JUN-1998; 98US-089598P.
PR      17-JUN-1998; 98US-089599P.
PR      17-JUN-1998; 98US-089600P.
PR      17-JUN-1998; 98US-089653P.
PR      18-JUN-1998; 98US-089801P.
PR      18-JUN-1998; 98US-089907P.
PR      18-JUN-1998; 98US-089908P.
PR      28-AUG-2001; 2001US-0941992.
XX      (GETH ) GENENTECH INC.
PA

```

X I Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 I I Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Gowski PJ;  
 I I Grimaldi JC, Gurney AL, Kijavlin IU, Napier MA, Pan J, Paoni NF;  
 I I Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WI;  
 I I Zhang Z;  
 X R WFI: 2003-066810/06.  
 R R P-PSDB; ABU10879.  
 X X Novel secreted and transmembrane polypeptide for modulating biological  
 T activity of cell expressing the polypeptide, identifying agonists or  
 T antagonists of polypeptide, and as molecular weight markers -  
 X S Claim 2: Fig 156; 655pp; English.  
 X C The invention relates to a secreted and transmembrane polypeptide, termed  
 C PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 C useful for detecting PRO polypeptides and for linking a bioactive  
 C molecule to a cell expressing the above polypeptides, where the bioactive  
 C molecule is a toxin, radiolabel or an antibody. The bioactive material  
 C causes the death of the cell. The polypeptide is useful for identifying  
 C agonists or antagonists of the PRO polypeptide, for preparing variants of  
 C PRO, as a molecular weight marker for protein electrophoresis purposes  
 C and the PRO polynucleotide is useful for recombinantly expressing those  
 C markers. The polynucleotide is also useful as a hybridisation probe, in  
 C chromosome and gene mapping, in generation of antisense RNA and DNA, in  
 C the preparation of PRO polypeptide, for generating transgenic animals or  
 C knockout animals which in turn are useful in the development and  
 C screening of therapeutically useful reagents, to construct hybridisation  
 C probes for mapping the gene which encodes PRO and for the genetic  
 C analysis of individuals with genetic disorders, in gene therapy, for  
 C chromosome identification, as a chromosome marker and for generating  
 C probes for PCR, Northern analysis, Southern analysis and Western  
 C analysis. This sequence represents a human PRO polynucleotide of the  
 C invention.  
 X Q Sequence 2185 BP; 527 A; 666 C; 519 G; 473 T; 0 other;

Query Match 100.0%; Score 2185; DB 25; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTCTCTTCCGAGGCAAAATCCAGGCAATGGTGAATATGAAAGTGGCCACCATGA 60  
 1 GTTCTCTTCCGAGGCAAAATCCAGGCAATGGTGAATATGAAAGTGGCCACCATGA 60  
 61 AGCTCTTGTGCGAGTAACGTGTCACACACACACCTGGAGTGCATCTGCTCCGCTCG 120  
 61 AGCTCTTGTGCGAGTAACGTGTCACACACACACCTGGAGTGCATCTGCTCCGCTCG 120  
 121 TCTACCTCAGCGGCAAGTGTGGATTCTGTGTCAGGCAATGCTGTGCTGCGGCTCAGCG 180  
 121 TCTACCTCAGCGGCAAGTGTGGATTCTGTGTCAGGCAATGCTGTGCTGCGGCTCAGCG 180  
 181 GGGCCGAGAACTGCGCTTGTGTCGTCAGTAAACCAATTCAGCAAGTGGTGTGCA 240  
 181 GGGCCGAGAACTGCGCTTGTGTCGTCAGTAAACCAATTCAGCAAGTGGTGTGCA 240  
 241 CGCGCCGGGGCTCTCCGAGGTCCGCGAGGATATCCCTCGAACACCGGTACCTCAAC 300  
 241 CGCGCCGGGGCTCTCCGAGGTCCGCGAGGATATCCCTCGAACACCGGTACCTCAAC 300  
 301 TCATGGAGAACACATCCAGATGATCCAGGCGACACCTTCGCGCACTCCACCACTGG 360  
 301 TCATGGAGAACACATCCAGATGATCCAGGCGACACCTTCGCGCACTCCACCACTGG 360  
 361 AGGTCCTGCAAGTGGGAGCAATCCCATCCGAGATTTAGAGTGGGGGCTTCAACGGGC 420  
 361 AGGTCCTGCAAGTGGGAGCAATCCCATCCGAGATTTAGAGTGGGGGCTTCAACGGGC 420  
 421 TGGCCAGCCTCAACACCTGAGCTGTGTGCAAACTGGCTGACAGTCACTCCCTAGCGGG 480

Db 421 TGGCCAGCCTCAACACCTTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG 480  
 Qy 481 CTTTGAATACCTGTCCAAAGTCCGGAGCTCTGGCTTCGCAACACCCCTCGAAAGCA 540  
 Db 481 CTTTGAATACCTGTCCAAAGTCCGGAGCTCTGGCTTCGCAACACCCCTCGAAAGCA 540  
 Qy 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTTGGAGCTTGGGGAGCTCA 600  
 Db 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTTGGAGCTTGGGGAGCTCA 600  
 Qy 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGTGTTCAACCTCAAGTATCTGA 660  
 Db 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGTGTTCAACCTCAAGTATCTGA 660  
 Qy 661 ACTTGGGCTGTCGAACATTAAGACATGCCCAATCTCAACCCCTGCTGGGCTGGAGG 720  
 Db 661 ACTTGGGCTGTCGAACATTAAGACATGCCCAATCTCAACCCCTGCTGGGCTGGAGG 720  
 Qy 721 AGCTGGAGATGTCCAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTTCCATGGCTGA 780  
 Db 721 AGCTGGAGATGTCCAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTTCCATGGCTGA 780  
 Qy 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGACTCAGCTCAGCTGATGAGCGGAATGCTT 840  
 Db 781 GCTCCCTCAAGAGCTCTGGGTATGAACTCAGACTCAGCTCAGCTGATGAGCGGAATGCTT 840  
 Qy 841 TTGACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATAAACCCTCTCTTTTTC 900  
 Db 841 TTGACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATAAACCCTCTCTTTTTC 900  
 Qy 901 CCCATGACCTTTTACCCCTGAGTACCTGTGTGAGTGTGATCTACACCAACCTCTT 960  
 Db 901 CCCATGACCTTTTACCCCTGAGTACCTGTGTGAGTGTGATCTACACCAACCTCTT 960  
 Qy 961 GGAATCTGATTTGACATCTGTGGCTAGCTGCTGCTTGGAGTATATACCCACCA 1020  
 Db 961 GGAATCTGATTTGACATCTGTGGCTAGCTGCTGCTTGGAGTATATACCCACCA 1020  
 Qy 1021 ATTCCACTGCTGTGGCGCTGTCTCCATGCAATGCAATGCAATGCAATGCAATGCA 1080  
 Db 1021 ATTCCACTGCTGTGGCGCTGTCTCCATGCAATGCAATGCAATGCAATGCAATGCA 1080  
 Qy 1081 AGGTGACCAAGGCTCTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Db 1081 AGGTGACCAAGGCTCTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Qy 1141 TCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGTGGAGTCTCCCTCTATGCTCCG 1200  
 Db 1141 TCAACATTTCTGAGGGTGGATGGCAGAACTTAAGTGTGGAGTCTCCCTCTATGCTCCG 1200  
 Qy 1201 TGAAGTGGTGTGCTGCCAATGGGACAGTGTCTCAGCCAGCTCCCGCACCCAGGATCT 1260  
 Db 1201 TGAAGTGGTGTGCTGCCAATGGGACAGTGTCTCAGCCAGCTCCCGCACCCAGGATCT 1260  
 Qy 1261 CTGTCTCTCAACGAGGCACTCTGAACTTTTCCCACTGCTGCTTTCAGACACTGGGGTGT 1320  
 Db 1261 CTGTCTCTCAACGAGGCACTCTGAACTTTTCCCACTGCTGCTTTCAGACACTGGGGTGT 1320  
 Qy 1321 ACACATGCTGTGAGCAATGTTGCGAGGCACTCTCAGAGCTGCTTACCTCAAGTGA 1380  
 Db 1321 ACACATGCTGTGAGCAATGTTGCGAGGCACTCTCAGAGCTGCTTACCTCAAGTGA 1380  
 Qy 1381 GCAGGCTGAGCTTTAACCACTCTCAACTTCTTCCACAGTAACAGTGGAGACCA 1440  
 Db 1381 GCAGGCTGAGCTTTAACCACTCTCAACTTCTTCCACAGTAACAGTGGAGACCA 1440  
 Qy 1441 CGGAGATCTCGCTGAGGACCAACCGGAAAGTAAAGCTGTTCCTACCCGCTCCACTG 1500  
 Db 1441 CGGAGATCTCGCTGAGGACCAACCGGAAAGTAAAGCTGTTCCTACCCGCTCCACTG 1500  
 Qy 1501 GTTACAGCGGGATATACCACTCTACCGGTGCTCATTTAGAGTACCTCCGCTGCCCA 1560  
 Db 1501 GTTACAGCGGGATATACCACTCTACCGGTGCTCATTTAGAGTACCTCCGCTGCCCA 1560

2y	1561	AGCAGTGGCAGTACCGCGACGACACACCACTGACAGATGACAGCAGCCTCGATGAAG	1620	PR	02-MAR-2000;	2000US-0186350.
2y	1561	AGCAGTGGCAGTACCGCGACGACACCACTGACAGATGACAGCAGCCTCGATGAAG	1620	PR	16-MAR-2000;	2000US-0189874.
2y	1561	AGCAGTGGCAGTACCGCGACGACACCACTGACAGATGACAGCAGCCTCGATGAAG	1620	PR	17-MAR-2000;	2000US-0190076.
2y	1621	TCATGAAGACCAACCAAGATCATCTGGCTGCTTTGTGGCAGTGACTCTGCTAGCTGCCG	1680	PR	18-APR-2000;	2000US-0198123.
2y	1621	TCATGAAGACCAACCAAGATCATCTGGCTGCTTTGTGGCAGTGACTCTGCTAGCTGCCG	1680	PR	19-MAY-2000;	2000US-0205515.
2y	1681	CCATGTTGATGTTCTTCTATTAACCTTCGTAAAGCGCACCGAGCGGAGTACAGTCAAG	1740	PR	07-JUN-2000;	2000US-0209467.
2y	1681	CCATGTTGATGTTCTTCTATTAACCTTCGTAAAGCGCACCGAGCGGAGTACAGTCAAG	1740	PR	28-JUN-2000;	2000US-0214886.
2y	1741	CCGCCCCGAGCTGTTGAGATATCCAGGTGACGACGAAGACATCCCGACGAGCAATCCCGCAG	1800	PR	30-JUN-2000;	2000US-0215135.
2y	1741	CCGCCCCGAGCTGTTGAGATATCCAGGTGACGACGAAGACATCCCGACGAGCAATCCCGCAG	1800	PR	07-JUL-2000;	2000US-0216647.
2y	1801	CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGGCAGTAGTCTGCCCAATTC	1860	PR	07-JUL-2000;	2000US-0216880.
2y	1801	CAGCAACAGCAGCTCCGTCGGGTGATCAGGTGAGGGGGCAGTAGTCTGCCCAATTC	1860	PR	11-JUL-2000;	2000US-0217487.
2y	1861	ATGACCATATTAACTACAAACACCTTACAAACAGCAGCAGTGGGGCCACTGGACAGAAAACA	1920	PR	11-JUL-2000;	2000US-0217496.
2y	1861	ATGACCATATTAACTACAAACACCTTACAAACAGCAGCAGTGGGGCCACTGGACAGAAAACA	1920	PR	14-JUL-2000;	2000US-0218290.
2y	1921	GCCTGGGGAATCTCTGACCCGACAGTACCACTATCTCTGAACTTATATTAATTCAGA	1980	PR	26-JUL-2000;	2000US-0220963.
2y	1921	GCCTGGGGAATCTCTGACCCGACAGTACCACTATCTCTGAACTTATATTAATTCAGA	1980	PR	26-JUL-2000;	2000US-0220964.
2y	1981	CCCATACCAAGGACAGGTACGAGAACTCAATATGACTCCCTCCCGCAAAACTTTA	2040	PR	14-AUG-2000;	2000US-0224518.
2y	1981	CCCATACCAAGGACAGGTACGAGAACTCAATATGACTCCCTCCCGCAAAACTTTA	2040	PR	14-AUG-2000;	2000US-0224519.
2y	2041	TAAATGCAATAGAAATGACACCAAGGACAGCACTTTGTACAGAGTGGGGAGAGACTTT	2100	PR	14-AUG-2000;	2000US-0225213.
2y	2041	TAAATGCAATAGAAATGACACCAAGGACAGCACTTTGTACAGAGTGGGGAGAGACTTT	2100	PR	14-AUG-2000;	2000US-0225214.
2y	2101	TTCCTGTATATGCTTATATATTTAGTCTATGGCTGTTAAAGAAACAGATTATATTA	2160	PR	14-AUG-2000;	2000US-0225266.
2y	2101	TTCCTGTATATGCTTATATATTTAGTCTATGGCTGTTAAAGAAACAGATTATATTA	2160	PR	14-AUG-2000;	2000US-0225267.
2y	2161	AATTTAAGACAAAAGTCAAAACA	2185	PR	14-AUG-2000;	2000US-0225270.
2y	2161	AATTTAAGACAAAAGTCAAAACA	2185	PR	14-AUG-2000;	2000US-0225447.
AC	AAS28823; standard; cDNA; 2324 BP.					
AC	AAS28823;					
DT	07-NOV-2001 (first entry)					
DE	Human immunoglobulin encoding cDNA SEQ ID No 69.					
KW	Immunoglobulin; primer; signal transduction pathway protein; cancer; ss;					
KW	antisense therapy; gene therapy; neurological disorder; renal disorder;					
KW	cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;					
KW	reproductive disorder; immune system disorder; proliferative disorder;					
KW	muscular disorder.					
OS	Homo sapiens.					
PN	WC20015315-A2.					
XX	02-AUG-2001.					
PD	17-JAN-2001; 2001WO-US01326.					
PF	31-JAN-2000; 2000US-0179065.					
XX	04-FEB-2000; 2000US-0180628.					
PR	24-FEB-2000; 2000US-0184664.					
PR	02-OCT-2000; 2000US-0237037.					
PR	02-OCT-2000; 2000US-0237038.					
PR	02-OCT-2000; 2000US-0237039.					







C and nucleic acid molecules encoding such polypeptides. Sequences of the  
C invention are useful for treating diseases such as Alzheimer's disease,  
C amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases  
C of the immune system, haematopoietic disease, inflammation, anxiety,  
C schizophrenia, feeding disorders, anorexia, depression, social, sexual  
C and memory alteration, cardiovascular disease, sleep disorder, learning  
C cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment  
C of transsexuals, growth abnormalities, obesity, infections, autoimmune  
C diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,  
C disorders associated with healthy maintenance of gastric mucosa and  
C repair of acute and chronic mucosal lesion, lung carcinoma, cerebral  
C ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,  
C annesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,  
C congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,  
C viral and non-viral hepatitis, type I and type II diabetes mellitus,  
C glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic  
C paralyses, tendinitis and malignant hyperthermia. Polypeptides of the  
C invention are used to identify membrane bound and soluble receptors.  
C They are also useful as vaccines for inducing an immunological response  
C in a mammal. Polynucleotides of the invention are used in gene therapy.  
C They are also valuable for chromosome localisation studies and tissue  
C expression studies.

X Sequence 1962 BP; 444 A; 622 C; 482 G; 414 T; 0 other;

Query Match 87.5%; Score 1911; DB 22; Length 1962;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1962; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

57 ATGAAGCTCTTGTGGAGTAACTGTGCACACACACCTGGATCCATCTGCTCCCG 116  
1 ATGAAGCTCTTGTGGAGTAACTGTGCACACACACCTGGATCCATCTGCTCCCG 60  
117 TTCTCTACTCTCAGCGCAAGTGTGATCTCTGTGACGACCATCTGCTGCGGCTCA 176  
61 TTCTCTACTCTCAGCGCAAGTGTGATCTCTGTGACGACCATCTGCTGCGGCTCA 120  
177 GCGGGGCCCCAGAACTCCGCTCGTGTGCTGCGAGTAAACAGTTGACGAAGTGGTG 236  
121 GCGGGGCCCCAGAACTCCGCTCGTGTGCTGCGAGTAAACAGTTGACGAAGTGGTG 180  
237 TGCAAGCGCGCGGGCCCTCCGAGGTCCCGAGGTATTCCTCGAACACCCGGTACCTC 296  
181 TGCAAGCGCGCGGGCCCTCCGAGGTCCCGAGGTATTCCTCGAACACCCGGTACCTC 240  
297 AACCTCATGGAGAACATCCAGATATCCAGCCGACACCTTCCGCCACTCCACCAC 356  
241 AACCTCATGGAGAACATCCAGATATCCAGCCGACACCTTCCGCCACTCCACCAC 300  
357 CTGAGGTCTCGAGTTGGGCGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAAC 416  
301 CTGAGGTCTCGAGTTGGGCGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAAC 360  
417 GCGCTGGCCAGCTTCAACACCTTGAGTGTTCGACAACTGGTGCAGTATCCCTAGC 476  
361 GCGCTGGCCAGCTTCAACACCTTGAGTGTTCGACAACTGGTGCAGTATCCCTAGC 420  
477 GGGGCTTTGAATACCTGTCAAGCTGGGGAGCTCTGGCTTGGCAACACCCATCGAA 536  
421 GGGGCTTTGAATACCTGTCAAGCTGGGGAGCTCTGGCTTGGCAACACCCATCGAA 480  
537 AGCATCCCTCTTACGCTTCAACCGGGTGCCTTCCCTCATGGCCCTGGAATTTGGGGGAG 596  
481 AGCATCCCTCTTACGCTTCAACCGGGTGCCTTCCCTCATGGCCCTGGAATTTGGGGGAG 540  
597 CTCAGAAAGCTGGAGTATCTCTGAGGAGCTTTTGAAGGGGTGTTTCAACCTCAAGTAT 656  
541 CTCAGAAAGCTGGAGTATCTCTGAGGAGCTTTTGAAGGGGTGTTTCAACCTCAAGTAT 600  
657 CTGAATTTGGGCATGTGCACATTAAGACATGCCCAATCTCAACCCCTTGGTGGGCTG 716  
601 CTGAATTTGGGCATGTGCACATTAAGACATGCCCAATCTCAACCCCTTGGTGGGCTG 660

717 GAGAGCTGCGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTTGGCTCTTCCATGGC 776  
661 GAGAGCTGCGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTTGGCTCTTCCATGGC 720  
777 CTGAGCTTCCCTCAAGAGCTCTGGTTCATGAACCTCAGCTCAGCTGAGTGGGGGAT 836  
721 CTGAGCTTCCCTCAAGAGCTCTGGTTCATGAACCTCAGCTCAGCTGAGTGGGGGAT 780  
837 GCTTTTGAAGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCCACAAATAACCTCTTCTT 896  
781 GCTTTTGAAGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCCACAAATAACCTCTTCTT 840  
897 TTGCCCATCACTCTTTTACCCCGCTGAGTACTCTGCTGAGTGTGATCTACACCAAC 956  
841 TTGCCCATCACTCTTTTACCCCGCTGAGTACTCTGCTGAGTGTGATCTACACCAAC 900  
957 CTTTGGAACTGTGATTTGTGACATTTCTGGTGTAGCTTGGTGGCTTCGAGATATATACC 960  
901 CTTTGGAACTGTGATTTGTGACATTTCTGGTGTAGCTTGGTGGCTTCGAGATATATACC 960  
1017 ACCAATTCCTCCTGCTGTGGCCGCTGTGATGCTTCCATGCAATGCGAGGCGCTACCTC 1076  
961 ACCAATTCCTCCTGCTGTGGCCGCTGTGATGCTTCCATGCAATGCGAGGCGCTACCTC 1020  
1077 GTGAGGTGAGACAGGCTCTTCCAGTGTCTGCCCCCTTTCATCATGACGACCTCGA 1136  
1021 GTGAGGTGAGACAGGCTCTTCCAGTGTCTGCCCCCTTTCATCATGACGACCTCGA 1080  
1137 GACCTCAACATTTCTGAGGCTCGGATGGCAGAACTTAAAGTGTGCGACTCCCCCTATGTCC 1196  
1081 GACCTCAACATTTCTGAGGCTCGGATGGCAGAACTTAAAGTGTGCGACTCCCCCTATGTCC 1140  
1197 TCCGTGAAGTGTGCTGCCCCAATGGGACAGTGTCTGAGCCGCTCCCGCCACCCAGG 1256  
1141 TCCGTGAAGTGTGCTGCCCCAATGGGACAGTGTCTGAGCCGCTCCCGCCACCCAGG 1200  
1257 ATCTCTGCTCTCAAGACGCGCACTTGAACCTTTTCCCACTGCTGCTTTTTCAGACCTGGG 1316  
1201 ATCTCTGCTCTCAAGACGCGCACTTGAACCTTTTCCCACTGCTGCTTTTTCAGACCTGGG 1260  
1317 GTGTACACATGATGTGTGAGGACATCTCCAGCGCTGCTGAGCTTACCTCAAT 1376  
1261 GTGTACACATGATGTGTGAGGACATCTCCAGCGCTGCTGAGCTTACCTCAAT 1320  
1377 GTGAGCAGGCTGAGCTTAACTCACTCACTACAGTCTTTCACACAGTAAACAGTGGAG 1436  
1321 GTGAGCAGGCTGAGCTTAACTCACTCACTACAGTCTTTCACACAGTAAACAGTGGAG 1380  
1437 ACCACGAGATCTCCCTGAGGACACAACCGGAAAGTACAGCTGTTCTTACACGCTCC 1496  
1381 ACCACGAGATCTCCCTGAGGACACAACCGGAAAGTACAGCTGTTCTTACACGCTCC 1440  
1497 ACTGTTTACAGCGGCTATACCACTCTTACCACTGCTCATTCAGACTTACCGCTGTG 1556  
1441 ACTGTTTACAGCGGCTATACCACTCTTACCACTGCTCATTCAGACTTACCGCTGTG 1500  
1557 CCCAAGCAGTGGCAGTACCCCGGACAGACACCACTGACAAAGATGACAGCAGCTGGAT 1616  
1501 CCCAAGCAGTGGCAGTACCCCGGACAGACACCACTGACAAAGATGACAGCAGCTGGAT 1560  
1617 GAAGTCTGAAGAACCAACCAAGATCATCTTGGCTGCTTTTGGGAGTACTCTGCTAGCT 1676  
1561 GAAGTCTGAAGAACCAACCAAGATCATCTTGGCTGCTTTTGGGAGTACTCTGCTAGCT 1620  
1677 GCGGCACTGTTGATTTCTTCTTAAACTTCTGTAAGGGGACACAGCAGCGGAGTACAGTC 1736  
1621 GCGGCACTGTTGATTTCTTCTTAAACTTCTGTAAGGGGACACAGCAGCGGAGTACAGTC 1680  
1737 ACAGCCCGCGGACTGTTGAGATTAATCCAGGTGGAACGACATCCAGCAGCAACATCC 1796  
1681 ACAGCCCGCGGACTGTTGAGATTAATCCAGGTGGAACGACATCCAGCAGCAACATCC 1740













b 1141 ACTGGTTACCGCGCATATACCACTCTACCGGCTGCTCATTAGACTACCGCTGTG 1200  
 y 1557 CCCAAGCAGGTGGCAGTACCCGGGAGAGACACCACTGACCAAGATGACAGACCGCTGGAT 1616  
 b 1201 CCCAAGCAGGTGGCAGTACCCGGGAGAGACACCACTGACCAAGATGACAGACCGCTGGAT 1260  
 y 1617 GAAGTCATGAAGACCAACCAAGATCATCTATGGCTGCTTTGGGAGTGAATCTGTAGCT 1676  
 b 1261 GAAGTCATGAAGACCAACCAAGATCATCTATGGCTGCTTTGGGAGTGAATCTGTAGCT 1320  
 y 1677 GCGCCATGTTGATGCTTCTATATAAATCTGTAAGCGGCACAGCGGAGTACAGTC 1736  
 b 1321 GCGCCATGTTGATGCTTCTATATAAATCTGTAAGCGGCACAGCGGAGTACAGTC 1380  
 y 1737 ACAGCCGCGGAGCTGTGAGATAATCCAGGTGGAGAGACATCCAGCAGCAACATCC 1796  
 b 1381 ACAGCCGCGGAGCTGTGAGATAATCCAGGTGGAGAGACATCCAGCAGCAACATCC 1440  
 y 1797 GCAGCAGCAACAGCAGCTCGTCCGCTGTATCAGGTGAGGGGGCAGTGTGCTGCCACA 1856  
 b 1441 GCAGCAGCAACAGCAGCTCGTCCGCTGTATCAGGTGAGGGGGCAGTGTGCTGCCACA 1500  
 y 1857 ATTCTAGCACCATTAACTAACACACTTACAAACCAAGCAGCAGTGGGCCCCACTGGACAGAA 1916  
 b 1501 ATTCTAGCACCATTAACTAACACACTTACAAACCAAGCAGCAGTGGGCCCCACTGGACAGAA 1560  
 y 1917 AACAGCCTGGGGAATCTCTGCAACCCAGTCCACCACTATCTCTGAACCTTATATAT 1976  
 b 1561 AACAGCCTGGGGAATCTCTGCAACCCAGTCCACCACTATCTCTGAACCTTATATAT 1620  
 y 1977 CAGACCCATACCAAGGACAGGTACAGGAATCTCAATATGACTCCCTCCGCCCAAAAAA 2036  
 b 1621 CAGACCCATACCAAGGACAGGTACAGGAATCTCAATATGACTCCCTCCGCCCAAAAAA 1680  
 y 2037 CTTATAAATTAAGACAAAAAGTCAAAAAA 2185  
 b 1681 CTTATAAATTAAGACAAAAAGTCAAAAAA 1740  
 y 2097 CTTTTCTTGTATGCTTATATATTAATTAAGTCTATGGCTGTTAAAAAACAAGATTATA 2156  
 b 1741 CTTTTCTTGTATGCTTATATATTAATTAAGTCTATGGCTGTTAAAAAACAAGATTATA 1800  
 y 2157 TTAATAATTAAGACAAAAAGTCAAAAAA 2185  
 b 1801 TTAATAATTAAGACAAAAAGTCAAAAAA 1829

RESULT 21

BVB3908

D ABV83908 standard; cDNA; 2159 BP.

X C

X C

X 09-DEC-2002 (first entry)

X Human polynucleotide SEQ ID NO 237.

X Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;  
 W immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;  
 W antiparasitic; antisickling; antianemic; antiarthritic; cancer;  
 W antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 W antiallergic; antidiabetic; antileuk; anticonvulsant; antifungal;  
 W antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
 W neurological disease; infection; nephrotropic; gene therapy; vaccine;  
 W gene; ss.

X Homo sapiens.

X X

X US2002090672-A1.

X X

X 11-JUL-2002.

X

PF 17-JAN-2001; 2001US-0764853.  
 XX 31-JAN-2000; 2000US-179065P.  
 PR 04-FEB-2000; 2000US-180628P.  
 PR 28-JUN-2000; 2000US-214886P.  
 PR 07-JUL-2000; 2000US-216647P.  
 PR 07-JUL-2000; 2000US-216880P.  
 PR 11-JUL-2000; 2000US-217487P.  
 PR 11-JUL-2000; 2000US-217496P.  
 PR 14-JUL-2000; 2000US-218290P.  
 PR 26-JUL-2000; 2000US-220963P.  
 PR 26-JUL-2000; 2000US-220964P.  
 PR 14-AUG-2000; 2000US-224518P.  
 PR 14-AUG-2000; 2000US-224519P.  
 PR 14-AUG-2000; 2000US-225267P.  
 PR 14-AUG-2000; 2000US-225268P.  
 PR 14-AUG-2000; 2000US-225270P.  
 PR 14-AUG-2000; 2000US-225447P.  
 PR 14-AUG-2000; 2000US-225757P.  
 PR 14-AUG-2000; 2000US-225758P.  
 PR 22-AUG-2000; 2000US-226888P.  
 PR 30-AUG-2000; 2000US-228944P.  
 PR 01-SEP-2000; 2000US-229287P.  
 PR 01-SEP-2000; 2000US-229343P.  
 PR 01-SEP-2000; 2000US-229344P.  
 PR 01-SEP-2000; 2000US-229345P.  
 PR 05-SEP-2000; 2000US-229509P.  
 PR 05-SEP-2000; 2000US-229513P.  
 PR 08-SEP-2000; 2000US-231413P.  
 PR 21-SEP-2000; 2000US-234223P.  
 PR 21-SEP-2000; 2000US-234274P.  
 PR 25-SEP-2000; 2000US-234997P.  
 PR 27-SEP-2000; 2000US-235834P.  
 PR 29-SEP-2000; 2000US-236327P.  
 PR 29-SEP-2000; 2000US-236367P.  
 PR 29-SEP-2000; 2000US-236368P.  
 PR 29-SEP-2000; 2000US-236369P.  
 PR 29-SEP-2000; 2000US-236370P.  
 PR 02-OCT-2000; 2000US-236802P.  
 PR 02-OCT-2000; 2000US-237037P.  
 PR 02-OCT-2000; 2000US-237038P.  
 PR 02-OCT-2000; 2000US-237039P.  
 PR 02-OCT-2000; 2000US-237040P.  
 PR 13-OCT-2000; 2000US-239935P.  
 PR 20-OCT-2000; 2000US-240960P.  
 PR 20-OCT-2000; 2000US-241785P.  
 PR 20-OCT-2000; 2000US-241809P.  
 PR 01-NOV-2000; 2000US-244617P.  
 PR 17-NOV-2000; 2000US-249299P.  
 PR 08-DEC-2000; 2000US-251856P.  
 PR 08-DEC-2000; 2000US-251868P.  
 PR 08-DEC-2000; 2000US-251869P.

(ROSE/) ROSEN C A.

(RUBE/) RUBEN S M.

(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2002-681727/73.

P-PSDB; ABP66936.

Novel polypeptide useful for diagnosis, prognosis, prevention, and  
 treatment of immune, hyperproliferative, renal, respiratory, and  
 cardiovascular, reproductive, endocrine, gastrointestinal and  
 neurological disorders -

Claim 1; SEQ ID NO 237; 369pp + Sequence Listing; English.

The invention relates to novel genes (ABV83682-ABV84101) and proteins  
 (ABP6710-ABP67129) useful for preventing, treating or ameliorating  
 medical conditions e.g. by protein or gene therapy. The genes are  
 isolated from a range of human tissues disclosed in the specification.



CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2159 BP; 569 A; 585 C; 512 G; 493 T; 0 other;  
Query Match 81.4%; Score 1778; DB 24; Length 2159;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
357 CTGGAGGCTCTGCTGAGGAGGAACTCCATCCGGGAGATGAGTGGGGCCCTTCAAC 416  
Db 1 CTGGAGGCTCTGCTGAGGAGGAACTCCATCCGGGAGATGAGTGGGGCCCTTCAAC 60  
417 GSCCTGGCCAGCTCAACACCTCGAGCTGTTCGAACTGGCTGACAGTCATCCCTAGC 476  
Db 61 GSCCTGGCCAGCTCAACACCTCGAGCTGTTCGAACTGGCTGACAGTCATCCCTAGC 120  
477 GGGGGCTTTGAAATGCTGCTCAAGCTGGGGAGCTCTGGCTTGGCAACACCCCATGAA 536  
Db 121 GGGGGCTTTGAAATGCTGCTCAAGCTGGGGAGCTCTGGCTTGGCAACACCCCATGAA 180  
537 AGCATCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGACTGGGGGAG 596  
Db 181 AGCATCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGACTGGGGGAG 240  
597 CTCAGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTGTTCAAACCTCAAGTAT 656  
Db 241 CTCAGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTGTTCAAACCTCAAGTAT 300  
657 CTGAACCTGGGCAATGCAACATTAAGACATGCCAATCTACCCCTCGTGGGGCTG 716  
Db 301 CTGAACCTGGGCAATGCAACATTAAGACATGCCAATCTACCCCTCGTGGGGCTG 360  
717 GAGGAGCTGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGC 776  
Db 361 GAGGAGCTGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGC 420  
777 CTGAGCTCCCTCAAGAGCTCTGGGTGATGAATCTACAGGTGAGCTGATGAGGGGAT 836  
Db 421 CTGAGCTCCCTCAAGAGCTCTGGGTGATGAATCTACAGGTGAGCTGATGAGGGGAT 480  
837 GCTTTTGAAGGGCTGCTTCACTTGTGGAATCTCACTTGGCCCAATAAATCTCTTCT 896  
Db 481 GCTTTTGAAGGGCTGCTTCACTTGTGGAATCTCACTTGGCCCAATAAATCTCTTCT 540  
897 TTGCCCAATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTCATCTACACAGAC 956  
Db 541 TTGCCCAATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTCATCTACACAGAC 600  
957 CTTTGGATCTGTGATGTGACATCTCTGCTGAGCTGGTGGCTTTCGAGAGTATATACC 1016  
Db 601 CTTTGGATCTGTGATGTGACATCTCTGCTGAGCTGGTGGCTTTCGAGAGTATATACC 660  
1017 ACCAATTCACCTGCTGTGGCGCTGTATGCTGCCATGCAATCGAGGGCGCTTACCTC 1076  
Db 661 ACCAATTCACCTGCTGTGGCGCTGTATGCTGCCATGCAATCGAGGGCGCTTACCTC 720  
1077 GTGGAGGAGGACAGGCTCTTCCAGTGTCTGCTGCCCTTCAATGATGAGCAGCTCGA 1136  
Db 721 GTGGAGGAGGACAGGCTCTTCCAGTGTCTGCTGCCCTTCAATGATGAGCAGCTCGA 780

QY 1137 GACCTCAACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGGACTCCCCCTATGTCC 1196  
Db 781 GACCTCAACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGGACTCCCCCTATGTCC 840  
QY 1197 TCCGTGAAAGTGGTGTCTGCGCAATGGACAGTGTCTAGCCAGCGCTCCCGCCACCAAGG 1256  
Db 841 TCCGTGAAAGTGGTGTCTGCGCAATGGACAGTGTCTAGCCAGCGCTCCCGCCACCAAGG 900  
QY 1257 ATCTCTGTCTCTCAAGAGGCGACCTTGAACCTTTTCCACGCTGTGCTTTCAGACACTGGG 1316  
Db 901 ATCTCTGTCTCTCAAGAGGCGACCTTGAACCTTTTCCACGCTGTGCTTTCAGACACTGGG 960  
1317 GTGTACACATGATGCTGACCAATGTTTGGAGCAACTCCAAAGCTTCGGCTACCTCAAT 1376  
Db 961 GTGTACACATGATGCTGACCAATGTTTGGAGCAACTCCAAAGCTTCGGCTACCTCAAT 1020  
1377 GTGAGCAGGCTGAGCTTAAACCTCTCAACTAGCTTCTTCAACAGTAACAGTGGAG 1436  
Db 1021 GTGAGCAGGCTGAGCTTAAACCTCTCAACTAGCTTCTTCAACAGTAACAGTGGAG 1080  
QY 1437 ACCACGGAGATCTCGCTGAGCAGACACACGGAAGTACAAGCCTGTTCTTACCACTGCC 1496  
Db 1081 ACCACGGAGATCTCGCTGAGCAGACACACGGAAGTACAAGCCTGTTCTTACCACTGCC 1140  
1497 ACTGTTACAGCGCGCATATACACCTCTTACAGGTGCTCATTCAGACTACCGGTGG 1556  
Db 1141 ACTGTTACAGCGCGCATATACACCTCTTACAGGTGCTCATTCAGACTACCGGTGG 1200  
QY 1557 CCCAAGCAGGTGGAGTACCGCGCAGACACCACTGACAAGATGACAGCAGCGCTGGAT 1616  
Db 1201 CCCAAGCAGGTGGAGTACCGCGCAGACACCACTGACAAGATGACAGCAGCGCTGGAT 1260  
1617 GAAGTATGAAGACCAACCAAGATCATATGCTGCTTTTGGGAGTACTCTGCTAGCT 1676  
Db 1261 GAAGTATGAAGACCAACCAAGATCATATGCTGCTTTTGGGAGTACTCTGCTAGCT 1320  
QY 1677 GCGGCACTGCTGATGCTTCTTATAAATCTTGAAGCGGCAACAGCGGAGTACAGTC 1736  
Db 1321 GCGGCACTGCTGATGCTTCTTATAAATCTTGAAGCGGCAACAGCGGAGTACAGTC 1380  
1737 ACAGCGCCCGGAGCTGTTGAGATAATCCAGGTGGAAGAGACATCCAGCAGCAACATCC 1796  
Db 1381 ACAGCGCCCGGAGCTGTTGAGATAATCCAGGTGGAAGAGACATCCAGCAGCAACATCC 1440  
QY 1797 GCGAGCAGCAAGCAGCTCGTCCGCTGATGAGGTGAGGGGAGTACTGCTGCCACA 1856  
Db 1441 GCGAGCAGCAAGCAGCTCGTCCGCTGATGAGGTGAGGGGAGTACTGCTGCCACA 1500  
1857 ATTCAATGACCATATTAATTAACCTACAACTTACAACTTACAACTTACAACTTACAA 1916  
Db 1501 ATTCAATGACCATATTAATTAACCTTACAACTTACAACTTACAACTTACAACTTACAA 1560  
QY 1917 AACAGCTGGGGAATCTCTGACCCGACAGTCACTATCTCTGAGACTTATATAT 1976  
Db 1561 AACAGCTGGGGAATCTCTGACCCGACAGTCACTATCTCTGAGACTTATATAT 1620  
1977 CAGACCCATACCAAGGACAAAGGTACAGGAACTCAAATATGACTCCCTCCGCCAAAAA 2036  
Db 1621 CAGACCCATACCAAGGACAAAGGTACAGGAACTCAAATATGACTCCCTCCGCCAAAAA 1680  
QY 2037 CTTTAAATGCAATAGAAATGACCAAGAGACGAACTTTTGTACAGAGTGGGAGAGA 2096  
Db 1681 CTTTAAATGCAATAGAAATGACCAAGAGACGAACTTTTGTACAGAGTGGGAGAGA 1740  
2097 CTTTAAATGCAATAGAAATGACCAAGAGACGAACTTTTGTACAGAGTGGGAGAGA 2156  
Db 1741 CTTTAAATGCAATAGAAATGACCAAGAGACGAACTTTTGTACAGAGTGGGAGAGA 1800  
2157 TTTAAATTTTAAAGACAAAAGTCAAAACA 2185  
Db 1801 TTTAAATTTTAAAGACAAAAGTCAAAACA 1829



RESULT 22	SQ	Sequence 2607 BP; 681 A; 752 C; 619 G; 555 T; 0 other;	
AA93621		Query Match	
AAA93621 standard; DNA; 2607 BP.		Best Local Similarity 65.9%; Score 1440; DB 21; Length 2607;	
AAA93621;		Mismatches 1740; Conservative 99.7%; Pred. No. 0;	
16-JAN-2001 (first entry)		Mismatches 1740; Conservative 99.7%; Pred. No. 0;	
Human SLIT protein-like splice variant SECX 3552358-2 DNA.		Mismatches 1740; Conservative 99.7%; Pred. No. 0;	
SECX protein; human; secreted; membrane-associated; cancer;	QY	1 GTTCTCTTTCGAGCCAAATCCGAGCGGATGGTGAATTAAGAACGTGCCACACCATGA	60
proliferation regulator; differentiation regulator; non-malignant tumour;	DB	159 GTTCTCTTTCGAGCCAAATCCGAGCGGATGGTGAATTAAGAACGTGCCACACCATGA	218
immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;	QY	61 AGCTCTTGTGGCAGGTAATCTGTGACACCAACACCTGGAATGCCATCTCTCTCCGTTGG	120
infection; inflammatory disorder; arthritis; haematopoietic disorder;	DB	219 AGCTCTTGTGGCAGGTAATCTGTGACACCAACACCTGGAATGCCATCTCTCTCCGTTGG	278
skin disorder; cardiovascular disorder; atherosclerosis; restenosis;	QY	121 TCTACTCTACGCGCGCAAGTGTGATCTGTGTGACGACCATCGCTGTCCGCTCAGCGG	180
neurological disease; Alzheimer's disease; cytostatic; wounding;	DB	279 TCTACTCTACGCGCGCAAGTGTGATCTGTGTGACGACCATCGCTGTCCGCTCAGCGG	338
spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;	QY	181 GGCCCCAGAACTGCCCCCTCCGTTTCTGCTGTCAGTAAACAGTTCAGCAAGGTGGTGTGA	240
anti-HIV; antiinflammatory; antiarthritis; antiarteriosclerotic;	DB	339 GGCCCCAGAACTGCCCCCTCCGTTTCTGCTGTCAGTAAACAGTTCAGCAAGGTGGTGTGA	398
neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;	QY	241 CGCGCGGCGGCTCTTCCGAGGTCGCGAGGATTCCTCTCGAAACACCGGATACCTCAACC	300
dermatological; gene therapy; ds.	DB	399 CGCGCGGCGGCTCTTCCGAGGTCGCGAGGATTCCTCTCGAAACACCGGATACCTCAACC	458
Homo sapiens.	QY	301 TCATGGAGAAACAAATCCAGATGATCCAGGCGGACACCTCCGCGACCTCCACACCTGG	360
	DB	459 TCATGGAGAAACAAATCCAGATGATCCAGGCGGACACCTCCGCGACCTCCACACCTGG	518
	QY	361 AGSTCTCAGTGTGGCAGGAACTCCATCCGCGAGATGAGTGGGGGCTTCACAAAGGCC	420
	DB	519 AGSTCTCAGTGTGGCAGGAACTCCATCCGCGAGATGAGTGGGGGCTTCACAAAGGCC	578
	QY	421 TGGCAGGCTCAACAGCCTGAGGCTGTTGCAACATGCGCTGACAGTCACTCCCTGAGCGGG	480
	DB	579 TGGCAGGCTCAACAGCCTGAGGCTGTTGCAACATGCGCTGACAGTCACTCCCTGAGCGGG	638
	QY	481 CTTTGAATACCTGTCCAGCTGCGGAGCTCTGCTTCGCAACACCCCAACCCCAACGCA	540
	DB	639 CTTTGAATACCTGTCCAGCTGCGGAGCTCTGCTTCGCAACACCCCAACCCCAACGCA	698
	QY	541 TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGGCTGAGCTTGGGGGAGCTCA	600
	DB	699 TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGGCTGAGCTTGGGGGAGCTCA	758
	QY	601 AGAAGCTGAGTATATCTCTCAGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA	660
	DB	759 AGAAGCTGAGTATATCTCTCAGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA	818
	QY	661 ACTTGGGATGTGCAAACTTAAAGCATGCCAAATCTCAACCCCTCGTGGGGCTGGAGG	720
	DB	819 ACTTGGGATGTGCAAACTTAAAGCATGCCAAATCTCAACCCCTCGTGGGGCTGGAGG	778
	QY	721 AGCTGAGATGTGAGGAAACCACTTCCTCGAGATCAGGCTGGCTCTCTCCATGGCTGA	780
	DB	879 AGCTGAGATGTGAGGAAACCACTTCCTCGAGATCAGGCTGGCTCTCTCCATGGCTGA	938
	QY	781 GCTCCTCAAGAAGCTCTGGGTGTGAAGTCACTCAGGTCAGCTGATTAAGCGGAATGCTT	840
	DB	939 GCTCCTCAAGAAGCTCTGGGTGTGAAGTCACTCAGGTCAGCTGATTAAGCGGAATGCTT	998
	QY	841 TTGAGGGGCTGCTTCACTTCTGGAATCTCACTTTGGGCGCAATAAATCTCTCTCTTTC	900
	DB	999 TTGAGGGGCTGCTTCACTTCTGGAATCTCACTTTGGGCGCAATAAATCTCTCTCTTTC	1058
	QY	901 CCCATGACCTCTTTACCCCGCTGAGGTACCTGTGGAGTGTGCATCTACACCAACCCCTT	960
	DB	1059 CCCATGACCTCTTTACCCCGCTGAGGTACCTGTGGAGTGTGCATCTACACCAACCCCTT	1118
	QY	961 GGAATGTGATGTGACATTTCTGTGGCTAGCTGGTGGCTTGGAGATATATACCCACCA	1020
	DB	1119 GGAATGTGATGTGACATTTCTGTGGCTAGCTGGTGGCTTGGAGATATATACCCACCA	1178

Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (A93629-B23048). The SECX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing the presence of, or predisposition to, a disease associated with altered levels of SECX proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used to detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders.

Claim 3; Fig 6; 15ipp; English.

Novel human membrane associated or secreted polypeptides and polynucleotides useful for diagnosis, prevention and treatment of pathological states such as cancer, immune, cardiovascular and neurological disorders

Shinkets RA;

WPI; 2000-594318/56.

P-PSDB; AAB23034.

(CURA-) CURAGEN CORP.

09-MAR-2000; 2000NO-US06280.

09-MAR-1999; 99US-0123667.

08-MAR-2000; 2000US-0123667.

14-SEP-2000.

WO200053742-A2.

1021 ATTCCACCTGCTGGCGCTGTCATGCTCCCATGCACATGGAGGCGCTACCTCGTG 1080  
 1179 ATTCCACCTGCTGGCGCTGTCATGCTCCCATGCACATGGAGGCGCTACCTCGTG 1238  
 1081 AGGTGGACCAAGGCTCTTCCAGTGTCTGCCCCCTTCATATGAGACGACCTGAGACC 1140  
 1239 AGGTGGACCAAGGCTCTTCCAGTGTCTGCCCCCTTCATATGAGACGACCTGAGACC 1298  
 1141 TCACATTTCTGAGGTCGATGCGAGATGCTTAAGTGTGCGACTCCCTATGCTCTCG 1200  
 1299 TCACATTTCTGAGGTCGATGCGAGATGCTTAAGTGTGCGACTCCCTATGCTCTCG 1358  
 1201 TGAAGTGTGCTGCTGCCCAATGTTGAGGACAGTGTCTAGCCACGCTCCGCCCAAGGATCT 1260  
 1359 TGAAGTGTGCTGCTGCCCAATGTTGAGGACAGTGTCTAGCCACGCTCCGCCCAAGGATCT 1418  
 1261 CTGTCTCTCAAGACGACCTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1320  
 1419 CTGTCTCTCAAGACGACCTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1478  
 1321 ACACATGATGTTGACCAATGTTTGGAGGCAACTCCAAACGCTCGGCTTACCTCAATGTGA 1380  
 1479 ACACATGATGTTGACCAATGTTTGGAGGCAACTCCAAACGCTCGGCTTACCTCAATGTGA 1538  
 1381 GCACGGCTGAGCTTAACACCTCCAACTACAGCTTCTTCCACAGTAACTGAGACCA 1440  
 1539 GCACGGCTGAGCTTAACACCTCCAACTACAGCTTCTTCCACAGTAACTGAGACCA 1598  
 1441 CGGAGATCTGCTCCCTGAGGACACACAGCGAAAGTACAGCTGTCTTACCACTCCACTG 1500  
 1599 CGGAGATCTGCTCCCTGAGGACACACAGCGAAAGTACAGCTGTCTTACCACTCCACTG 1658  
 1501 GTTACACGCGGCAATATACCACTCTTACCAAGTGTCTTACCACTCCACTG 1560  
 1659 GTTACACGCGGCAATATACCACTCTTACCAAGTGTCTTACCACTCCACTG 1718  
 1561 AGCAGGTGGAGTACCGCGGACACACACCTGACAGATGTCAGACGCTGGATGAAG 1620  
 1719 AGCAGGTGGAGTACCGCGGACACACACCTGACAGATGTCAGACGCTGGATGAAG 1778  
 1621 TCATGAGACACCAAGATATATACCACTCTTACCAAGTGTCTTACCACTCCACTG 1680  
 1779 TCATGAGACACCAAGATATATACCACTCTTACCAAGTGTCTTACCACTCCACTG 1838  
 1681 CCATGTTGATGCTTCTTATTAATCTTCTAAGCGGACACGAGCGGAGTACAGTACAG 1740  
 1839 CCATGTTGATGCTTCTTATTAATCTTCTAAGCGGACACGAGCGGAGTACAGTACAG 1898  
 1741 CCGCCC 1746  
 1899 CCGCCC 1904

RESULT 23  
 AAC77300  
 ID AAC77300 standard; cDNA, 1805 BP.  
 XX  
 AC AAC77300;  
 XX  
 CT 08-FEB-2001 (first entry)  
 XX  
 DE Human ORFX ORF2855 polynucleotide sequence SEQ ID NO:5709.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnary; antipariatic; antiparkinsonian; nootropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antitubercular; antithyroid;  
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive; ss.  
 XX Homo sapiens.  
 OS WO200058473-A2.  
 XX  
 PN 05-OCT-2000.  
 XX  
 PD 31-MAR-2000; 2000WO-US08621.  
 XX  
 PF 31-MAR-1999; 99US-0127607.  
 XX  
 PR 02-APR-1999; 99US-0127636.  
 PR  
 PR 05-APR-1999; 99US-0127728.  
 PR  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shimkets RA, Leach M;  
 PI WPI; 2000-602362/57.  
 XX  
 DR P-PSDB; ABA43091.  
 DR  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX  
 XX Claim 5; Page 4876-4877; 5507pp; English.  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
 CC antipariatic; antiparkinsonian; nootropic; neuroprotective;  
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antitubercular;  
 CC antithyroid; and antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat arthritis,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX  
 XX Sequence 1805 BP; 484 A; 486 C; 416 G; 419 T; 0 other;

Query Match 61.8%; Score 1351; DB 21; Length 1805;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1471; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 715 TGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTCGCTTCCATG 774  
 DB 23 TGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTCGCTTCCATG 82  
 QY 775 GCCTGAGCTCCCTCAAGAGCTCTGGGTCTATGAACTCAGAGTCAAGCTGATGAGCGGA 834  
 DB 83 GCCTGAGCTCCCTCAAGAGCTCTGGGTCTATGAACTCAGAGTCAAGCTGATGAGCGGA 142  
 QY 835 ATGCTTTTGGAGGCTGGCTTCACTCTGGAACCTCAACTTGGCCCAATAAATCTCTTT 894  
 DB 143 ATGCTTTTGGAGGCTGGCTTCACTCTGGAACCTCAACTTGGCCCAATAAATCTCTTT 202  
 QY 895 CTTTCCCTCATGACCTCTTTTCCCTCCCTGCTGAGTACCTGGTGGAGTTGATACACCA 954



or genetic lesions in the SECK gene. They may also be used to modulate SECK expression (e.g., using antisense oligonucleotides). SECK nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECK primers or probes are useful for detecting the presence of SECK nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECK proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumors, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, retinosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders.

Sequence 1356 BP; 283 A; 437 C; 339 G; 297 T; 0 other;

Query Match 53.9%; Score 1178; DB 21; Length 1356;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1328; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

204 TGCTGTCAGTAACAGTTCAGCAAGTGTGTGTCACGGCGCGGGGCTCTCCGAGTTC 263  
22 TGCTGTCAGTAACAGTTCAGCAAGTGTGTGTCACGGCGCGGGGCTCTCCGAGTTC 81  
264 CGCAGGATATTCCTCGAACAACCGGTGTAACCTCATGTGAGAGAACATCCAGATG 323  
82 CGCAGGATATTCCTCGAACAACCGGTGTAACCTCATGTGAGAGAACATCCAGATG 141  
324 ATCCAGGCGGACACCTCCGCGACCTCCACCACTGGAGTTCCTGCAAGTTGGGCGAGAAC 383  
142 ATCCAGGCGGACACCTCCGCGACCTCCACCACTGGAGTTCCTGCAAGTTGGGCGAGAAC 201  
384 TCCATCCGCGGAGATGAGTGGGGGCTTCGAAACCGCTGCGAGCTCCGCAACCTCGGAG 443  
202 TCCATCCGCGGAGATGAGTGGGGGCTTCGAAACCGCTGCGAGCTCCGCAACCTCGGAG 261  
444 CTGTTTCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503  
262 CTGTTTCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321  
504 CGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563  
322 CGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 381  
564 GTGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623  
382 GTGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441  
624 GGAGCTTTTGAGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCTGCTGCAACATTA 683  
442 GGAGCTTTTGAGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCTGCTGCAACATTA 501  
684 GACATGCCAATCTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743  
502 GACATGCCAATCTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561  
744 TTCCCTGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803  
562 TTCCCTGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
804 ATGAACCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863  
622 ATGAACCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681  
864 GAACTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923  
682 GAACTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741  
924 AGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 983  
742 AGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801

984 TGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043  
802 TGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861  
1044 CATGCTCCCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1103  
862 CATGCTCCCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 921  
1104 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163  
922 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981  
1164 GAGAACTTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1223  
982 GCAGAACTTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1041  
1224 ACAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1283  
1042 ACAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1101  
1284 AACTTTTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343  
1102 AACTTTTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161  
1344 GCAGCAACTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403  
1162 GCAGCAACTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221  
1404 AACTTACAGCTTCTTCAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1463  
1222 AACTTACAGCTTCTTCAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1281  
1464 ACAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1523  
1282 ACAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1341  
1524 TCTACCAAGCT 1534  
1342 TCTACCAAGCT 1352  
RESULT 25  
ABA06744  
ID ABA06744 standard; cDNA; 1168 BP.  
AC ABA06744;  
XX  
XX  
DT 10-JAN-2002 (first entry)  
XX  
Human cDNA SEQ ID NO: 410.  
DE Human; gene therapy; neural disorder; immune system disorder;  
XX muscular disorder; reproductive disorder; gastrointestinal disorder;  
XX pulmonary disorder; cardiovascular disorder; renal disorder;  
XX proliferative disorder; inflammation; ss.  
OS Homo sapiens.  
XX  
XX WO200154474-A2.  
XX  
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XX  
XX 17-JAN-2001; 2001WO-US01349.  
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XX 31-JAN-2000; 2000US-179065P.  
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476161/51.  
P-FSDS; ABB10522.

Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.

Claim 1; SEQ ID NO: 410; 859pp + Sequence Listing; English.

The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a cDNA of the invention.

CC

XX SQ Sequence 1166 BP; 243 A; 364 C; 291 G; 264 T; 6 other;  
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 778 TGAGCTCCCTCAGAGCTCTGGGTGATGACTCAGAGTCAAGTATGAGCGGAATG 837  
 419 TGAGCTCCCTCAGAGCTCTGGGTGATGACTCAGAGTCAAGTATGAGCGGAATG 478  
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 599 CTTGGAATGTAATGTGACATCTTGTGGCTAGCTGTTGGCTTCGAGAGTATATACCCA 658  
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 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human immunoglobulin encoding cDNA SEQ ID No 118.

XX KW Immunoglobulin; primer; signal transduction pathway protein; cancer; ss;  
 KW antisense therapy; gene therapy; neurological disorder; renal disorder;  
 KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;  
 KW reproductive disorder; immune system disorder; proliferative disorder;  
 XX muscular disorder.  
 OS Homo sapiens.  
 XX WO200155315-A2.  
 XX PD 02-AUG-2001.  
 XX PF 17-JAN-2001; 2001WO-US01326.  
 XX PR 31-JAN-2000; 2000US-0179065.  
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XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-457725/49.  
DR P-PSDB; AAU18084.  
XX  
PT Isolated novel immunoglobulin polypeptide for monitoring the presence  
PT and progression of diseases and for diagnosis -  
XX  
PS Claim 1; SEQ ID No 118; 551pp; English.  
XX  
XX Sequences AAS28765-AAS28877 represent cDNA molecules, which encode the  
CC immunoglobulin polypeptides of the invention, and primers for the  
CC polynucleotides. The polynucleotides and polypeptides can be used to  
CC diagnose a pathological condition or a susceptibility to a pathological  
CC condition in a subject by determining the presence or absence of a  
CC mutation in a DNA sequence or determining the presence or amount of  
CC expression of the protein. Alternatively the identification of a binding  
CC partner to a sequence allows determination of changes in protein  
CC activity. The sequences can be used as research tools for receptors or  
CC other signal transduction pathway proteins that interact with the  
CC polypeptides of the invention and can be used to treat, prevent or  
CC diagnose various types of disorders such as neurological disorders,  
CC cardiovascular disorders, gastrointestinal disorders, reproductive  
CC disorders, immune system disorders, renal disorders, muscular disorders,  
CC pulmonary disorders, proliferative disorders and cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [fp.wipo.int/pub/published\\_pct\\_sequences](http://fp.wipo.int/pub/published_pct_sequences).  
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QY 359 AGGAGCTGGAGATGTCAGGGAACCTTCCCTGAGATCAGGCTGCTCTTCCATGGCC 418  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 778 TGAGCTCCCTCAAGAGCTCTGGGTGATGAACTCAGCTCAGCTGATGAGCGGAATG 837  
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QY 419 TGAGCTCCCTCAAGAGCTCTGGGTGATGAACTCAGCTCAGCTGATGAGCGGAATG 478  
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QY 898 TGGCCCATGATGACCTTTTACCCCGCTGAGGTACTGCTGAGTTGCTATCACCACCAACC 957  
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QY 539 TGGCCCATGATGACCTTTTACCCCGCTGAGGTACTGCTGAGTTGCTATCACCACCAACC 598  
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QY 958 CTTTTCAGCGGCTGGCTTCACTTGTGGAATCAACTGGCCCACTACCTCTCTTCTT 1017  
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QY 599 CTTTTCAGCGGCTGGCTTCACTTGTGGAATCAACTGGCCCACTACCTCTCTTCTT 658  
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1b	839	CCGTGAAGTGTTCTCTCCCAATGGGACACAGTCTCAGCCAAGCCTCCGGCAACCCAAAGGA	898
1y	1258	TCTCTGTCCTCAACGACGGCACCTTGAACCTTTTCCCAAGTCTGCTGCTTTCAGACACTGGGG	1317
1b	899	TCTCTGTCCTCAACGACGGCACCTTGAACCTTTTCCCAAGTCTGCTTTCAGACACTGGGG	958
1y	1318	TGTACACATGCATGGTGAACCAATGTTTGCAGGCAACTCCAAAGCCTCGGCCTACCTCAATG	1377
1b	959	TGTACACATGCATGGTGAACCAATGTTTGCAGGCAACTCCAAAGCCTCGGCCTACCTCAATG	1018
1y	1378	TGACACAGCGTGAAGCTTAAACACCTCCAACTACAGCTTCTTCCACCAACAGTAACAGTGGAGA	1437
1b	1019	TGACACAGCGTGAAGCTTAAACACCTCCAACTACAGCTTCTTCCACCAACAGTAACAGTGGAGA	1078
1y	1438	CCACGGAGATCTCGCTTGAGGACACAAACGGGAAGTACAGCCTGTTCCTTACCACGTTCCA	1497
1b	1079	CCACGGAGATCTCGCTTGAGGACACAAACGGGAAGTACAGCCTGTTCCTTACCACGTTCCA	1138
1y	1498	CTGCTTACCACGGCGGCATATACCACCTCT	1526
1b	1139	CTGCTTACCACGGCGGCATATACCACCTCT	1167

RESULT 27  
 ABV84081  
 ID ABV84081 standard; cDNA; 1168 BP.  
 X  
 X ABV84081;

RESIST 27

1BV84081

:D ABV84081 standard; cDNA; 1168 BP.

5

1C ABV8

X

T 09-D

X

Human

100

Human

Case	Age	Sex	Site	Pathologic	Survival
1	65	M	Rectum	Adenocarcinoma	10 months
2	68	F	Rectum	Adenocarcinoma	12 months
3	70	M	Rectum	Adenocarcinoma	14 months
4	72	F	Rectum	Adenocarcinoma	16 months
5	75	M	Rectum	Adenocarcinoma	18 months
6	78	F	Rectum	Adenocarcinoma	20 months
7	80	M	Rectum	Adenocarcinoma	22 months
8	82	F	Rectum	Adenocarcinoma	24 months
9	85	M	Rectum	Adenocarcinoma	26 months
10	88	F	Rectum	Adenocarcinoma	28 months
11	90	M	Rectum	Adenocarcinoma	30 months
12	92	F	Rectum	Adenocarcinoma	32 months
13	95	M	Rectum	Adenocarcinoma	34 months
14	98	F	Rectum	Adenocarcinoma	36 months
15	100	M	Rectum	Adenocarcinoma	38 months
16	102	F	Rectum	Adenocarcinoma	40 months
17	105	M	Rectum	Adenocarcinoma	42 months
18	108	F	Rectum	Adenocarcinoma	44 months
19	110	M	Rectum	Adenocarcinoma	46 months
20	112	F	Rectum	Adenocarcinoma	48 months
21	115	M	Rectum	Adenocarcinoma	50 months
22	118	F	Rectum	Adenocarcinoma	52 months
23	120	M	Rectum	Adenocarcinoma	54 months
24	122	F	Rectum	Adenocarcinoma	56 months
25	125	M	Rectum	Adenocarcinoma	58 months
26	128	F	Rectum	Adenocarcinoma	60 months
27	130	M	Rectum	Adenocarcinoma	62 months
28	132	F	Rectum	Adenocarcinoma	64 months
29	135	M	Rectum	Adenocarcinoma	66 months
30	138	F	Rectum	Adenocarcinoma	68 months
31	140	M	Rectum	Adenocarcinoma	70 months
32	142	F	Rectum	Adenocarcinoma	72 months
33	145	M	Rectum	Adenocarcinoma	74 months
34	148	F	Rectum	Adenocarcinoma	76 months
35	150	M	Rectum	Adenocarcinoma	78 months
36	152	F	Rectum	Adenocarcinoma	80 months
37	155	M	Rectum	Adenocarcinoma	82 months
38	158	F	Rectum	Adenocarcinoma	84 months
39	160	M	Rectum	Adenocarcinoma	86 months
40	162	F	Rectum	Adenocarcinoma	88 months
41	165	M	Rectum	Adenocarcinoma	90 months
42	168	F	Rectum	Adenocarcinoma	92 months
43	170	M	Rectum	Adenocarcinoma	94 months
44	172	F	Rectum	Adenocarcinoma	96 months
45	175	M	Rectum	Adenocarcinoma	98 months
46	178	F	Rectum	Adenocarcinoma	100 months
47	180	M	Rectum	Adenocarcinoma	102 months
48	182	F	Rectum	Adenocarcinoma	104 months
49	185	M	Rectum	Adenocarcinoma	106 months
50	188	F	Rectum	Adenocarcinoma	108 months
51	190	M	Rectum	Adenocarcinoma	110 months
52	192	F	Rectum	Adenocarcinoma	112 months
53	195	M	Rectum	Adenocarcinoma	114 months
54	198	F	Rectum	Adenocarcinoma	116 months
55	200	M	Rectum	Adenocarcinoma	118 months
56	202	F	Rectum	Adenocarcinoma	120 months
57	205	M	Rectum	Adenocarcinoma	122 months
58	208	F	Rectum	Adenocarcinoma	124 months
59	210	M	Rectum	Adenocarcinoma	126 months
60	212	F	Rectum	Adenocarcinoma	128 months
61	215	M	Rectum	Adenocarcinoma	130 months
62	218	F	Rectum	Adenocarcinoma	132 months
63	220	M	Rectum	Adenocarcinoma	134 months
64	222	F	Rectum	Adenocarcinoma	136 months
65	225	M	Rectum	Adenocarcinoma	138 months
66	228	F	Rectum	Adenocarcinoma	140 months
67	230	M	Rectum	Adenocarcinoma	142 months
68	232	F	Rectum	Adenocarcinoma	144 months
69	235</				

[illegible]

anti anti

anti-

neur  
neur

gene





SC Homo



PN .US20



PD 11-J

1  
 2  
 3  
 4

PF 17-0

XX 31-1

PR 31-5  
DD 04-5

Dr. R. J. B. & Dr. R. J. B.

PR 07-J

07-J  
PR11-J  
DR

PR 11-J

PR 14-J

PR 26-5

PR 26-J

PR 14-A

PR 14-A

Claim 1: SEO TD NO 410: 369pp + Sequence Listing: English;

The invention relates to novel genes (ABV83682-ABV84101) and proteins (ABP6710-ABP7129) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast, ovarian, bladder, prostate, lung, colorectal, pancreatic, endometrial, myeloid, and non-Hodgkin's lymphoma; (b) autoimmune diseases, e.g. rheumatoid arthritis, multiple sclerosis, myasthenia gravis, Sjögren's syndrome, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftn.wipo.int/pub/pub](mailto:ftn.wipo.int/pub/pub) published pct sequences.

Sequence 1168 BP: 243 A: 364 C: 291 G: 264 T: 6 other;

Query Match 34.7%: Score 758; DB 24; Length 1168;

Query Pattern	Best Local Similarity	Pred. No. 0;
Query Pattern	99.98%	Pred. No. 0;

Local similarity	Matches	Mismatches	Indels	Gaps
Conservative	808	0	1	0







AAC58254;  
29-JAN-2001 (first entry)  
Human PRO1111 hybridisation probe SEQ ID NO:47.  
Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
proliferation; tumorigenesis; identification; cancer; PCR primer;  
hybridisation; probe; cytostatic; neurotrophic; neuroprotective;  
anti-inflammatory; immunosuppressive; immunostimulant; antiangiogenic;  
leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;  
astrocytal disorder; hypothalamic disorder; glandular disorder;  
macrophagal disorder; epithelial disorder; stromal disorder;  
blastocoele disorder; inflammatory disorder; angiogenic;  
immunologic disorder; ss.  
Homo sapiens.  
WO2000053755-A2.  
14-SEP-2000.  
06-JAN-2000; 2000WO-US00376.  
08-MAR-1999; 99WO-US05028.  
02-JUN-1999; 99WO-US12252.  
23-JUN-1999; 99US-0141037.  
07-JUL-1999; 99US-0143048.  
26-JUL-1999; 99US-0145698.  
30-NOV-1999; 99WO-US28313.  
20-DEC-1999; 99WO-US30911.  
05-JAN-2000; 2000WO-US00219.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
Watanabe CK, Wood WI;  
WPI; 2000-572270/53.  
Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
treatment, diagnosis and prevention of cancer -  
Example 17; Page 125; 286pp; English.  
The present invention describes an isolated antibody that binds to  
one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
PRO1025, PRO1030, PRO1037, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
growth. The PRO polypeptides and nucleotides are useful in the  
treatment, diagnosis and prevention of cancer. The antibodies and other  
anti-tumour compounds may be used to treat various conditions, including  
those characterised by overexpression and/or activation of the amplified  
PRO genes. Exemplary conditions or disorders to be treated with such  
antibodies and other compounds include benign or malignant tumours  
(e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
leukaemia and lymphoid malignancies, other disorders such as neuronal,  
glial, astrocytal, hypothalamic and other glandular, macrophagal,  
epithelial, stromal and blastocoele disorders, and inflammatory,  
angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
primers and hybridisation probes used in the isolation of the human PRO  
sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
PRO polynucleotide and protein sequences given in the exemplification of  
the present invention.  
Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;

Query Match 2.3%; Score 50; DB 21; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6.3e-14;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 350 CCACCACTGGAGTCTGAGTGGGAGGAACTCCATCCGCGAGATTG 399  
Db 1 CCACCACTGGAGTCTGAGTGGGAGGAACTCCATCCGCGAGATTG 50  
RESULT 32  
AAZ65183  
ID AAZ65183 standard; DNA; 50 BP.  
AC AAZ65183;  
DT 05-APR-2000 (first entry)  
DE Probe specific for human PRO1111.  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
pharmaceutical; receptor immunoadhesin; gene mapping; probe; ss.  
Homo sapiens.  
WO9963088-A2.  
09-DEC-1999.  
02-JUN-1999; 99WO-US12252.  
02-JUN-1998; 98US-0087607.  
02-JUN-1998; 98US-0087609.  
02-JUN-1998; 98US-0087759.  
03-JUN-1998; 98US-0087827.  
04-JUN-1998; 98US-0088021.  
04-JUN-1998; 98US-0088025.  
04-JUN-1998; 98US-0088028.  
04-JUN-1998; 98US-0088029.  
04-JUN-1998; 98US-0088030.  
04-JUN-1998; 98US-0088033.  
04-JUN-1998; 98US-0088326.  
05-JUN-1998; 98US-0088167.  
05-JUN-1998; 98US-0088202.  
05-JUN-1998; 98US-0088212.  
05-JUN-1998; 98US-0088217.  
09-JUN-1998; 98US-0088655.  
10-JUN-1998; 98US-0088722.  
10-JUN-1998; 98US-0088730.  
10-JUN-1998; 98US-0088734.  
10-JUN-1998; 98US-0088738.  
10-JUN-1998; 98US-0088740.  
10-JUN-1998; 98US-0088741.  
10-JUN-1998; 98US-0088742.  
10-JUN-1998; 98US-0088810.  
10-JUN-1998; 98US-0088811.  
10-JUN-1998; 98US-0088824.  
10-JUN-1998; 98US-0088825.  
10-JUN-1998; 98US-0088826.  
11-JUN-1998; 98US-0088858.  
11-JUN-1998; 98US-0088861.  
11-JUN-1998; 98US-0088863.  
11-JUN-1998; 98US-0088876.  
12-JUN-1998; 98US-0089090.  
12-JUN-1998; 98US-0089105.  
16-JUN-1998; 98US-0089440.  
16-JUN-1998; 98US-0089512.  
16-JUN-1998; 98US-0089514.  
17-JUN-1998; 98US-0089532.  
17-JUN-1998; 98US-0089538.  
17-JUN-1998; 98US-0089598.  
17-JUN-1998; 98US-0089599.  
17-JUN-1998; 98US-0089600.  
17-JUN-1998; 98US-0089653.  
18-JUN-1998; 98US-0089801.  
18-JUN-1998; 98US-0089907.

PR 18-JUN-1998; 98US-0089903.  
 PR 19-JUN-1998; 98US-0089947.  
 PR 19-JUN-1998; 98US-0089948.  
 PR 19-JUN-1998; 98US-0089952.  
 PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091544.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091645.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 07-JUL-1998; 98US-0091982.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 12-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096959.

PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.

(GETH ) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 Wood WI, Yuan J;

WPI; 2000-072883/06.

Membrane-bound proteins and related nucleotide sequences

Example 67; Page 431; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;

Query Match 2.3%; Score 50; DB 21; Length 50;

Best Local Similarity 100.0%; Pred. NO. 6.3e-14; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 CCACCACCTGGAGGTCCTGCAGTTGGCGCAGGAATCCATCCGCGCAGATTG 399

1 CCACCACCTGGAGGTCCTGCAGTTGGCGCAGGAATCCATCCGCGCAGATTG 50  
 |||||

RESULT 33

AAF44340

ID AAF44340 standard; DNA; 50 BP.

XX

AC AAF44340;

XX

DT 02-APR-2001 (first entry)

XX

DE Human PRO1111 hybridisation probe SEQ ID NO:251.

XX Human; secreted and transmembrane protein; PRO; cytostatic;

KW Cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

KW diagnostic assay; PCR primer; hybridisation; probe; ss.

XX Homo sapiens.

OS

XX

PN WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

XX 15-SEP-1999; 99WO-US21090.

XX 13-SEP-1999; 99WO-US21547.

XX 08-OCT-1999; 99US-0158663.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US05004.

XX 28-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

(GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Borstein D, Deanovers L, Eaton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi CJ, Gurney AL, Kijavini JJ, Napier MA, Pan J, Pechi NF;

XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;

XX Zhang Z;

XX WPI; 2001-032160/04.

XX PRO polynucleotides used to produce polypeptides used to target

XX bioactive molecules such as toxins, radiolabels or antibodies, to

XX specific cells, to cause targeted cell death -

XX Example 67; Page 457; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

XX proteins. The PRO proteins have cytostatic activity. The PRO proteins

XX can be used for targeted delivery of bioactive molecules, such as

XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

XX sequences, and their fragments, can be used as hybridisation probes, in

XX chromosomal and gene mapping, and in the generation of anti-sense RNA

XX and DNA. They may also be used to produce transgenic animals which are

XX used to develop and screen therapeutically useful reagents. The PRO

XX nucleotide and protein sequence can be used for tissue typing and in

XX treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

XX AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

XX in the isolation of human PRO sequences. AAF44087 to AAF44269 and

XX AAB65154 to AAB65300 represent human PRO polynucleotide and protein

XX sequences given in the exemplification of the present invention.

XX Q Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;

XX Query Match 2.3%; Score 50; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 6.3e-14;

XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Y 350 CCACCACCTGGAGTCTCGAGTGGGCGAGGACTCCATCCGCGAGATG 399

XX b 1 CCACCACCTGGAGTCTCGAGTGGGCGAGGACTCCATCCGCGAGATG 50

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ABX80286  
ID ABX80286 standard; DNA; 50 BP.  
XX AC ABX80286;  
XX DT 28-APR-2003 (first entry)  
XX DE Novel human secreted or transmembrane protein PRO1138 DNA.  
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX KW cardiac insufficiency disorder; cancer; tumour; immune response;  
XX KW adrenal cortical capillary endothelial growth; c-fos induction;  
XX KW vascular endothelial growth factor inhibition; VEGF inhibition;  
XX KW endothelial cell growth inhibitor; r-lymphocytes stimulation;  
XX KW retinal neurons cell survival; rod photoreceptor cell survival;  
XX KW retinal disorder; retinitis pigmentosa; kidney disorder;  
XX KW mammalian kidney mesangial cell proliferation; Berger disease;  
XX KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;  
XX KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX OS Homo sapiens.  
XX PN US2002132252-A1.  
XX PD 19-SEP-2002.  
XX PF 14-NOV-2001; 2001US-0990442.  
XX PR 05-NOV-1997; 97WO-US20069.  
XX PR 16-SEP-1998; 98WO-US19330.  
XX PR 17-SEP-1998; 98WO-US19437.  
XX PR 07-OCT-1998; 98WO-US21141.  
XX PR 01-DEC-1998; 98WO-US25108.  
XX PR 05-JAN-1999; 99WO-US00106.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 02-JUN-1999; 99WO-US12252.  
XX PR 15-SEP-1999; 99WO-US21090.  
XX PR 15-SEP-1999; 99WO-US21547.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 01-DEC-1999; 99WO-US28301.  
XX PR 01-DEC-1999; 99WO-US28634.  
XX PR 16-DEC-1999; 99WO-US30095.  
XX PR 20-DEC-1999; 99WO-US30911.  
XX PR 06-JAN-2000; 2000WO-US00219.  
XX PR 06-JAN-2000; 2000WO-US00376.  
XX PR 11-FEB-2000; 2000WO-US03565.  
XX PR 18-FEB-2000; 2000WO-US04341.  
XX PR 22-FEB-2000; 2000WO-US04414.  
XX PR 24-FEB-2000; 2000WO-US04914.  
XX PR 24-FEB-2000; 2000WO-US05004.  
XX PR 02-MAR-2000; 2000WO-US05841.  
XX PR 10-MAR-2000; 2000WO-US06319.  
XX PR 15-MAR-2000; 2000WO-US06884.  
XX PR 20-MAR-2000; 2000WO-US07377.  
XX PR 30-MAR-2000; 2000WO-US08439.  
XX PR 15-MAY-2000; 2000WO-US13358.  
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 PR 18-JUN-1998; 98US-089807P.  
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 PR 28-AUG-2001; 2001US-0941992.  
 (GETH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kijavini IG, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-247083/24.  
 DR P-PSDB; ABUS9117.  
 XX  
 DR Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments -  
 PT  
 XX Claim 2; Fig 170; 648pp; English.  
 PS  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186

CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO12 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.  
 XX  
 SQ Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;  
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 ID ABX80790 standard; DNA; 50 BP.  
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 DT 22-APR-2003 (first entry)  
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 DE Human secreted/transmembrane protein, probe #2.  
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 KW Human; probe; ss; PRO; secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioindicator; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
 XX  
 OS Homo sapiens.  
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 PN US2003027162-A1.  
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 PD 06-FEB-2003.  
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 PF 15-NOV-2001; 2001US-0997428.  
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 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
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 PR 07-OCT-1998; 98WO-US21141.  
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 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
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QY 350 CCACCACTGAGGCTCTGACCTGGCAGGAACTCCATCCGCGAGATTG 399
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AC ABX81173;
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DT 22-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO1138 DNA.
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumor; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
XX
OS Homo sapiens.
XX
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PD 06-FEB-2003.
XX
PF 14-NOV-2001; 2001US-0990562.
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XX AC ABX90263;  
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XX DE Human secreted/transmembrane protein, #93, probe.  
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XX KW pharmaceutical; diagnostic; therapeutic; gene therapy.  
XX OS Homo sapiens.  
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XX PD 31-OCT-2002.  
XX PF 14-NOV-2001; 2001US-0992598.  
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 PR 11-JUN-1998; 98US-088861P.  
 PR 12-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089807P.  
 PR 18-JUN-1998; 98US-089808P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX (GSH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 XX Ferrera N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;  
 XX Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
 XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 XX Zhang Z;  
 XX WPI; 2003-288106/28.

PT New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, or in generating probes -  
 XX Example 67; Page 247; 650pp; English.  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful in gene therapy, in chromosome  
 CC identification, as chromosome markers, or in generating probes. The PRO  
 CC polypeptides are useful as molecular markers for protein  
 CC electrophoresis, and the isolated nucleic acids may be used for  
 CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
 CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 CC in diagnostic assays for PRO, and in affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The sequences presented in  
 CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
 CC probes detecting the PRO polynucleotides of the invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;  
 SQ  
 Query Match 2.3%; Score 50; DB 25; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-14;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 350 CCACCACCTGGAGTCTGTCAGTTGGGCGAGCACTCCATCGGCAGATTG 399  
 DB 1 CCACCACCTGGAGTCTGTCAGTTGGGCGAGCACTCCATCGGCAGATTG 50  
 RESULT 38  
 ABX77874  
 ID ABX77874 standard; DNA; 50 BP.  
 XX AC ABX77874;  
 XX DT 14-APR-2003 (first entry)  
 XX DE Human PRO probe #26.  
 XX KW Human; PRO; ss; cytostatic; tumour; cancer; breast; lung; stomach;  
 KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; probe;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX OS Homo sapiens.  
 XX PN US2003027163-A1.  
 XX PD 06-FEB-2003.  
 XX PF 15-NOV-2001; 2001US-0997666.  
 XX PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.



PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097552P.  
PR 26-AUG-1998; 98US-097554P.  
PR 26-AUG-1998; 98US-097555P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 98US-123957P.  
PR 23-JUN-1999; 98US-141037P.  
PR 07-JUL-1999; 99US-143048P.  
  
Query Match 2.3%; Score 50; DB 25; length 50;  
Best Local Similarity 100.0%; Pred. No. 6.3e-14;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 350 CCACCCTGAGGTCCTGCGAGTGGCGAGCACTCCATCCGCGAGATTG 399  
Db 1 CCACCCTGAGGTCCTGCGAGTGGCGAGCACTCCATCCGCGAGATTG 50  
  
RESULT 39  
ABX79470  
ID ABX79470 standard; DNA; 50 BP.  
XX AC ABX79470;  
XX DT 17-Apr-2003 (first entry)  
XX DE Human secreted/transmembrane protein, probe #2.  
XX KW Human; probe; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; biosensor; bioindicator; tumor; therapeutic;  
KN colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
XX OS Homo sapiens.  
XX US2002142961-A1.  
XX PD 03-OCT-2002.  
XX PF 19-NOV-2001; 2001US-0989721.  
XX PR 05-NOV-1997; 97WO-US20069.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 03-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 09-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 11-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089536P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 18-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
  
(GETH ) GENENTECH INC.  
XX XX  
XX XX

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grisaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF, Roy MA, Stewart RA, Tumas D, Watanabe CK, Williams PM, Wood WI, Zhang Z;  
WPI; 2003-155950/15.  
New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Disclosure; SEQ ID NO 251; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX79290-ABX79675 are the genes encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention.

Note: The sequence data for this patent is also available in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 50 BP; 10 A; 15 C; 15 G; 9 T; 0 other;

Query Match 2.3%; Score 50; DB 25; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6.3e-14;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 350 CCACCACCTGGAGGTCCTGTCAGTGGGAGGAGCACTCCATCCGGCAGATTG 399  
C 1 CCACCACCTGGAGGTCCTGTCAGTGGGAGGAGCACTCCATCCGGCAGATTG 50

RESULT 40

YX64109

C ABX64109 standard; DNA; 50 BP.

C ABX64109;

I 26-FEB-2003 (first entry)

X Human PRO DNA probe #24.

X Human; PRO polypeptide; secreted protein; transmembrane protein;  
X Genetic disorder; antibacterial; immunosuppressive; probe; ss.

X Homo sapiens.

X US2002103125-A1.

X 01-AUG-2002.

X 20-NOV-2001; 2001US-0989731.

X 05-NOV-1997; 97WO-US200069.

X 16-SEP-1998; 98WO-US19330.

X 17-SEP-1998; 98WO-US19437.

X 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 28-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065316P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 03-JUN-1998; 98US-087759P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.



11-JUN-1998; 98US-088861P.  
 11-JUN-1998; 98US-088876P.  
 12-JUN-1998; 98US-089105P.  
 16-JUN-1998; 98US-089400P.  
 16-JUN-1998; 98US-089512P.  
 16-JUN-1998; 98US-089514P.  
 17-JUN-1998; 98US-089532P.  
 17-JUN-1998; 98US-089538P.  
 17-JUN-1998; 98US-089598P.  
 17-JUN-1998; 98US-089599P.  
 17-JUN-1998; 98US-089600P.  
 17-JUN-1998; 98US-089653P.  
 18-JUN-1998; 98US-089801P.  
 18-JUN-1998; 98US-089907P.  
 18-JUN-1998; 98US-089908P.  
 28-AUG-2001; 2001US-094132P.

(GETH ) GENENTECH LTD.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ,  
 Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoli NF,  
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 Zhang Z;  
 WPI; 2003-102117/09.

Novel secreted and transmembrane polypeptide for modulating biological

activity of cell expressing the polypeptide, identifying agonists or  
 antagonists of polypeptide, and as molecular weight markers

Example 67; Page 246; 649pp; English.

The present invention relates to the isolation of novel human PRO  
 polypeptides, and the polynucleotide sequences encoding them. The  
 PRO polypeptides are secreted and transmembrane proteins. The PRO  
 polypeptides are useful for detecting other PRO polypeptides, for  
 linking bioactive molecules to cells expressing PRO polypeptides,  
 for modulating biological activities of cells expressing PRO  
 polypeptides, and for identifying agonists or antagonists.  
 The polynucleotide sequences encoding PRO polypeptides are useful as  
 hybridisation probes, in chromosome and gene mapping, in the generation  
 of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
 generating transgenic animals or knockout animals, to construct  
 hybridisation probes for mapping the gene which encodes the PRO  
 polypeptide, and for the genetic analysis of individuals with genetic  
 disorders, in gene therapy, for chromosome identification, as  
 chromosome markers, and for generating probes for PCR, Northern  
 analysis, Southern analysis and Western analysis. The present sequence  
 represents a probe used in the examples of the present invention.  
 Note: The sequence data for this patent was obtained in electronic  
 format directly from the USPTO web site at  
 seqdata.uspto.gov/psipdbentry.html.

Sequence 50 BP; 10 A; 16 C; 15 G; 9 T; 0 other;

Query Match 2.3%; Score 50; DB 25; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-14;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

350 CCACCACTGGAGGTCCTGAGTTGGGAGGAACTCCATCGGCGAGATTG 399  
 1 CCACCACTGGAGGTCCTGAGTTGGGAGGAACTCCATCGGCGAGATTG 50

RESULT 41

ABX17073

ID ABX17073 standard; DNA; 50 BP.

XX

AC

ABX17073;

XX

04-FEB-2003 (first entry)

DT

DE Human PRO probe #25.  
 XX Human; PRO; probe; ss: secreted polypeptide; transmembrane polypeptide;  
 KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
 KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
 KW antibacterial.  
 XX OS  
 XX Homo sapiens.  
 XX US2002123463-A1.  
 XX 05-SEP-2002.  
 PD  
 XX 19-NOV-2001; 2001US-0989732.  
 XX 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.



CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,  
 CC epithelial, stromal and blastocellic disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 CC primers and hybridisation probes used in the isolation of the human PRO  
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 CC PRO polynucleotide and protein sequences given in the exemplification of  
 CC the present invention.

XX Sequence 31 BP; 7 A; 15 C; 2 G; 7 T; 0 other;

Query Match 1.4%; Score 31; DB 21; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 0.00613;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1930 ACTCTCTGCACCCACAGTCACCACTATCTC 1960  
 Db 1 ACTCTCTGCACCCACAGTCACCACTATCTC 31

RESULT 43  
 AAF44427  
 ID AAF44427 standard; DNA; 31 BP.

XX RAA44427;

AC RAA44427;

DT 02-APR-2001 (first entry)

DE Human PRO1111 hybridisation probe SEQ ID NO:466.

XX Human; secreted and transmembrane protein; PRO: cytostatic;

KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

KW diagnostic assay; PCR primer; hybridisation; probe; ss.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 08-OCT-1999; 99US-0158663.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 02-MAR-2000; 2000WO-US05004.

XX 15-MAR-2000; 2000WO-US05841.

XX 20-MAR-2000; 2000WO-US06984.

XX 20-MAR-2000; 2000WO-US07377.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Baton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PU;

XX Grimaldi CJ, Gurney AL, Kijavini IJ, Napier WA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI; 2001-032160/04.

DR PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Example 170; Page 542; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytostatic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA

CC and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in

CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and

CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 31 BP; 7 A; 15 C; 2 G; 7 T; 0 other;

Query Match 1.4%; Score 31; DB 22; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.00613;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1930 ACTCTCTGCACCCACAGTCACCACTATCTC 1960

Db 1 ACTCTCTGCACCCACAGTCACCACTATCTC 31

RESULT 44

ABX80436

ID ABX80436 standard; DNA; 31 BP.

XX ABX80436;

AC ABX80436;

XX 28-APR-2003 (first entry)

XX Human secreted or transmembrane protein related PCR primer #122.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

XX cardiac insufficiency disorder; cancer; tumour; immune response;

XX adrenal cortical capillary endothelial growth; c-fos induction;

XX vascular endothelial growth factor inhibition; VEGF inhibition;

XX endothelial cell growth inhibitor; T-lymphocytes stimulation;

XX retinal neurons cell survival; rod photoreceptor cell survival;

XX retinal disorder; retinitis pigmentosa; kidney disorder;

XX mammalian kidney mesangial cell proliferation; Berger disease;

XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;

XX chondrocyte redifferentiation; sports injury; arthritis; PCR;

XX primer; ss.

XX Homo sapiens.

XX US2002132252-A1.

XX 19-SEP-2002.

XX 14-NOV-2001; 2001US-0990442.

XX 05-NOV-1997; 97WO-US20069.

XX 16-SEP-1998; 98WO-US19330.

XX 17-SEP-1998; 98WO-US19437.

XX 07-OCT-1998; 98WO-US21141.

XX 01-DEC-1998; 98WO-US25108.

XX 05-JAN-1999; 99WO-US00106.

R 08-MAR-1999; 99WO-US05028.  
R 02-JUN-1999; 99WO-US12252.  
R 15-SEP-1999; 99WO-US21090.  
R 15-SEP-1999; 99WO-US21547.  
R 30-NOV-1999; 99WO-US28313.  
R 01-DEC-1999; 99WO-US28301.  
R 01-DEC-1999; 99WO-US28634.  
R 16-DEC-1999; 99WO-US30095.  
R 20-DEC-1999; 99WO-US30911.  
R 06-JAN-2000; 2000WO-US00219.  
R 06-JAN-2000; 2000WO-US00376.  
R 11-FEB-2000; 2000WO-US03565.  
R 18-FEB-2000; 2000WO-US04341.  
R 22-FEB-2000; 2000WO-US04414.  
R 24-FEB-2000; 2000WO-US04914.  
R 24-FEB-2000; 2000WO-US05004.  
R 02-MAR-2000; 2000WO-US05841.  
R 10-MAR-2000; 2000WO-US06319.  
R 15-MAR-2000; 2000WO-US06884.  
R 20-MAR-2000; 2000WO-US07177.  
R 30-MAR-2000; 2000WO-US08439.  
R 15-MAY-2000; 2000WO-US13358.  
R 17-MAY-2000; 2000WO-US13705.  
R 22-MAY-2000; 2000WO-US14042.  
R 30-MAY-2000; 2000WO-US14941.  
R 02-JUN-2000; 2000WO-US15264.  
R 28-JUL-2000; 2000WO-US20710.  
R 11-AUG-2000; 2000WO-US22031.  
R 23-AUG-2000; 2000WO-US23522.  
R 24-AUG-2000; 2000WO-US23328.  
R 08-NOV-2000; 2000WO-US30952.  
R 01-DEC-2000; 2000WO-US32678.  
R 28-FEB-2001; 2001WO-US06520.  
R 01-JUN-2001; 2001WO-US17800.  
R 29-JUN-2001; 2001WO-US19892.  
R 09-JUL-2001; 2001WO-US21066.  
R 16-JUN-1997; 97US-U021735.  
R 17-OCT-1997; 97US-U062250P.  
R 12-NOV-1997; 97US-U05186P.  
R 13-NOV-1997; 97US-U05311P.  
R 24-NOV-1997; 97US-U06770P.  
R 25-FEB-1998; 98US-U05945P.  
R 20-MAR-1998; 98US-U078910P.  
R 28-APR-1998; 98US-U083322P.  
R 07-MAY-1998; 98US-U094600P.  
R 28-MAY-1998; 98US-U097106P.  
R 02-JUN-1998; 98US-U097607P.  
R 02-JUN-1998; 98US-U097609P.  
R 02-JUN-1998; 98US-U097759P.  
R 04-JUN-1998; 98US-U087827P.  
R 04-JUN-1998; 98US-U088021P.  
R 04-JUN-1998; 98US-U088025P.  
R 04-JUN-1998; 98US-U088026P.  
R 04-JUN-1998; 98US-U088028P.  
R 04-JUN-1998; 98US-U088029P.  
R 04-JUN-1998; 98US-U088030P.  
R 04-JUN-1998; 98US-U088033P.  
R 04-JUN-1998; 98US-U088326P.  
R 05-JUN-1998; 98US-U088167P.  
R 05-JUN-1998; 98US-U088202P.  
R 05-JUN-1998; 98US-U088212P.  
R 05-JUN-1998; 98US-U088217P.  
R 09-JUN-1998; 98US-U088655P.  
R 10-JUN-1998; 98US-U088734P.  
R 10-JUN-1998; 98US-U088738P.  
R 10-JUN-1998; 98US-U088742P.  
R 10-JUN-1998; 98US-U088810P.  
R 10-JUN-1998; 98US-U088824P.  
R 10-JUN-1998; 98US-U088826P.  
R 11-JUN-1998; 98US-U088858P.  
R 11-JUN-1998; 98US-U088861P.  
R 11-JUN-1998; 98US-U088876P.

PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Kujavin IJ, Napier MA, Pan J, Paoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
XX WPI; 2003-247083/24.  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX are therapeutically useful for enhancing immune response and in cancer  
XX treatments -  
XX Example 170; Page 294; 648pp; English.  
XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
XX in modulating at least one biological activity of a cell expressing a PRO  
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,  
XX PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
XX useful for treating conditions or disorders where angiogenesis would be  
XX beneficial, e.g. wound healing and antagonist of this polypeptide are  
XX useful for treating cancerous tumours. PRO812 inhibits vascular  
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial  
XX cells and is thus useful for inhibiting endothelial cell growth in  
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,  
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
XX stimulated T-lymphocytes and are therapeutically useful for enhancing  
XX immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
XX rod photoreceptor cells) and therefore are useful for treating retinal  
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
XX and therefore are useful for treating kidney disorders associated with  
XX decreased mesangial cell function such as Berger disease or other  
XX nephropathies associated with dermatitis, herpiformis or Crohn's  
XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
XX proliferation and/or redifferentiation of chondrocytes in culture and  
XX are thus useful for treating sports injuries, and arthritis. This  
XX sequence represents a primer used in the isolation of DNA encoding  
XX novel human PRO polypeptides.  
XX Sequence 31 BP; 7 A; 15 C; 2 G; 7 T; 0 other;

Query Match 1.4%; Score 31; DB 25; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1930 ACTCTGACCCCACTGACCACTATCTC 1960  
Db 1 ACTCTGACCCCACTGACCACTATCTC 31

RESULT 45  
ABX80940  
ID ABX80940 standard; DNA; 31 BP.  
XX AC  
XX ABX80940;  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein, TaqMan probe #13.  
XX  
KW Human; probe; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; TaqMan;  
KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
JS Homo sapiens.  
XX  
XX US2003027162-A1.  
XX  
XX  
PD 06-FEB-2003.  
XX  
XX  
XX 15-NOV-2001; 2001US-0997428.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28303.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US40095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-US49787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-065770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-075910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088128P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088744P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089588P.  
PR 17-JUN-1998; 98US-089593P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090423P.  
PR 24-JUN-1998; 98US-090431P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
PR 24-JUN-1998; 98US-090472P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 24-JUN-1998; 98US-090542P.  
PR 24-JUN-1998; 98US-090557P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 25-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091519P.

R 02-JUL-1998; 98US-091626P.  
R 02-JUL-1998; 98US-091628P.  
R 02-JUL-1998; 98US-091633P.  
R 02-JUL-1998; 98US-091646P.  
R 02-JUL-1998; 98US-091673P.  
R 07-JUL-1998; 98US-091978P.  
R 07-JUL-1998; 98US-091982P.  
R 09-JUL-1998; 98US-092182P.  
R 10-JUL-1998; 98US-092472P.  
R 20-JUL-1998; 98US-093339P.  
R 30-JUL-1998; 98US-094651P.  
R 04-AUG-1998; 98US-095282P.  
R 04-AUG-1998; 98US-095285P.  
R 04-AUG-1998; 98US-095301P.  
R 04-AUG-1998; 98US-095302P.  
R 04-AUG-1998; 98US-095318P.  
R 04-AUG-1998; 98US-095321P.  
R 04-AUG-1998; 98US-095325P.  
R 10-AUG-1998; 98US-095916P.  
R 10-AUG-1998; 98US-095929P.  
R 11-AUG-1998; 98US-096012P.  
R 11-AUG-1998; 98US-096143P.  
R 12-AUG-1998; 98US-096146P.  
R 12-AUG-1998; 98US-096329P.  
R 17-AUG-1998; 98US-096757P.  
R 17-AUG-1998; 98US-096766P.  
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R 17-AUG-1998; 98US-096773P.  
R 17-AUG-1998; 98US-096791P.  
R 17-AUG-1998; 98US-096877P.  
R 17-AUG-1998; 98US-096891P.  
R 17-AUG-1998; 98US-096894P.  
R 17-AUG-1998; 98US-096895P.  
R 17-AUG-1998; 98US-096897P.  
R 18-AUG-1998; 98US-096949P.  
R 18-AUG-1998; 98US-096950P.  
R 18-AUG-1998; 98US-096959P.  
R 18-AUG-1998; 98US-096960P.  
R 18-AUG-1998; 98US-097022P.  
R 19-AUG-1998; 98US-097141P.  
R 20-AUG-1998; 98US-097218P.  
R 24-AUG-1998; 98US-097661P.  
R 24-AUG-1998; 98US-097652P.  
R 26-AUG-1998; 98US-097944P.  
R 26-AUG-1998; 98US-097955P.  
R 26-AUG-1998; 98US-097971P.  
R 26-AUG-1998; 98US-097974P.  
R 26-AUG-1998; 98US-097978P.  
R 26-AUG-1998; 98US-097979P.  
R 26-AUG-1998; 98US-097986P.  
R 26-AUG-1998; 98US-098014P.  
R 31-AUG-1998; 98US-098525P.  
R 16-SEP-1998; 98US-100634P.  
R 17-SEP-1998; 98US-100858P.  
R 22-DEC-1998; 98US-113296P.  
R 12-MAR-1999; 98US-123957P.  
R 23-JUN-1999; 98US-141037P.

Query Match 1.4%; Score 31; DB 25; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1930 ACTCTGACCCACAGTCACCACTATCTC 1960  
|||||  
b 1 ACTCTGACCCACAGTCACCACTATCTC 31

RESULT 46  
BX81323  
D AX81323 standard; DNA; 31 bp.  
X C AX81323;  
X

DT 22-APR-2003 (first entry)  
XX Human secreted or transmembrane protein related PCR primer #122.  
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; PCR;  
XX primer; ss.  
XX Homo sapiens.  
XX US2003027985-A1.  
XX 06-FEB-2003.  
XX 14-NOV-2001; 2001US-0990562.  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US00106.  
PR 08-MAR-1999; 98WO-US05028.  
PR 02-JUN-1999; 98WO-US12252.  
PR 15-SEP-1999; 98WO-US21090.  
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RESULT 47

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XX

AC ABX90413;

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DT 01-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, TaqMan probe #13.

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 KW Human; probe; ss; PRO; secreted; transmembrane; signal peptide;  
 KW pharmaceutical; diagnostic; therapeutic; gene therapy; TaqMan.  
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RESULT 48  
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XX AC ABX78024;  
XX DT 14-APR-2003 (first entry)  
XX DE Human PRO probe #51.  
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KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ABPT; probe;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX OS Homo sapiens.  
XX PN US2003027163-A1.  
XX PD 06-FEB-2003.  
XX PF 15-NOV-2001; 2001US-0997666.  
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70			PR	02-JUN-1998; 98US-087609P.	
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1 ACTCTCTGACCCACAGTCACCACTATCTC 31

RESULT 49

3X79620

ABX79620 standard; DNA; 31 BP.

ABX79620;

PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 11-JUN-1998; 98US-088838P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089807P.  
PR 18-JUN-1998; 98US-089808P.  
PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Rotstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-155950/15.

XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
PT PRO361 or PRO366) useful as targets for therapeutic intervention in  
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers

XX Example 170; Page 294; 647pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
CC biosensors or bioeffectors, for detecting or treating e.g. tumours in  
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, goats or  
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
CC colon, lung or breast cancers) and diagnostic determination of the  
CC presence of these cancers. The PRO polypeptides are also useful as  
CC molecular weight markers or for chromosome identification. The PRO genes  
CC are useful as hybridisation probes or for screening libraries of human  
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. The sequences  
CC presented in ABX7290-ABX79675 are the genes encoding, the primers  
CC amplifying and the probes detecting the PRO polynucleotides of the  
CC invention.

CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX SQ Sequence 31 BP; 7 A; 15 C; 2 G; 7 T; 0 other;

Query Match 1.4%; Score 31; DB 25; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1930 ACTCTCTCCACCCACAGTACCACTATCTC 1960

|||||

DB 1 ACTCTCTCCACCCACAGTACCACTATCTC 31

RESULT 50

ABX64259

ID ABX64259 standard; DNA; 31 BP.

AC ABX64259;

XX 26-FEB-2003 (first entry)

XX Human PRO DNA probe #49.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW Genetic disorder; antibacterial; immunosuppressive; probe; ss.

XX Homo sapiens.

XX US2002103125-A1.

XX 01-AUG-2002.

XX 20-NOV-2001; 2001US-0989731.

PR 05-NOV-1997; 97WO-US20069.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US26313.

PR 01-DEC-1999; 99WO-US26301.

PR 01-DEC-1999; 99WO-US26634.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 06-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US08439.

PR 15-MAY-2000; 2000WO-US13358.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23522.

PR 04-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US30952.

PR 01-DEC-2000; 2000WO-US32678.

28-FEB-2001; 2001WO-US06520.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
29-JUN-2001; 2001WO-US21066.  
09-JUL-2001; 2001WO-US21735.  
16-JUN-1997; 97US-049787P.  
17-OCT-1997; 97US-062250P.  
13-NOV-1997; 97US-065186P.  
13-NOV-1997; 97US-065311P.  
24-NOV-1997; 97US-066770P.  
25-FEB-1998; 98US-075945P.  
20-MAR-1998; 98US-078310P.  
28-APR-1998; 98US-083322P.  
07-MAY-1998; 98US-084600P.  
28-MAY-1998; 98US-087106P.  
02-JUN-1998; 98US-087609P.  
02-JUN-1998; 98US-087759P.  
03-JUN-1998; 98US-087827P.  
04-JUN-1998; 98US-088021P.  
04-JUN-1998; 98US-088025P.  
04-JUN-1998; 98US-088026P.  
04-JUN-1998; 98US-088028P.  
04-JUN-1998; 98US-088029P.  
04-JUN-1998; 98US-088030P.  
04-JUN-1998; 98US-088033P.  
04-JUN-1998; 98US-088326P.  
05-JUN-1998; 98US-088167P.  
05-JUN-1998; 98US-088202P.  
05-JUN-1998; 98US-088212P.  
05-JUN-1998; 98US-088217P.  
09-JUN-1998; 98US-088555P.  
10-JUN-1998; 98US-088734P.  
10-JUN-1998; 98US-088738P.  
10-JUN-1998; 98US-088742P.  
10-JUN-1998; 98US-088810P.  
10-JUN-1998; 98US-088824P.  
10-JUN-1998; 98US-088826P.  
11-JUN-1998; 98US-088858P.  
11-JUN-1998; 98US-088861P.  
11-JUN-1998; 98US-088876P.  
12-JUN-1998; 98US-089105P.  
16-JUN-1998; 98US-089440P.  
16-JUN-1998; 98US-089512P.  
16-JUN-1998; 98US-089514P.  
17-JUN-1998; 98US-089532P.  
17-JUN-1998; 98US-089538P.  
17-JUN-1998; 98US-089598P.  
17-JUN-1998; 98US-089599P.  
17-JUN-1998; 98US-089600P.  
17-JUN-1998; 98US-089653P.  
18-JUN-1998; 98US-089801P.  
18-JUN-1998; 98US-089907P.  
18-JUN-1998; 98US-089908P.  
28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH LTD.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kujavin LU, Napier MA, Pan J, Paoni NF;  
Roy MP, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI; 2003-102117/09.

Novel secreted and transmembrane polypeptide for modulating biological  
activity of cell expressing the polypeptide, identifying agonists or  
antagonists of polypeptide, and as molecular weight markers

Example 170; Page 294; 649pp; English.

The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for  
CC linking bioactive molecules to cells expressing PRO polypeptides,  
CC for modulating biological activities of cells expressing PRO  
CC polypeptides, and for identifying agonists or antagonists.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
CC generating transgenic animals or knockout animals, to construct  
CC hybridisation probes for mapping the gene which encodes the PRO  
CC polypeptide, and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as  
CC chromosome markers, and for generating probes for PCR, Northern  
CC analysis, Southern analysis and Western analysis. The present sequence  
CC represents a probe used in the examples of the present invention.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsiDEntry.html.

XX  
SQ Sequence 31 BP; 7 A; 15 C; 2 G; 7 T; 0 other;

Query Match 1.4%; Score 31; DB 25; Length 31;  
Best Local Similarity 100.0%; Pred.No. 0.00019;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1930 ACTCTCTGACCCACAGTCACCACTATCTC 1960  
Db 1 ACTCTCTGACCCACAGTCACCACTATCTC 31

Search completed: February 6, 2004, 02:47:46  
Job time : 591 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

Multiple nucleic - nucleic search, using sw model

Run on: February 5, 2004, 22:30:48 ; Search time 4163 Seconds  
(without alignments)  
12756.493 Million cell updates/sec

File: US-09-989-279-228  
Effect score: 2185  
Sequence: 1 gttcccttcgagccaaa.....aaagacaaaagtcaaaaaca 2185

Scoring table: OLIGO\_NUC  
Gap 60.0, Gapext 60.0

Aligned: 22781392 seqs, 12152238056 residues

Word size: 10

Total number of hits satisfying chosen parameters: 29496677

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database:

EST:

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hic.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_hic.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_bum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_pqg.\*
- 27: em\_gss\_vri.\*
- 28: gb\_ges1.\*
- 29: gb\_ges2.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
C 1	621	28.4	564	13	BQ185392
C 2	569	26.0	590	13	BQ185165
C 3	563	25.8	711	12	BM975435
C 4	540	24.7	540	13	BQ187977
					BQ185392 UI-E-EJ1-
					BQ185165 UI-E-EJ1-
					BM975435 UI-CF-EN1
					BQ187977 UI-E-EJ1-

806	9	AV709803
504	13	BX114395
478	9	AI769814
540	13	BQ189063
447	9	AI435407
514	13	BQ184873
609	13	BQ340625
780	14	CA310827
509	13	BU789069
504	13	BU789663
393	9	AI470931
389	13	BQ340622
424	10	AW954538
362	13	BQ340572
528	14	H23116
630	12	BM724722
472	14	TI5752
430	10	AI323304
458	14	R43906
428	14	R43906
468	12	BM975594
325	14	T13015
483	14	H23117
626	13	BU741381
254	9	AR077185
346	14	T16288
359	14	R71701
544	9	AW524479
224	10	BE550550
273	10	BF50908
336	9	AI845568
356	10	B8505784
485	14	CA9807028
883	11	AX0476781
283	13	BQ368354
505	9	AI769160
150	9	AA24351
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437	9	AI5168859
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288	9	AA232802
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256	10	BB700307
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565	12	BB009844
881	12	BB087668
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883	10	EF165865
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258	10	B8356521
293	10	B8333179
337	14	T27055
271	10	BB331347
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442	14	AI9556
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287	10	B8307316
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288	10	B8334107
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290	10	B8335857
470	12	BB664085
611	10	BB9654984
249	10	B8338748

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79	57	2.6	283	10	BQ330087	BQ330087	
80	56	2.6	177	10	BQ384608	BQ384608	
81	56	2.6	190	10	BQ170044	BQ170044	
82	56	2.6	190	10	BQ330516	BQ330516	
83	56	2.6	245	10	BQ332977	BQ332977	
84	56	2.6	251	10	BQ547634	BQ547634	
85	56	2.6	256	10	BQ346457	BQ346457	
86	56	2.6	258	10	BQ374788	BQ374788	
87	56	2.6	261	10	BQ332867	BQ332867	
88	56	2.6	266	10	BQ332941	BQ332941	
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93	56	2.6	274	10	BQ129082	BQ129082	
94	56	2.6	276	10	BQ332920	BQ332920	
95	56	2.6	277	10	BQ330616	BQ330616	
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97	56	2.6	278	10	BQ440461	BQ440461	
98	56	2.6	279	10	BQ329980	BQ329980	
99	56	2.6	279	10	BQ334018	BQ334018	
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101	56	2.6	280	10	BQ335811	BQ335811	
102	56	2.6	282	10	BQ333175	BQ333175	
103	56	2.6	284	10	BQ334104	BQ334104	
104	56	2.6	285	10	BQ346200	BQ346200	
105	56	2.6	291	10	BQ268633	BQ268633	
106	56	2.6	304	10	BQ257516	BQ257516	
107	56	2.6	308	10	BQ342834	BQ342834	
108	56	2.6	309	10	BQ265129	BQ265129	
109	56	2.6	439	10	BQ807460	BQ807460	
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111	55	2.5	250	10	BQ330286	BQ330286	
112	55	2.5	438	13	BY359783	BY359783	
113	54	2.5	213	10	BQ332842	BQ332842	
114	54	2.5	222	10	BQ328890	BQ328890	
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119	54	2.5	258	10	BQ335764	BQ335764	
120	54	2.5	259	10	BQ336204	BQ336204	
121	54	2.5	261	10	BQ330405	BQ330405	
122	54	2.5	267	10	BQ335306	BQ335306	
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124	54	2.5	274	10	BQ334203	BQ334203	
125	54	2.5	285	10	BQ329831	BQ329831	
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128	53	2.4	250	10	BQ267841	BQ267841	
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130	52	2.4	241	10	BQ169976	BQ169976	
131	52	2.4	250	10	BQ333010	BQ333010	
132	52	2.4	295	10	BQ332927	BQ332927	
133	52	2.4	427	10	BQ647479	UI-M-BH1-	
134	51	2.3	279	10	BQ333931	BQ333931	
135	51	2.3	287	10	BQ334056	BQ334056	
136	51	2.3	306	10	BQ333136	BQ333136	
137	51	2.3	317	10	BQ269855	BQ269855	
138	50	2.3	279	10	BQ331665	BQ331665	
139	50	2.3	286	10	BQ334084	BQ334084	
140	48	2.2	288	10	BQ336444	BQ336444	
141	48	2.2	487	29	BQ229666	CH230-272	
142	47	2.2	287	10	BQ330035	BQ330035	
143	47	2.2	395	10	BQ286666	ST451257	
144	46	2.1	255	10	BQ335765	BQ335765	
145	46	2.1	257	10	BQ333688	BQ333688	
146	46	2.1	281	10	BQ330892	BQ330892	
147	45	2.1	266	10	BQ331119	BQ331119	
148	45	2.1	290	10	BQ330450	BQ330450	
149	45	2.1	270	10	BQ335154	BQ335154	
150	42	1.9	267	10	BQ336098	BQ336098	

ALIGNMENTS

RESULT 1

BQ185392 664 bp mRNA linear EST 30-APR-2002  
UI-E-EJ1-aju-f-24-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone  
UI-E-EJ1-aju-f-24-0-UI 3', mRNA sequence.  
BQ185392.1 GI:20360943  
EST.  
BQ185392.1  
Homo sapiens  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (Bases 1 to 664)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-72, >POLY A#Simple\_repeat (matched complement) 399-429,  
>(CAG)n#Simple\_repeat (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clones="UI-E-EJ1-aju-f-24-0-UI"  
/tissue\_type="fetal eyes, lens, eye anterior segment,  
optic nerve, retina, Retina Foveal and Macular, RPE and  
Choroid"  
/dev\_stage="fetal and adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-EJ1"  
/note="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-EJ1 is a subtracted cDNA library constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pTT3-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tags for this library are: fetal eyes, AGAATCAGGA  
; lens, CGATACCGA; eye anterior segment, AATGCCGAT;  
Optic nerve, CCATTAGG; retina, CCGCG; Retina Foveal and  
Macular, GFGC; RPE and Choroid, CCTGA. This library was  
created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI).  
TAG LIB=UI-E-EJ1  
TAG\_TISSUE=Foveal and Macular Retina



```
BASE COUNT      134 a   136 c   162 g   232 t
ORIGIN
Query Match      28.4%; Score 621; DB 13; Length 664;
Best Local Similarity 100.0%; Pred. NO. 1.9e-294; Indels 0; Gaps 0;
Matches 621; Conservative 0; Mismatches 0;
1565 GGTGGCAGTACCCGCGACAGACACCACTGACAGATGACAGACGAGCTGGATGAAGTCAT 1624
1647 GGTGGCAGTACCCGCGACAGACACCACTGACAGATGACAGACGAGCTGGATGAAGTCAT 588
1625 GAAGACACCAAGATCATCTGCTGCTTTGGGAGTACTCTGCTAGCTCCGCCAT 1684
1687 GAAGACACCAAGATCATCTGCTGCTTTGGGAGTACTCTGCTAGCTCCGCCAT 528
1685 GTTCATTTGCTCTTATATAAATTCCTAGAGCGGACCCAGCAGCGAGTACAGTCACAGCCGC 1744
1627 GTTCATTTGCTCTTATATAAATTCCTAGAGCGGACCCAGCAGCGAGTACAGTCACAGCCGC 468
1745 CCGGACTGTTGAGATTAATCCAGGTGGAGAGACATCCAGAGCGCAACATCCGACGAGC 1804
1667 CCGGACTGTTGAGATTAATCCAGGTGGAGAGACATCCAGAGCGCAACATCCGACGAGC 408
1805 AACAGCAGCTCCGTCGCTGATCAGGTGAGGCGGACAGTGTGCTGCCACATTCATGA 1864
1607 AACAGCAGCTCCGTCGCTGATCAGGTGAGGCGGACAGTGTGCTGCCACATTCATGA 348
1865 CCATATTAACTTACAAACCTTACAAACAGCAGATGGGGCCCTCTGACAGAGAAACAGCCT 1924
1647 CCATATTAACTTACAAACCTTACAAACAGCAGATGGGGCCCTCTGACAGAGAAACAGCCT 288
1825 GGGGAACTCTGCAACCCAGCAGTACACATCTCTGAACTTATATATTTTATTTTATTTT 1984
1887 GGGGAACTCTGCAACCCAGCAGTACACATCTCTGAACTTATATATTTTATTTTATTTT 228
1885 TACCAAGCAGAGGTACAGGAACTCAATATGACTCCCTCCGCCCAAAATTTATAAA 2044
1627 TACCAAGCAGAGGTACAGGAACTCAATATGACTCCCTCCGCCCAAAATTTATAAA 168
1645 ATGCAATAGATGACACAAAGACAGAACTTTTGTACAGAGTGGGAGAGATTTTCT 2104
167 ATGCAATAGATGACACAAAGACAGAACTTTTGTACAGAGTGGGAGAGATTTTCT 108
2105 TGTATGCTTTATATTTAAGTCTATGCTGCTGTTAAATTTTATATTTAATTT 2164
107 TGTATGCTTTATATTTAAGTCTATGCTGTTAAATTTTATATTTAATTT 48
2165 TAAAGACAAAAGTCAAAACA 2185
47 TAAAGACAAAAGTCAAAACA 27
RESULT 2
90185165/c
JOCUS
DEFINITION
UI-E-EJ1-aju-e-03-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-aju-e-03-0-UI 3', mRNA sequence.
ACCESSION
JOCUS
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 590)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
8889548
COMMENT
Contact: Soares, MB
```

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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 385-415, >(CAG)n#Simple_repeat (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-aju-e-03-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_hosts="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;
optic nerve, CCATTAAGTG, retina, CCGG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG LIB=UI-E-EJ1
TAG_TISSUE=human retina
TAG_SEQ=CCGCG"
BASE COUNT      123 a   121 c   144 g   202 t
ORIGIN
Query Match      26.0%; Score 569; DB 13; Length 590;
Best Local Similarity 100.0%; Pred. NO. 8e-269;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1617 GAGTCATGAGACCAACAGATCATCTTGGTCTTTGTCGAGTACTCTGCTAGCT 1676
DB      581 GAGTCATGAGACCAACAGATCATCTTGGTCTTTGTCGAGTACTCTGCTAGCT 522
QY      1677 GCGGCCATGTTGATTGCTTCTATAAACTTCGTAAGCGGCCAGCAGCGGAGTACAGTC 1736
DB      521 GCGGCCATGTTGATTGCTTCTATAAACTTCGTAAGCGGCCAGCAGCGGAGTACAGTC 462
QY      1737 ACAGCGCCCGGAGCTGTTGAGATTAATCAGGTGGACGAGACATCCCGCAGCAGATCC 1796
DB      461 ACAGCGCCCGGAGCTGTTGAGATTAATCAGGTGGACGAGACATCCCGCAGCAGATCC 402
QY      1797 GCAGCAGCAACAGAGCTCCGTCGCTGTTATCAGGTGAGGGGCGAGTGTGCTGCCACA 1856
DB      401 GCAGCAGCAACAGAGCTCCGTCGCTGTTATCAGGTGAGGGGCGAGTGTGCTGCCACA 342
QY      1857 ATTCATGACCATATTAATCTACAACTTACAAACAGCAGATGGGGCCCTGTCAGCA 1916
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BASE COUNT 158 a 243 c 210 g 195 t  
ORIGIN  
Query Match 23.5%; Score 513; DB 9; Length 806;  
Best Local Similarity 100.0%; Pred. No. 3.2e-241;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 500 GCTCGGGAGCTCTGGCTTGGCAACACCCATCGAAAGCATCCCTCTTACGCCCTTCAA 559  
X 1 GCTCGGGAGCTCTGGCTTGGCAACACCCATCGAAAGCATCCCTCTTACGCCCTTCAA 60  
Y 560 CCGGCTGCCCTCCCTCATGTGGCTTGGGGAGCTCAAGAGCTGGAGTATATCTC 619  
X 61 CCGGCTGCCCTCCCTCATGTGGCTTGGGGAGCTCAAGAGCTGGAGTATATCTC 120  
Y 620 TGAGGAGCTTTTGAAGGCTTCAAGCTTCAAGTATCTGAATCTGGGATGGCAAT 679  
X 121 TGAGGAGCTTTTGAAGGCTTCAAGCTTCAAGTATCTGAATCTGGGATGGCAAT 180  
Y 680 TAAAGACATGCCCAATCTCAACCCCTGGTGGGGCTGGAGAGCTGGAGATGCGAGAA 739  
X 181 TAAAGACATGCCCAATCTCAACCCCTGGTGGGGCTGGAGAGCTGGAGATGCGAGAA 240  
Y 740 CCATCTCCCTGAGATCAGGCTGGCTTCCATGGCTGAGTCCCTCAAGAGCTCTG 799  
X 241 CCATCTCCCTGAGATCAGGCTGGCTTCCATGGCTGAGTCCCTCAAGAGCTCTG 300  
Y 800 GTCTATGAATCAGAGTCAAGCTGATTTGAGCGAATGCTTTTCAAGCGCTGGCTTCACT 859  
X 301 GTCTATGAATCAGAGTCAAGCTGATTTGAGCGAATGCTTTTCAAGCGCTGGCTTCACT 360  
Y 860 TGTGAATCTCAACTTGGCCCAATTAACCTCTCTTTTGGCCCATGACCTTTTACCCC 919  
X 361 TGTGAATCTCAACTTGGCCCAATTAACCTCTCTTTTGGCCCATGACCTTTTACCCC 420  
Y 920 GTGAGCTACCTGGTGGTGGCTTACACCAACCTTGGAGCTGATTTGAGTACAT 979  
X 421 GTGAGCTACCTGGTGGTGGCTTACACCAACCTTGGAGCTGATTTGAGTACAT 480  
Y 980 TCTGTGGCTAGCTGGCTGGCTTGGAGTATAT 1012  
X 481 TCTGTGGCTAGCTGGCTGGCTTGGAGTATAT 513  
RESULT 6  
BX114395/c  
LOCUS  
DEFINITION  
IMAGp998H10156 ; IMAGE:33723, mRNA sequence.  
ACCESSION  
BX114395  
VERSION  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 504)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rofls  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998H10156  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111

www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13u, Primer sequence: CGTTGTAAACACGACGCCAGT.  
Location/Qualifiers  
1. 504  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGp998H10156 ; IMAGE:33723"  
/sex="female"  
/dev\_stage="73 days post natal"  
/lab\_host="DHI08 (ampicillin resistant)"  
/clone\_lib="Soares infant brain INIB"  
/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not  
I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
I - oligo(dT) primer (5'  
TACTGGAGATTCGCGCGCCAGGAATTTTTTTTTTTT 3');  
double-stranded cDNA was ligated to Hind III adaptors  
(Pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the Lfamid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Patima Bonaide."  
BASE COUNT 101 a 97 c 123 g 183 t  
ORIGIN  
Query Match 22.3%; Score 488; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 6.7e-229;  
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1695 TTCTATAAATTCGTAGCGGCACACGAGCGAGTACAGTCACAGCGCGCGGACTGTT 1754  
DB 504 TTCTATAAATTCGTAGCGGCACACGAGCGAGTACAGTCACAGCGCGCGGACTGTT 445  
QY 1755 GAGATAATCCAGGTGGAGCAAGAGATCCAGCAGCAATCCCGCAGCAGCAACAGCAGCT 1814  
DB 444 GAGATAATCCAGGTGGAGCAAGAGATCCCGCAGCAGCAATCCCGCAGCAGCAGCT 385  
QY 1815 CCGTCCGGTGATCAGGTGAGGGGCGAGTGTGCTGCCCAATTCATGACCATATTAAAC 1874  
DB 384 CCGTCCGGTGATCAGGTGAGGGGCGAGTGTGCTGCCCAATTCATGACCATATTAAAC 325  
QY 1875 TACAACACTTACAACACAGCAGCATGGGGCCCATCTGGAGCAGAAACAGCCTGGGAACTCT 1934  
DB 324 TACAACACTTACAACACAGCAGCATGGGGCCCATCTGGAGCAGAAACAGCCTGGGAACTCT 265  
QY 1935 CTGACCCCGCAGCTACCCACTATCTCTGAACCTTATATATTCAGACCCATACCAAGGAC 1994  
DB 264 CTGACCCCGCAGCTACCCACTATCTCTGAACCTTATATATTCAGACCCATACCAAGGAC 205  
QY 1995 AAGGTACAGGAAACTCAAATATGACTCCCTCCCGCCAAATAATGCAATAG 2054  
DB 204 AAGGTACAGGAAACTCAAATATGACTCCCTCCCGCCAAATAATGCAATAG 145  
QY 2055 ATGCACACAGAGCAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCT 2114  
DB 144 ATGCACACAGAGCAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCT 85  
QY 2115 TATATATTAAAGTCTATGGGCTGGTGTAAATAAAGAGAGTATATTTAAATTTAAAGACAAA 2174  
DB 84 TATATATTAAAGTCTATGGGCTGGTGTAAATAAAGAGAGTATATTTAAATTTAAAGACAAA 25  
QY 2175 AAGTCAAA 2182  
DB 24 AAGTCAAA 17  
RESULT 7  
BX1769814/c  
LOCUS  
DEFINITION  
wJ26h10.x1 NC1\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2404003 3',  
mRNA sequence.  
ACCESSION  
BX1769814

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VERSION
EYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

A1769814.1 GI:5236323
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 629 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 462.
Location/Qualifiers
1. .478
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2404003"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
/clone_lib="NCI CGAP Kid12"
/notes="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Patima Bonaldo."
ASE COUNT 97 a 96 c 121 g 164 t
RIGIN

Query Match 21.9%; Score 478; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 5.7e-224;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1703 ACTTGTGAGCGGACAGCAGCGGAGTACAGTCAAGCGCGCCCGGACTGTTGAGATAT 1762
|
|
|
b 478 ACTTGTGAGCGGACAGCAGCGGAGTACAGTCAAGCGCGCCCGGACTGTTGAGATAT 419
|
|
|
Y 1763 CCAGGTGGAGAGACATCCAGCAGCATCCGAGCAGCAACAGCAGCTCGGCGG 1822
|
|
|
b 418 CCAGGTGGAGAGACATCCAGCAGCAACATCCGAGCAGCAACAGCAGCTCGGCGG 359
|
|
|
Y 1823 TGTATCAGGTGAGGGGCGAGTGTGCGCCCAATTCATGACCAATTAATTAACACAC 1882
|
|
|
b 358 TGTATCAGGTGAGGGGCGAGTGTGCGCCCAATTCATGACCAATTAATTAACACAC 299
|
|
|
Y 1883 CTACAAACAGCAGCAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1942
|
|
|
b 298 CTACAAACAGCAGCAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
|
|
|
Y 1943 CACAGTCACCACTATCTCTGAACCTTATATTAATTCAGACCCATACCAAGCAGGTACA 2002
|
|
|
b 238 CACAGTCACCACTATCTCTGAACCTTATATTAATTCAGACCCATACCAAGCAGGTACA 179
|
|
|
Y 2003 GGAACTCAATATGATCTCCCTCCCGCCCAAAACCTTATTAATGCAATGATGACAC 2062
|
|
|
b 178 GGAACTCAATATGATCTCCCTCCCGCCCAAAACCTTATTAATGCAATGATGACAC 119
|
|
|

Qy 2063 AAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTATATATT 2122
|
|
|
Db 118 AAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTATATATT 59
|
|
|
Qy 2123 AAGTCTATGGCTGGTTAAAGAAAAACAGATTTATTTAAATTTAAAGACAAAAGTCA 2180
|
|
|
Db 58 AAGTCTATGGCTGGTTAAAGAAAAACAGATTTATTTAAATTTAAAGACAAAAGTCA 1
|
|
|

RESULT 8
BQ189063
LOCUS
DEFINITION
BQ189063 540 bp mRNA linear EST 30-APR-2002
UI-E-EJI-aju-f-24-0-UI.r1 UI-E-EJI Homo sapiens cDNA clone
UI-E-EJI-aju-f-24-0-UI.5', mRNA sequence.
BQ189063.1 GI:20364614
VERSION
BQ189063
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 540)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 218-248, >(CAG)n#simple_repeat
Seq primer: M13 REVERSE.
Location/Qualifiers
1. .540
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJI-aju-f-24-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJI"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJI is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATVAGCGA; eye anterior segment, AATGCCCAT;
optic nerve, CCATTAGTGT; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual

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System, supported by National Eye Institute (NEI)."

```
BASE COUNT      165 a      151 c      119 g      104 t      1 others
ORIGIN
Query Match      21.1%; Score 462; DB 13; Length 540;
Best Local Similarity 99.8%; Pred. No. 4.4e-216;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1566 GTGGCAGTACCGGACAGACACCACTGCAAGATGCGAGCAGCCTGGATGAAGTCAATG 1625
DB 1 GTGGCAGTACCGGACAGACACCACTGCAAGATGCGAGCAGCCTGGATGAAGTCAATG 60
1626 AGAGACACCAAGATCATCTGCTGGCTTGTGGCAGTCACTCTGCTAGCTGCGGCCATG 1685
DB 61 AGAGACACCAAGATCATCTGCTGGCTTGTGGCAGTCACTCTGCTAGCTGCGGCCATG 120
1686 TTGATTGTCTTCTATAAACTTGTAAAGCGGACCAACGAGCGAGTACAGTCACAGCGGCC 1745
DB 121 TTGATTGTCTTCTATAAACTTGTAAAGCGGACCAACGAGCGAGTACAGTCACAGCGGCC 180
1746 CGGACTGTTGAGATATCCAGTGTGAGGAGACATCCGACGAGCAATCCGACGAGCA 1805
DB 181 CGGACTGTTGAGATATCCAGTGTGAGGAGACATCCGACGAGCAATCCGACGAGCA 240
1806 ACAGCAGCTCCCTCGCGTGTATCAGTGTGAGGCGGAGTGTGCTGCCACAAATTCATCAC 1865
DB 241 ACAGCAGCTCCCTCGCGTGTATCAGTGTGAGGCGGAGTGTGCTGCCACAAATTCATCAC 300
1866 CATATTAACTACAACTTACAAACAGACATGATGGGGCCCTGTGACAGAAACAGCTG 1925
DB 301 CATATTAACTACAACTTACAAACAGACATGATGGGGCCCTGTGACAGAAACAGCTG 360
1926 GGGACTCTCTGACCCCACTGACCACTATCTCTGAACTTATATATTAATTCAGACCCAT 1985
DB 361 GGGACTCTCTGACCCCACTGACCACTATCTCTGAACTTATATATTAATTCAGACCCAT 420
1986 ACCAAGCAAGGTACAGAACTCAATATATGACTCCCTCCCTCCCAAAAACCTTATAAAA 2045
DB 421 ACCAAGCAAGGTACAGAACTCAATATATGACTCCCTCCCTCCCAAAAACCTTATAAAA 480
2046 TSCATATAGATGCACAAAGACAGCACTTTT 2078
DB 481 TSCATATAGATGCACAAAGACAGCACTTTT 513
```

```
RESULT 9
AI435407/c
LOCUS      447 bp      mRNA      linear      EST 30-MAR-1999
DEFINITION      th94b04.x1 Soares NSF F8 9W OT PA_P S1 Homo sapiens cDNA clone
IMAGE:2126287 3', mRNA sequence.
ACCESSION      AI435407
VERSION      AI435407.1 GI:4302966
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 447)
JOURNAL      NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 674 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 418.
FEATURES
Location/Qualifiers
1..447
/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:2126287"
/lab_host="DH10B"
/clone_lib="Soares NSF F8 9W OT PA_P S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and as circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was from
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NBSP pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
```

```
BASE COUNT      92 a      85 c      108 g      162 t
ORIGIN
Query Match      20.2%; Score 441; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 9.9e-206;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1743 GCCCGACTGTTGAGATATCCAGTGTGAGGAGCAATCCGACGAGCAATCCGACGCA 1802
DB 447 GCCCGACTGTTGAGATATCCAGTGTGAGGAGCAATCCGACGAGCAATCCGACGCA 388
1803 GCACAGCAGCTCCCTCGCGTGTATCAGTGTGAGGCGGAGTGTGCTGCCACAAATTCAT 1862
DB 387 GCACAGCAGCTCCCTCGCGTGTATCAGTGTGAGGCGGAGTGTGCTGCCACAAATTCAT 328
1863 GACCATATTAATACACACCTTACAAACAGACACATGCGGCCCTGTCGACAGAAACAGC 1922
DB 327 GACCATATTAATACACACCTTACAAACAGACACATGCGGCCCTGTCGACAGAAACAGC 268
1923 CTGGGAACTCTCTGACCCCACTGACCACTATCTCTGAACTTATATATTAATTCAGACC 1982
DB 267 CTGGGAACTCTCTGACCCCACTGACCACTATCTCTGAACTTATATATTAATTCAGACC 208
1983 CATACACGACAGGTGACGAACTCAATATGACTCCCTCCCTCCCAAAAACCTTATA 2042
DB 207 CATACACGACAGGTGACGAACTCAATATGACTCCCTCCCTCCCAAAAACCTTATA 148
2043 AAATGCAATAGAAATGCACAAAGACAGCAACTTTGTACAGGTGGGAGAGACTTTT 2102
DB 147 AAATGCAATAGAAATGCACAAAGACAGCAACTTTGTACAGGTGGGAGAGACTTTT 88
2103 CTTGTATATGCTTATATATTAATTAATGCTGCTGTTAAATAAAACAGATATATATAA 2162
DB 87 CTTGTATATGCTTATATATTAATTAATGCTGCTGTTAAATAAAACAGATATATATAA 28
2163 TTTAAAGCAAAAAGTCAAAA 2183
DB 27 TTTAAAGCAAAAAGTCAAAA 7
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```
RESULT 10
BQ184873/c
LOCUS      514 bp      mRNA      linear      EST 30-APR-2002
DEFINITION      UI-B-EJ1-ajr-d-10-0-UI.s1 UI-B-EJ1 Homo sapiens cDNA clone
ACCESSION      BQ184873
VERSION      BQ184873.1 GI:20360424
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
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**AUTHORS**  
**TITLE**  
**JOURNAL**  
**MEDLINE**  
**PUBMED**  
**COMMENT**

Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 889548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 376-406, >(CAG)n#Simple\_repeat (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=No.

**FEATURES**  
 source

1. .514  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ1-ajr-d-10-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Foveal and Macular, RPE and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-EJ1"  
 /notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR; Site 2: Not I;  
 UI-E-EJ1 is a subtracted cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into p773-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes, AGAATCAAGA  
 ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCGAT;  
 optic nerve, CCGATTAGTG; retina, CCGCG; Retina Foveal and  
 Macular, GTCC; RPE and Choroid, ACCTA. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI).  
 TAG LIB=UI-E-EJ1  
 TAG TISSUE=human fetal eyes  
 TAG SEQ=AGAATCAAGA"  
 BASE COUNT 110 a 104 c 125 g 175 t  
 RIGIN

Query Match 19.7%; Score 431; DB 13; Length 514;  
 Best Local Similarity 99.8%; Pred. No. 8.4e-201;  
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1702 AACTTCGTAGCGGCACACAGCGAGTACATCCAGCGCCGCGATGTGAGTAA 1761  
 487 AACATCGTAGCGGCACACAGCGAGTACATCCAGCGCCGCGATGTGAGTAA 428  
 1762 TCCAGGTGGAGAGACATCCAGCGACACATCCGAGCAGCAACAGCAGCTCCGTCG 1821  
 427 TCCAGGTGGAGAGACATCCAGCGACACATCCGAGCAGCAACAGCAGCTCCGTCG 368  
 1822 GTGTATCAGGTGAGCGGCGAGTGTGTGCGCCACATTCATGACATTAACACACA 1881  
 367 GTGTATCAGGTGAGCGGCGAGTGTGTGCGCCACATTCATGACATTAACACACA 308

1882 CCTCAAAACACAGCAGCATGGGCCCTGAGCAGAGAAACAGAGCTGGGAACTCTCTGCACC 1941  
 307 CTTCAAAACACAGCAGCATGGGCCCTGAGCAGAGAAACAGAGCTGGGAACTCTCTGCACC 248  
 1942 CCACTGTCACCACTATCTCTGAAACCTTATATTAATTCAGACCCATACCAAGGCAAGGTAC 2001  
 247 CCACTGTCACCACTATCTCTGAAACCTTATATTAATTCAGACCCATACCAAGGCAAGGTAC 188  
 2002 AGGAACCTCAATATGACCTCCCTCCCAAAACCTTATAAAATGCAATAGATGCAACA 2061  
 187 AGGAACCTCAATATGACCTCCCTCCCAAAACCTTATAAAATGCAATAGATGCAACA 128  
 2062 CAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATAT 2121  
 127 CAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATAT 68  
 2122 TAAGTCTATGGCTGGTAAATAAAACAGATATATTAATAATTTAAAGCAAAAAGTCAA 2181  
 67 TAAGTCTATGGCTGGTAAATAAAACAGATATATTAATAATTTAAAGCAAAAAGTCAA 8  
 2182 AA 2183  
 7 AA 6

RESULT 11  
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 LOCUS  
 DEFINITION  
 BQ340625  
 ACCSSION  
 BQ340625.1 GI:21001706  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM

Homo sapiens  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 609)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zsago, M.A., Bordin, S., Costa, F.P.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PMO&t2=PMO-NN0258-  
 220501-001-f07&t3=2001-05-22&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 12  
 High quality sequence stop: 601.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="NN0258"  
 /notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products



derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

BASE COUNT      128 a  195 c  142 g  144 t
ORIGIN
Query Match      18.9%; Score 412; DB 13; Length 609;
Best Local Similarity 99.5%; Pred. No. 2e-191;
Matches 562; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 874 TGGCCCAACATTAACCTCTCTCTTTGGCCCATGACCTCTTTACCCGCTGAGGTACTCTG 933
b 44 TGGCCCAACATTAACCTCTCTCTTTGGCCCATGACCTCTTTACCCGCTGAGGTACTCTG 103
Y 934 TGGAGTTGCATCTACACACAAACCTTTGGAACCTGATTTGTGACATCTCTGCTAGCCT 993
b 104 TGGAGTTGCATCTACACACAAACCTTTGGAACCTGATTTGTGACATCTCTGCTAGCCT 163
Y 994 GTGGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCGCTGTCATGCTCCCA 1053
b 164 GTGGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCGCTGTCATGCTCCCA 223
Y 1054 TGCACATGCGAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 1113
b 224 TGCACATGCGAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 283
Y 1114 CTTTCATGCGAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 1173
b 284 CTTTCATGCGAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 343
Y 1174 AGTGTGCGAGCTCCCTTATGCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 1233
b 344 AGTGTGCGAGCTCCCTTATGCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 403
Y 1234 GCGAGGCTCCCGCAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 1293
b 404 GCGAGGCTCCCGCAGGCGCTACTCTCTGAGGTGACACAGGCTCTCTTCCAGTGTCTGCCC 463
Y 1294 ACCTGCTGCTTTTACAGACCTGGGCTGTACACATGCTGCTGACCAATGTTGCGAGCACT 1353
b 464 ACCTGCTGCTTTTACAGACCTGGGCTGTACACATGCTGCTGACCAATGTTGCGAGCACT 523
Y 1354 CCAACGCTCGGCTACTCTATGAGTACAGGCTGAGCTTAACACTTCAACTACAGCT 1413
b 524 CCAACGCTCGGCTACTCTATGAGTACAGGCTGAGCTTAACACTTCAACTACAGCT 583
Y 1414 TCTTCAACACAGTAACTGAGGAC 1438
b 584 TCTTCAACACAGTAACTGAGGAC 608

RESULT 12
LOCUS      CA310827/c
DEFINITION UI-CF-PNO-afb-f-01-0-UI.s1 UI-CF-PNO Homo sapiens cDNA clone
ACCESSION CA310827
VERSION   CA310827.1 GI:24528925
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 780)
AUTHORS   Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   9704477
PubMed    889548
COMMENT   Contact: McCray, PB

```

McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-58, >POLY A#simple repeat (matched complement) 386-416,  
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Seq primer: M13 FORWARD  
POLYA=yes.

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FEATURES
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/clone="UI-CF-PNO-afb-f-01-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (11 phage resistant)"
/clone_lib="UI-CF-PNO"
/notes="Organ; Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-PNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) the library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG LIB=UI-CF-PNO
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_SEQ=CTGCTCAGGT"
BASE COUNT 154 a 161 c 207 g 257 t 1 others
ORIGIN
Query Match      18.1%; Score 395; DB 14; Length 780;
Best Local Similarity 99.8%; Pred. No. 4.7e-183;
Matches 515; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1669 TGCTAGCTGCGCCGCAATGTTGATTGTTCTTTATTAACCTTCTGTAAGCGCGCAGCAGCGGA 1728
b 530 TGCTAGCTGCGCCGCAATGTTGATTGTTCTTTATTAACCTTCTGTAAGCGCGCAGCAGCGGA 471
QY 1729 GTACAGTCACAGCGCGCGGACTGTTGAGATATCCAGGTGGAGCAAGACATCCCGAGCAG 1788
b 470 GTACAGTCACAGCGCGCGGACTGTTGAGATATCCAGGTGGAGCAAGACATCCCGAGCAG 411
QY 1789 CAACATCCGAGCAGCAGCAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGC 1848
b 410 CAACATCCGAGCAGCAGCAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGC 351
QY 1849 TGCCCAAAATTCATGACCATATTAATTAACCAACCTTACAAACCCAGCAGCATGGGGCCCACT 1908
b 350 TGCCCAAAATTCATGACCATATTAATTAACCAACCTTACAAACCCAGCAGCATGGGGCCCACT 291
QY 1909 GGACAGAAAACAGCTGGGGAACTCTCTGCAACCCCACTCACTATCTCTGAAACCTT 1968
b 290 GGACAGAAAACAGCTGGGGAACTCTCTGCAACCCCACTCACTATCTCTGAAACCTT 231
QY 1969 ATATAATTCAGCCCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCC 2028
b 230 ATATAATTCAGCCCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCC 171
QY 2029 CC-AAAAAACTTATATAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAT 2087
b 170 CCAAAAAAACTTATATAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAT 111

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Y 2088 GGGGAGAGACTTTTCTGTATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAAA 2147  
 b 110 GGGGAGAGAGACTTTTCTGTATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAAA 51  
 Y 2148 CAGATTATATTAAGTTTAAAGACAAATTAAGTCAAAA 2183  
 b 50 CAGATTATATTAAGTTTAAAGACAAATTAAGTCAAAA 15

RESULT 13  
 U789069/c  
 CCUS  
 DEFINITION  
 1039405.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6128696  
 2' similar to SW:INS\_CERAE P30407 INSULIN PRECURSOR. ; mRNA  
 sequence.  
 BU789069 509 bp mRNA linear EST 11-OCT-2002  
 1039405.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6128696  
 2' similar to SW:INS\_CERAE P30407 INSULIN PRECURSOR. ; mRNA  
 sequence.  
 CESSION  
 BU789069 GI:23838200  
 ERSION  
 EYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 509)  
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
 Lemishka, I., Secorce, M., Brestelli, J., Gadowhi, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas  
 M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T.,  
 Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohpc.harvard.edu  
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to  
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington  
 University Genome Sequencing Center for information on obtaining a  
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 392.  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6128696"  
 /tissue\_type="insulinoma"  
 /lab\_host="pH10B (phage-resistant)"  
 /clone\_lib="Human insulinoma"  
 /note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:  
 XhoI; Site: 2: EcoRI; Constructed with lambda ZAPII system  
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to  
 pBluescript SK- by Dr. H. Inoue following the Washington  
 University protocol  
 (http://genome.wustl.edu/est/lambda\_protocol.shtml).  
 please contact Hiroshi Inoue, MD/PhD for further  
 information on this library (Metabolism Division, Permutt  
 Laboratory, Washington University School of Medicine, Box  
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this  
 is a Washington University Pancreas EST project library. "  
 101 a 104 c 127 g 177 t

BASE COUNT  
 101 a 104 c 127 g 177 t  
 18.0%; Score 394; DB 13; Length 509;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.5e-182; Indels 0; Gaps 0;  
 Matches 394; Conservative 0; Mismatches 0;

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 14  
 B0186663  
 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bent-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
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 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Poveal and Macular, RPE and

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 15  
 B0186663  
 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bent-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
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 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Poveal and Macular, RPE and

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 16  
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 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bent-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
 i. .504  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ1-ajr-d-10-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Poveal and Macular, RPE and

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 17  
 B0186663  
 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bent-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
 i. .504  
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 /clone="UI-E-EJ1-ajr-d-10-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Poveal and Macular, RPE and

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 18  
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 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
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 Fax: 319 335 9565  
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 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
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 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ1-ajr-d-10-0-UI"  
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 optic nerve, retina, Retina Poveal and Macular, RPE and

FEATURES  
 source  
 LOCATION  
 COMMENT

RESULT 19  
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 LOCUS  
 DEFINITION  
 UI-E-EJ1-ajr-d-10-0-UI.x1 UI-E-EJ1 Homo sapiens cDNA clone  
 UI-E-EJ1-ajr-d-10-0-UI 5', mRNA sequence.  
 ACCESSION  
 B0186663  
 VERSION  
 B0186663.1 GI:20362214  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 504)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 AUTHORS  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA  
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 Fax: 319 335 9565  
 Email: bent-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 100-130. >(CAG)n#simple\_repeat  
 Seq primer: M13 REVERSE.  
 Location/Qualifiers  
 i. .504  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ1-ajr-d-10-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Poveal and Macular, RPE and

Choroid  
/dev stage="fetal and adult"  
/lab host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone lib="UI-B-EJ1"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not I; UI-B-EJ1 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CCATTAGGGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAGG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 175 a 123 c 99 g 105 t  
ORIGIN  
Query Match 17.7%; Score 387; DB 13; Length 504;  
Best Local Similarity 99.8%; Pred. No. 4.1e-179;  
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1684 TGTGATTGCTCTTATTAACCTGTAAGCGGCACGAGCGGAGTACAGTCACAGCGG 1743  
Db 1 TGTGATTGCTCTTATTAACCTGTAAGCGGCACGAGCGGAGTACAGTCACAGCGG 60  
QY 1744 CCGGAGCTGTTGAGATTAATCCAGTGGACGAGACATCCAGCAGCAGCATCCGCGAGCAG 1803  
Db 61 CCGGAGCTGTTGAGATTAATCCAGTGGACGAGACATCCAGCAGCAGCATCCGCGAGCAG 120  
QY 1804 CAACAGCAGCTCCGTCGGTGATCAGTGGAGGGGAGTGTGCTGCCCAATTCATG 1863  
Db 121 CAACAGCAGCTCCGTCGGTGATCAGTGGAGGGGAGTGTGCTGCCCAATTCATG 180  
QY 1864 ACCATTAATTAACACACCTCAACACGACATCCAGCAGCAGCATCCGCGAGCAGC 1923  
Db 181 ACCATTAATTAACACACCTCAACACGACATCCAGCAGCAGCATCCGCGAGCAGC 240  
QY 1924 TGGGGAATCTCTGCACTCCACAGTACACATCTCTGACCTTATTAATTCAGACCC 1983  
Db 241 TGGGGAATCTCTGCACTCCACAGTACACATCTCTGACCTTATTAATTCAGACCC 300  
QY 1984 ATACAGGACAGGTACAGGAACTCAATATATGATCTCCCTCCGCGAGGAGAGCTTTTC 2043  
Db 301 ATACAGGACAGGTACAGGAACTCAATATATGATCTCCCTCCGCGAGGAGAGCTTTTC 360  
QY 2044 AATGCAATAGATGCACACAGCAGCAGTCTTGTACAGAGTGGGAGAGCTTTTC 2103  
Db 361 AATGCAATAGATGCACACAGCAGCAGTCTTGTACAGAGTGGGAGAGCTTTTC 420  
QY 2104 TGTATATGCTTATATAT 2121  
Db 421 TGTATATGCTTATATAT 438

RESULT 15  
LOCUS A1470931/C  
DEFINITION t191c05.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:219368 3', mRNA sequence.  
ACCESSION A1470931  
VERSION A1470931.1 GI:4333021  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 393)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA library preparation: M. Bento Soares, Ph.D.  
cDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.lnl.gov/bbrp/image/image.html  
Insert Length: 815 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 364.  
Location/Qualifiers  
FEATURES  
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1..393  
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/clone="IMAGE:219368"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Kid11"  
/note="Organ: kidney; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP Kid11 was prepared, and ss circles were made in vitro. Following RAP hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 85 a 72 c 97 g 139 t  
ORIGIN  
Query Match 17.6%; Score 385; DB 9; Length 393;  
Best Local Similarity 100.0%; Pred. No. 4e-178;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1795 CCGCAGCAGCAGCAGCAGCTCCGTCGGTGATCAGTGGAGGGGAGTAGTCTGCCCA 1854  
Db 385 CCGCAGCAGCAGCAGCAGCTCCGTCGGTGATCAGTGGAGGGGAGTAGTCTGCCCA 326  
QY 1855 CAATTCATGACCATATTAACCTAACAACCTTACAAACAGCAGCAGTGGGCGCCACTGGACAG 1914  
Db 325 CAATTCATGACCATATTAACCTAACAACCTTACAAACAGCAGCAGTGGGCGCCACTGGACAG 266  
QY 1915 AAAACAGCTGGGGAACCTCTCTGCACCCACAGTCACCTCTCTGAACCTTATATAA 1974  
Db 265 AAAACAGCTGGGGAACCTCTCTGCACCCACAGTCACCTCTCTGAACCTTATATAA 206  
QY 1975 TTTCAGACCCATACCAAGGACAAAGGTACAGGAACTCAATATGATCTCCCTCCGCGAGG 2034  
Db 205 TTTCAGACCCATACCAAGGACAAAGGTACAGGAACTCAATATGATCTCCCTCCGCGAGG 146  
QY 2035 AACCTTATAAATGCAATAGATGACACCAAGGACAGCACTTTGTACAGAGTGGGAGAG 2094  
Db 145 AACCTTATAAATGCAATAGATGACACCAAGGACAGCACTTTGTACAGAGTGGGAGAG 86  
QY 2095 GACTTTTCTTGTATATGCTTATATATTAAGTCTATGGGCTGTGTTAAAAAACAATTA 2154  
Db 85 GACTTTTCTTGTATATGCTTATATATTAAGTCTATGGGCTGTGTTAAAAAACAATTA 26  
QY 2155 TATTAAAAATTTAAAGACAAAAAGTC 2179  
Db 25 TATTAAAAATTTAAAGACAAAAAGTC 1

RESULT 16

Q0340622 B0340622 389 bp mRNA linear EST 20-MAY-2002  
 LOCUS PM0-NN0258-220501-001-c05 NN0258 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION B0340622  
 ACCESSION B0340622.1 GI:21001702  
 ERSION  
 EYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 389)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 W.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM0&t2=PM0-NN0258-  
 220501-001-c05&t3=2001-05-22&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 9  
 High quality sequence stop: 389.  
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 /dev\_stage="Adult"  
 /clone\_lib="NN0258"  
 /note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORSTS PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 76 a 120 c 91 g 102 t  
 ORIGIN  
 Query Match 15.0%; Score 327; DB 13; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-149; Indels 0; Gaps 0;  
 Matches 32; Conservative 0; Mismatches 0;  
 Y 878 CCACATAACCTCTCTTTTGGCCCATGACCTCTTTACCCCGCTGAGTACCTGGTGA 937  
 b 63 CCACATAACCTCTCTTTTGGCCCATGACCTCTTTACCCCGCTGAGTACCTGGTGA 122  
 Y 938 GTTGCANTACACACACCTTGGACTGTGATGTGACATTCGTGGCTAGCTGGTG 997  
 b 123 GTTGCATCTACACACACCTTGGACTGTGATGTGACATTCGTGGCTAGCTGGTG 182  
 Y 998 GTTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCGCTGTCATGCTCCCATGCA 1057  
 b 183 GTTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCGCTGTCATGCTCCCATGCA 242  
 Y 1058 CATGCGAGGCGGTACTCTGTGAGGTGGACCAAGGCTCTTCCAGTGTCTGCCCCCTT 1117  
 b 243 CATGCGAGGCGGTACTCTGTGAGGTGGACCAAGGCTCTTCCAGTGTCTGCCCCCTT 302

Qy 1118 CATCATGAGGACCTCGAGACCTCAACATTTCTGAGCTCGATGGAGACTTAAGTG 1177  
 Db 303 CATCATGAGGACCTCGAGACCTCAACATTTCTGAGCTCGATGGAGACTTAAGTG 362  
 Y 1178 TCGGACTCCCCCTATGCTCTCCGTGAA 1204  
 Db 363 TCGGACTCCCCCTATGCTCTCCGTGAA 389  
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 LOCUS EST366608 424 bp mRNA linear EST 01-JUN-2000  
 DEFINITION EST366608 MAGE resequencences, MAGE Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW954538  
 VERSION AW954538.1 GI:8144221  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 424)  
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt  
 J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and  
 Quackenbush,J.  
 TITLE Assessment of gene expression patterns in a model of colon tumor  
 metastasis using a 19,200 element cDNA microarray  
 JOURNAL Unpublished  
 COMMENT Contact: John Quackenbush  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 3528  
 Fax: 301 838 0208  
 Email: johnq@tigr.org  
 Plate: 65  
 Seq primer: Reverse  
 Location/Qualifiers  
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 Y 894 TCCTTGGCCCATGACCTCTTTACCCCGCTGAGTACCTGGTGGAGTTGCATCTACACCAC 953  
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 Y 954 AACCCCTTGGAACTGTGATTTGTGACATTTCTGTGGCTAGCTGTGGCTTCGAGAGTATATA 1013  
 Db 88 AACCCCTTGGAACTGTGATTTGTGACATTTCTGTGGCTAGCTGTGGCTTCGAGAGTATATA 147  
 Y 1014 CCACACCAATTCACCTGCTGTGGCGCTGTCACTGCCATGCACATGAGGAGGCCCTAC 1073  
 Db 148 CCCACCAATTCACCTGCTGTGGCGCTGTCACTGCCATGCACATGAGGAGGCCCTAC 207  
 Y 1074 CTCGTGAGGTGACACAGGCTCTCTTCCAGTGTCTGTGCCCTTCATCATGAGCAGCACT 1133  
 Db 208 CTCGTGAGGTGACACAGGCTCTCTTCCAGTGTCTGTGCCCTTCATCATGAGCAGCACT 267  
 Y 1134 CGAGACCTCAACATTTCTGAGGTGAGTGGCAGAACTTAAGTGTGCGACTCCCCCTATG 1193  
 Db 268 CGAGACCTCAACATTTCTGAGGTGAGTGGCAGAACTTAAGTGTGCGACTCCCCCTATG 327  
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 Db 328 TCCTCCGTGAGTGTGTGCTGCCCAATGGACAGTCTCAGCCACGCCCT 376



778 TGAGCTCCCTCAAGAGCTCTGGTCTATGAACTCACAGGTGAGCTGAGTGGCGGAATG 837  
87 TGAGCTCCCTCAAGAGCTCTGGTCTATGAACTCACAGGTGAGCTGAGTGGCGGAATG 146  
838 CTTTGGAGGGCTGGCTTCACTTGGAGCTCACTTGGAGCTCACTTGGAGCTCACTTGGAGCT 897  
147 CTTTGGAGGGCTGGCTTCACTTGGAGCTCACTTGGAGCTCACTTGGAGCTCACTTGGAGCT 206  
898 TGCCCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCACTTACACCAACC 957  
207 TGCCCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCACTTACACCAACC 266  
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267 CTTGGAATCTGATGTCGACATTCCTGGCTAGCCTG 304

SULT 20  
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KUS  
DEFINITION  
UI-E-EJ0-ais-i-18-0-UI-r1 UI-E-EJ0 Homo sapiens cDNA clone  
UI-E-EJ0-ais-i-18-0-UI 5', mRNA sequence.  
BM724722  
BM724722.1 GI:19046053  
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Homo sapiens (human)  
Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 632)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.regen.com).  
The following repetitive elements were found in this cDNA  
sequence: 597-627, >AT rich/Low complexity (matched complement)  
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/dev\_stage="fetal and adult"  
/lab\_host="DH10B (life technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-EJ0"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-EJ0 is a subtracted cDNA library constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dfr)18 tail. The  
sequence tags for this library are: fetal eyes, AGAATCAGA  
; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT;  
optic nerve, CCATTAAAGTG; retina, CCGCG; Retina Foveal and  
Macular, GTCC; RPE and Choroid, ACCTA. This library was  
created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI)."

BASE COUNT 227 a 113 c 133 g 159 t  
ORIGIN

Query Match 11.9%; Score 261; DB 12; Length 632;  
Best Local Similarity 100.0%; Pred. No. 5.3e-117;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1925 GGGGAACCTCTCTGACACCCACAGTCACCATCTCTGAACCTTATATATTCAGACCA 1984  
DB 37 GGGGAACCTCTCTGACACCCACAGTCACCATCTCTGAACCTTATATATTCAGACCA 96  
QY 1985 TACCAGGACAGGTACAGGAACTCAAAATATGACTCCCTCCCAAAAAAATTATAA 2044  
DB 97 TACCAGGACAGGTACAGGAACTCAAAATATGACTCCCTCCCAAAAAAATTATAA 156  
QY 2045 ATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCT 2104  
DB 157 ATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCT 216  
QY 2105 TGTATATCTTATATATTAAGTCTATGCTGCTGTTAAAAAAACAGATTATATTAAT 2164  
DB 217 TGTATATCTTATATATTAAGTCTATGCTGCTGTTAAAAAAACAGATTATATTAAT 276  
QY 2165 TAAAGACAAAAAGTCAAAACA 2185  
DB 277 TAAAGACAAAAAGTCAAAACA 297

RESULT 21  
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LOCUS  
DEFINITION  
T15752 Infant brain, Bento Soares Homo sapiens cDNA 3'end, mRNA  
sequence.  
T15752  
T15752.1 GI:517914  
VERSION  
EST.  
KEYWORDS  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 470)  
Berry, R., Stevens, J., Walter, N.A.R., Wilcox, A.S., Rubano, T.,  
Hopkins, J.A., Weber, J., Gould, R., Soares, M.B. and Sikela, J.M.,  
Gene-based Sequence Tagged Sites (STSS) as the basis for a human  
gene map  
Nat. Genet. 10, 415-423 (1995)  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Sikela JM  
Department of Pharmacology  
University of Colorado Health Sciences Center  
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236  
Tel: 3032708637  
Fax: 3032707097  
Email: nikkie@ally.uchsc.edu  
Seq primer: -21mi3 Universal.  
Location/Qualifiers  
1..470  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/lab\_host="E. coli DH5-alpha"  
/clone\_lib="Infant brain, Bento Soares"  
/note="Vector: BA, M13-derived; Site\_1: HindIII; Site\_2:

NotI; The infant brain library, constructed by Bento Soares, Columbia University, was oligo-(dT) primed and directionally cloned into an M13-derived plasmid using total brain mRNA from a 72-day old human female afflicted with spinal muscular atrophy. "

BASE COUNT	95 a	95 c	120 g	156 t	4 others
ORIGIN					
Query Match	11.5%	Score 252;	DB 14;	Length 470;	
Best Local Similarity	99.7%	Pred. No. 1.4e-112;			
Matches 302;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Y	1882	CCTACAAACAGCAGCATGGGCGCCACTGGACAGAAAGAGCTGGGAACTCTCTGACCC	1941		
b	303	CCTACAAACAGCAGCATGGGCGCCACTGGACAGAAAGAGCTGGGAACTCTCTGACCC	244		
Y	1942	CCACAGTCACCATCTCTGAAACCTTATATATTCAGACCCATCCAGGACCAAGGTAC	2001		
b	243	CCACAGTCACCATCTCTGAAACCTTATATATTCAGACCCATCCAGGACCAAGGTAC	184		
Y	2002	AGGAACTCAATATGACTCCCTCCGCCAAAACCTTATAAATGCAATGAGTCAAC	2061		
b	183	AGGAACTCAATATGACTCCCTCCGCCAAAACCTTATAAATGCAATGAGTCAAC	124		
Y	2062	CAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATAT	2121		
b	123	CAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATAT	64		
Y	2122	TAACTCTATGGCTGGTGTAAATAAAGACAGATTATATAAATTAAGACAAAGTCAA	2181		
b	63	TAACTCTATGGCTGGTGTAAATAAAGACAGATTATATAAATTAAGACAAAGTCAA	4		
Y	2182	AAC 2184			
b	3	AAC 1			

RESULT 22  
 LOCUS R43906/c 452 bp mRNA linear EST 13-FEB-1999  
 DEFINITION qp37e09.x1 Soares\_fetal\_lung\_NbHL19w Homo sapiens cDNA clone  
 IMAGE:1930984 3', mRNA sequence.  
 ACCESSION A1332304  
 VERSION A1332304.1 GI:4068963  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 452)  
 AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbe@mail.nih.gov  
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 340 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 450.  
 Location/Qualifiers  
 1. .452  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1930984"  
 /dev\_stage="13 weeks"  
 /lab\_host="NBHL19w (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19w"  
 /note="Organ: lung; Vector: pPT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer"

[5'-TGTTACCAATCTGAAGTCGGAGCGCCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Ronaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19w."

BASE COUNT	111 a	89 c	84 g	168 t	
ORIGIN					
Query Match	11.0%	Score 241;	DB 9;	Length 452;	
Best Local Similarity	100.0%	Pred. No. 3.8e-107;			
Matches 241;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1945	CAGTCACCACTATCTCTGAACCTTATATATTCAGACCCATCCAGGACCAAGGTACAGG	2004		
DB	399	CAGTCACCACTATCTCTGAACCTTATATATTCAGACCCATCCAGGACCAAGGTACAGG	340		
QY	2005	AAACTCAATATGACTCCCTCCGCCAAAACCTTATAAATGCAATGAGTCAACAA	2064		
DB	339	AAACTCAATATGACTCCCTCCGCCAAAACCTTATAAATGCAATGAGTCAACAA	280		
QY	2065	AGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATTA	2124		
DB	279	AGACAGCAACTTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATTA	220		
QY	2125	GTCATGCGCTGGTGTAAATAAAGACAGATTATATAAATTAAGACAAAGTCAAAAC	2184		
DB	219	GTCATGCGCTGGTGTAAATAAAGACAGATTATATAAATTAAGACAAAGTCAAAAC	160		
QY	2185	A 2185			
DB	159	A 159			

RESULT 23  
 LOCUS R43906/c 428 bp mRNA linear EST 22-MAY-1995  
 DEFINITION V226h05.sl Soares infant brain IN1B Homo sapiens cDNA clone  
 IMAGE:33723 3', mRNA sequence.  
 ACCESSION R43906  
 VERSION R43906.1 GI:821784  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 428)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished  
 COMMENT On May 9, 1995 this sequence version replaced gi:802630.  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1458  
 High quality sequence stops: 328 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1458 Std Error: 0.00  
 Seq primer: Promega -21ml3  
 High quality sequence stop: 328.  
 Location/Qualifiers  
 1. .428  
 /organism="Homo sapiens"



/mol\_type="mRNA"  
/db\_xref="CDB:406070"  
/db\_xref="taxon:9606"  
/clone="IMAGE:33723"  
/sex="female"

/dev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares infant brain INB"  
/notes="Organ: whole brain; Vector: Lfamid BA; Site:1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15'  
AACTGAAGAATTCGCGCGCGCGAATTTTCTTTTCTTTT 3';  
double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lfamid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

87 a 72 c 112 g 154 t 3 others

Query Match 10.8%; Score 235; DB 14; Length 428;  
Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1951 CCATCTCTCTGAACTTATATATTCAGACCCTACCAAGGACAGGTACAGAACTC 2010  
|||||  
243 CCATCTCTCTGAACTTATATATTCAGACCCTACCAAGGACAGGTACAGAACTC 184  
|||||

2011 AATATGACTCCCTCCCTCCCAAACTTATAAAATGCAATGACACACAAAGACAG 2070  
|||||

183 AATATGACTCCCTCCCTCCCAAACTTATAAAATGCAATGACACACAAAGACAG 124  
|||||

2071 CAATTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATTAAGTCTAT 2130  
|||||

123 CAATTTTGTACAGAGTGGGAGAGACTTTTCTGTATATGCTTATATTAAGTCTAT 64  
|||||

2131 GGGCTGTTTAAATAAACAAGATTATATTAATAATTTAAAGCAAAAGTCAAAACA 2185  
|||||

63 GGGCTGTTTAAATAAACAAGATTATATTAATAATTTAAAGCAAAAGTCAAAACA 9  
|||||

RESULT 24  
LOCUS BM975594/c 468 bp mRNA linear EST 21-FEB-2003  
DEFINITION UI-CF-ENI-acu-d-14-0-UI.s1 UI-CF-ENI Homo sapiens cDNA clone  
BM975594  
BM975594.1 GI:19593185  
EST.  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 468)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-53, >AT-richLow\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source  
Location/Qualifiers  
1. 468  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-ENI-acu-d-14-0-UI"  
/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
Cells"

/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-ENI"  
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-ENI is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT7T3-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGGT.

TAG\_L11B=UI-CF-ENI  
TAG\_T11SUB=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG\_SEQ=CTGCTCAGGT"

BASE COUNT 128 a 103 c 104 g 133 t  
ORIGIN

Query Match 10.3%; Score 224; DB 12; Length 468;  
Best Local Similarity 100.0%; Pred. No. 9.1e-99;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1208 GTTGCTGCCCAATGGGACAGTGTCTCAGCCACCGCTCCGCCACCCCAAGGATCTCTCT 1267

DB 434 GTTGCTGCCCAATGGGACAGTGTCTCAGCCACCGCTCCGCCACCCCAAGGATCTCTCTCT 375

QY 1268 CAACGAGCGCACTTGACATTTTCCACGCTGCTGCTTTCAGACACTGGGGTGTACACATG 1327

DB 374 CAACGAGCGCACTTGACATTTTCCACGCTGCTGCTTTCAGACACTGGGGTGTACACATG 315

QY 1328 CATGGTGACCAATGTTGCAGGCAACTCCAAACGCTCGGCTACCTCAATGTGAGCAGCGC 1387

DB 314 CATGGTGACCAATGTTGCAGGCAACTCCAAACGCTCGGCTACCTCAATGTGAGCAGCGC 255

QY 1388 TGAGCTTAAACACTCCCACTACAGCTTCTTCCACCAAGTAACAG 1431

DB 254 TGAGCTTAAACACTCCCACTACAGCTTCTTCCACCAAGTAACAG 211

RESULT 25  
T33015/c 325 bp mRNA linear EST 06-SEP-1995  
LOCUS BST56321 Human Brain Homo sapiens cDNA 3, end similar to None, mRNA  
DEFINITION sequence.  
T33015  
T33015.1 GI:615113  
VERSION  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 325)  
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT



Y 2162 ATTAAAGCAAAAGTCAAAACA 2185  
 J741381/c  
 CCUS  
 b 34 ATTAAAGCAAAAGTCAAAACA 11

RESULT 27  
 J741381/c  
 DEFINITION  
 UI-E-EJ0-ais-1-18-0-UI si UI-E-EJ0 Homo sapiens cDNA clone  
 UI-E-EJ0-ais-1-18-0-UI 3', mRNA sequence.

CESSION  
 ESION  
 EYWORDS  
 URCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 626)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

CONTACT: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA  
 sequence: 1-30, >Atrich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source  
 1..626  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ0-ais-1-18-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Foveal and Macular, RPE and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-EJ0"  
 /notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-E-EJ0 is a subtracted cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into p773-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes, AGAATCAAGA  
 ; lens, CCATTAGGCA; eye anterior segment, AATGCCGCAT;  
 optic nerve, CCATTAGTGT; retina, CCGCG; Retina foveal and  
 Macular, GTCC; RPE and Choroid, ACCTA. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI).  
 TAG LIB=UI-E-EJ0  
 TAG\_TISSUE=human retina

BASE COUNT 159 a 131 c 110 g 226 t  
 ORIGIN  
 Query Match 9.1%; Score 199; DB 13; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-86;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1987 CCAAGGACAAAGTACAGGAACCTCAATATATGCTCCCTCCCGAAAAAAGCTATATAAT 2046  
 Db 528 CCAAGGACAAAGTACAGGAACCTCAATATATGCTCCCTCCCGAAAAAAGCTATATAAT 469  
 QY 2047 GCATATAGATGCACACAAAGCAGCAACTTTTGTACAGATGGGGAGAGACTTTTCTTG 2106  
 Db 468 GCATATAGATGCACACAAAGCAGCAACTTTTGTACAGATGGGGAGAGACTTTTCTTG 409  
 QY 2107 TATATGCTTATATATTAAGTCTTATGGCTGGTGTAAAAAACAAGATTATATAAATTTA 2166  
 Db 408 TATATGCTTATATATTAAGTCTTATGGCTGGTGTAAAAAACAAGATTATATAAATTTA 349  
 QY 2167 AAGACAAAAGTCAAAACA 2185  
 Db 348 AAGACAAAAGTCAAAACA 330

RESULT 28  
 AA077185 254 bp mRNA linear EST 24-SEP-1999  
 LOCUS 7B09E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens CDNA  
 DEFINITION clone 7B09E10, mRNA sequence.

ACCESSION AA077185  
 VERSION AA077185  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 254)  
 Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,  
 Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.  
 2006 expressed-sequence tags derived from human chromosome  
 7-enriched cDNA libraries  
 Genome Res. 7 (3), 281-292 (1997)

JOURNAL 97228905  
 MEDLINE 9074931  
 PUBMED  
 COMMENT  
 Contact: Eric D. Green  
 Genome Technology Branch  
 National Human Genome Research Institute/NIH  
 49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892  
 Tel: 3014020201  
 Email: egreen@nhgri.nih.gov  
 Plate: 09 row: E column: 10  
 Seq primer: -21M13 (ABI).  
 Fax: 3014024735

FEATURES  
 source  
 1..254  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="7B09E10"  
 /sex="female and male mixture"  
 /tissue\_type="brain"  
 /dev\_stage="pool of 9 week and 12 week"  
 /lab\_host="E. coli strain DH5 alpha"  
 /clone\_lib="Chromosome 7 Fetal Brain cDNA Library"  
 /notes="Organ: brain; Vector: pAMP10; CDNA was generated  
 from cytoplasmic RNA using a mixture of random DNA  
 hexamers and oligo(dT). From this pool of cDNA, human  
 chromosome 7-enriched cDNA was isolated by direct cDNA  
 selection using chromosome 7 genomic DNA (cosmids). The  
 resulting direct-selected cDNA was cloned into a plasmid  
 vector using a non-directional uracil DNA glycosylase (UDG  
 )-mediated cloning strategy."

BASE COUNT 47 a 44 c 72 g 91 t

Query Match 8.8%; Score 193; DB 9; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GGGCAGTAGTGTGCCCAATTCATGACCATATTAATCAACACCTTACAAACAGCAC 1896  
 DB 254 GGGCAGTAGTGTGCCCAATTCATGACCATATTAATCAACACCTTACAAACAGCAC 195  
 QY 1897 ATGGGGCCCACTGGACAGAAACAGCCCTGGGAACTCTCGACCCACAGTCCACCACTA 1956  
 DB 194 ATGGGGCCCACTGGACAGAAACAGCCCTGGGAACTCTCGACCCACAGTCCACCACTA 135  
 QY 1957 TCTCTGAACCTTATATTAATTCAGACCCATACCAAGGACAGGTACAGGAACTCAATAT 2016  
 DB 134 TCTCTGAACCTTATATTAATTCAGACCCATACCAAGGACAGGTACAGGAACTCAATAT 75  
 QY 2017 GACTCCCTCCCC 2029  
 DB 74 GACTCCCTCCCC 62

RESULT 29  
 LOCUS T16288/c 346 bp mRNA linear EST 25-JUL-1996  
 DEFINITION NIB1062 Normalized infant brain, Bento Soares Homo sapiens cDNA  
 3' end, mRNA sequence.

ACCESSION T16288  
 VERSION T16288.1 GI:518450  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 346)  
 AUTHORS Berry, R., Stevens, T.J., Walter, N.A.R., Wilcox, A.S., Rubano, T.,  
 Hopkins, J.A., Weber, J., Goold, R., Soares, M.B. and Sikela, J.M.  
 TITLE Gene-based Sequence Tagged Sites (STS) as the basis for a human  
 gene map  
 JOURNAL Nat. Genet. 10, 415-423 (1995)  
 MEDLINE 95400322  
 PUBMED 7670491  
 COMMENT Contact: Sikela JM  
 Department of Pharmacology  
 University of Colorado Health Sciences Center  
 Box C236, 4200 E. 9th Ave, Denver CO 80262-0236  
 Tel: 3032708637  
 Fax: 3032708637  
 Email: nikki@ally.uchsc.edu  
 Seq primer: -21M13 Universal.

FEATURES  
 source  
 1..346  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /lab\_host="E. coli DH5-alpha"  
 /clone\_lib="Normalized infant brain, Bento Soares"  
 /note="Vector: BA, M13-derived; Site 1: HindIII; Site 2:  
 NotI; The normalized infant brain library, constructed by  
 Bento Soares, Columbia University, was oligo-(dT) primed  
 and directionally cloned into an M13-derived plasmid using  
 total brain mRNA from a 72-day old human female afflicted  
 with spinal muscular atrophy. The library was normalized  
 as described elsewhere."

BASE COUNT 77 a 55 c 83 g 129 t 2 others  
 ORIGIN  
 Query Match 8.8%; Score 193; DB 14; Length 346;  
 Best Local Similarity 99.1%; Pred. No. 1.7e-83;  
 Matches 343; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1839 GCAGTAGTGTGCCCAATTCATGACCATATTAATCAACACCTTACAAACAGCACAT 1898  
 DB 346 GCAGTAGTGTGCCCAATTCATGACCATATTAATCAACACCTTACAAACAGCACAT 287  
 QY 1899 GGGGGCCCACTGGACAGAAACAGCCCTGGGAACTCTCTGACCCACAGTCCACCACTATC 1958  
 DB 286 GGGGGCCCACTGGACAGAAACAGCCCTGGGAACTCTCTGACCCACAGTCCACCACTATC 227  
 QY 1959 TCTGAACCTTATATTAATTCAGACCCATACCAAGGACAGGTACAGGAACTCAATATGA 2018  
 DB 226 TCTGAACCTTATATTAATTCAGACCCATACCAAGGACAGGTACAGGAACTCAATATGA 167  
 QY 2019 CTCCTCCCTCCCCAARAACTTATTAATTCAGATGACACACAAAGACAGCACTTTT 2078  
 DB 166 CTCCTCCCTCCCCAARAACTTATTAATTCAGATGACACACAAAGACAGCACTTTT 107  
 QY 2079 GTACAGAGTGGGAGAGACTTTTCTCTGATATATCTTATATTAATTAAGTCTATGGCTGGT 2138  
 DB 106 GTACAGAGTGGGAGAGACTTTTCTCTGATATATCTTATATTAATTAAGTCTATGGCTGGT 47  
 QY 2139 TAAAAAACAACAGATTATTAATTAATTAAGACAAAGAGTCAAAAC 2184  
 DB 46 TAAAAAACAACAGATTATTAATTAATTAAGACAAAGAGTCAAAAC 1

RESULT 30  
 LOCUS R71701 359 bp mRNA linear EST 02-JUN-1995  
 DEFINITION YJ85c08.r1 Soares breast 2Ndbest Homo sapiens cDNA clone  
 IMAGE:15534 5' similar to SP:B3665 B3665 SLIT PROTEIN 2  
 PRECURSOR - FRUIT FLY 1, mRNA sequence.

ACCESSION R71701  
 VERSION R71701.1 GI:845733  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 359)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston  
 R., Willamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Willson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1447  
 High quality sequence stops: 149  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 1447 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 149.  
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 /dev\_stage="adult"  
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 /clone\_lib="Soares breast 2Ndbest"  
 /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'

FEATURES  
 source  
 1..359  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:573441"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:15534"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares breast 2Ndbest"  
 /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'

	ASE COUNT	68 a	107 c	87 g	91 t	6 others
RIGIN						
Query Match		8.5%;	Score 186;	DB 14;	Length 359;	
Best Local Similarity		99.6%;	Pred. No. 4.9e-80;			
Matches 236;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;	
y	894	TCCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACCTGTGGAGTTGCATCTACACCAC	953			
b	18	TCCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACCTGTGGAGTTGCATCTACACCAC	77			
y	954	AACCCCTTGGAACTGTGATTTGCACATTCCTGTGGCTAGCCTGTGGCTTCGAGAGTATATA	1013			
b	78	AACCCCTTGGAACTGTGATTTGCACATTCCTGTGGCTAGCCTGTGGCTTCGAGAGTATATA	137			
y	1014	CCACACAAATTCACACCTGTGTGGCGCTGTGCATGCTCCCATGCAATGCGAGGCGCGCTAC	1073			
b	138	CCACACAAATTCACACCTGTGTGGCGCTGTGCATGCTCCCATGCAATGCGAGGCGCGCTAC	157			
y	1074	CTCGTGGAGGTGGACACAGCGCTCTCTTCCAGTNGCTCTGTGCCCTTTCATCATGGACGCA	1130			
b	198	CTCGTGGAGGTGGACACAGCGCTCTCTTCCAGTNGCTCTGTGCCCTTTCATCATGGACGCA	254			

RESULT 31	AW524479/c	544 bp	linear	EST 06-MAR-2000
OCUS			mRNA	
EFINITION	UI-R-B00-abx-h-11-0-UI.51 UI-R-B00			Rattus norvegicus cDNA clone
	UI-R-B00-abx-h-11-0-UI 3'			mRNA sequence.
CCSSION	AW524479			
ERSION	AW524479.1	GI:7166864		
EWORDS	EST.			
OURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
ERENCE	1 (bases 1 to 544)			
AUTHORS	Bonafido,M.F., Lennon,G. and Soares,M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene			
	discovery			
JOURNAL	Genome Res. 6 (1996) 791-806 (1996)			

8889948  
PUBMED  
COMMENT

Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road , 4156 MEERF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized thalamus library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com)) The following repetitive elements were found in this cDNA sequence: 1-41, >AT-rich#Low\_complexity 363-395, >(CAG)n#Simple repeat

Seq primer: M13 Forward  
pol:YA=Yes.

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FEATURES      Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:10116"
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/notes="Vector: pYT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-BOO) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
rarest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG LIB=UI-R-BOO
TAG TISSUE=thalamus
TAG SEQ=GATCG"

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Query Match	8.1%	Score 177;	DB 9;	Length 544;
Best Local Similarity	99.6%;	Prod. No. 1.3e-75;		
Matches 227;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1797	GCAGCAGCAACAGCAGCTCCGTCGGTGATCAGGTGAGGGGGCAGTAGTGTGCGCCACA	1856	
DB	381	GCAGCAGCAACAGCAGCTCCGTCGGTGATCAGGTGAGGGGGCAGTAGTGTGCGCCACA	322	
QY	1857	ATTCATGACCCATATTAACAACAACCTTAAACAGACACATGGGGCCACTGGACAGAA	1916	
DB	321	ATCCATGACCATATTAACAACAACCTTAAACAGACACATGGGGCCACTGGACAGAA	262	
QY	1917	ACACGCTGGGGAACTCTCTGCACCCCAAGTCACACATCTCTGGAACCTTATATAATT	1976	
DB	261	ACACGCTGGGGAACTCTCTGCACCCCAAGTCACACATCTCTGGAACCTTATATAATT	202	
QY	1977	CAGACCCATACAAGGACAAGGTACAGGAACTCAAAATATGATCTCCCC	2024	
DB	201	CAGACCCATACAAGGACAAGGTACAGGAACTCAAAATATGATCTCCCC	154	

[illegible]

1073/800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 and  
Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RCL-HT0268-200  
 400-016-g10at3=2000-04-20&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 18  
 High quality sequence stop: 224.  
 Location/Qualifiers  
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 derived from ORSTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 low stringency conditions."  
 45 a 53 c 69 g 57 c

BASE COUNT  
 ORIGIN

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 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 GAACCTTTCCGACGCTGCTTTCAGACACTGGGGTGACACATGCTGACCAATGT 1342  
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 QY 1343 TCAGGCAACTCCACGCGCTCGCCCTACTCAATGTGAGCAGCGCTGAGCTTAACACCTC 1402  
 DB 152 TCAGGCAACTCCACGCGCTCGCCCTACTCAATGTGAGCAGCGCTGAGCTTAACACCTC 93  
 QY 1403 CAACCTACAGCTTCTTCCACACAGTACAGTGGGACACGACGATCTCGCTGAG 1457  
 DB 92 CAACCTACAGCTTCTTCCACACAGTACAGTGGGACACGACGATCTCGCTGAG 38

RESULT 33  
 BF850808  
 LOCUS  
 DEFINITION CM3-EN0111-231100-507-f07 EN0111 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF850808  
 VERSION BF850808.1 GI:12237970  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 273)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922

Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0111-  
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 High quality sequence start: 12  
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 /dev\_stage="Adult"  
 /clone\_lib="EN0111"  
 /note="Organ: lung normal; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORSTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 low stringency conditions."  
 52 a 86 c 71 g 64 t

BASE COUNT  
 ORIGIN

Query Match 7.8%; Score 170; DB 10; Length 273;  
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 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 CGAGGCCCTACCTCTGAGAGTGAGCCAGCCCTCTTCCAGTCTCTGCCCTTCATC 1121  
 DB 87 CGAGGCCCTACCTCTGAGAGTGAGCCAGCCCTCTTCCAGTCTCTGCCCTTCATC 146  
 QY 1122 ATGAGCAGCCTCGAGACCTCAACATTTCTGAGGTGGATGGCAGAACTTAAGTTCGG 1181  
 DB 147 ATGAGCAGCCTCGAGACCTCAACATTTCTGAGGTGGATGGCAGAACTTAAGTTCGG 206  
 QY 1182 ACTCCCTCTATGCTCTCTCGTGAAGTGTGCTGCCCAATGGGACAGTCT 1231  
 DB 207 ACTCCCTCTATGCTCTCTCGTGAAGTGTGCTGCCCAATGGGACAGTCT 256

RESULT 34  
 AI845568/c  
 LOCUS  
 DEFINITION UI-M-A01-adx-a-11-0-UI-s1 NIH BMAP\_MHI N Mus musculus cDNA clone  
 UI-M-A01-adx-a-11-0-UI 3', mRNA sequence.  
 ACCESSION AI845568  
 VERSION AI845568.1 GI:5489474  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 336)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 8899548  
 Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20832-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 1-57, >AT rich#low complexity  
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POLYA=yes.

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TAG LIB=NIH BMAP MHI N  
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Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1860 CATGACCATATTAACTACACACTACAAACAGCAGCATGGGCCCTGGACAGAAAC 1919  
334 CATGACCATATTAACTACACACTACAAACAGCAGCATGGGCCCTGGACAGAAAC 275  
1920 AGCTGGGGAACTCTCTGACCCCAAGTCACCACTATCTCTGAACCTTATATATTCAG 1979  
274 AGCTGGGGAACTCTCTGACCCCAAGTCACCACTATCTCTGAACCTTATATTCAG 215  
1980 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 2024  
214 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 170

RESULT 35  
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LOCUS  
DEFINITION B805784 RIKEN full-length enriched, 1 month neonate cerebellum Mus musculus cDNA clone G63007F10 3', mRNA sequence.  
ACCESSION B805784  
VERSION B805784.1 GI:16978413  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 356)  
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imocani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE  
JOURNAL  
COMMENT  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)  
Unpublished  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanaki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
e mouse tissues  
Location/Qualifiers  
i. 336  
/organism="Mus musculus"  
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61 CATGACCATATTAACTACACACTACAAACAGCAGCATGGGCCCTGGACAGAAAC 120  
1920 AGCTGGGGAACTCTCTGACCCCAAGTCACCACTATCTCTGAACCTTATATTCAG 1979  
121 AGCTGGGGAACTCTCTGACCCCAAGTCACCACTATCTCTGAACCTTATATTCAG 180  
1980 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 2024  
181 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 225

RESULT 36  
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DEFINITION B016B05-3N NIA Mouse Neural Stem Cell (Differentiated) cDNA Library (long) Mus musculus cDNA clone NIA:B016B05 IMAGE:30099664 3', mRNA sequence.  
ACCESSION CA890728  
VERSION CA890728.1 GI:27342277  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)



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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 485)
AUTHORS Piao Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
JOURNAL CDNA Library (Long)
COMMENT Unpublished
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
Plate: B0161 row: B column: 05
Seq primer: -21M13 Forward
High quality sequence stop: 485
POLYA=Yes.

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            /dev_stage="Adult"
            /lab_host="DH10B"
            /clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
            CDNA Library (Long)"
            /note="Vector: pSPOR1 (Invitrogen); Site 1: SalI; Site 2:
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            National Institute on Aging (NIA). Intramural Research
            Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is
            a long-transcript enriched cDNA library (Ref. Genome Res.
            11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
            obtained from Dr. Angelo L. Vescovi (Institute for Stem
            Cell Research, Italy). Double-stranded cDNAs were
            synthesized with an oligo(dT) primer [Invitrogen:
            5'-pGACGTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3'] from
            2.0 microgram of total RNA, treated with T4 DNA polymerase
            and purified by ethanol-precipitation. The cDNAs were
            ligated to lone-linker LU-Sal4, purified by
            phenol/chloroform, and separated from free linkers by
            Centricion 100. Then, the cDNAs were amplified by
            long-range high fidelity PCR using Ex Tag polymerase
            (Takara) with a primer Sal4-S. The products were purified
            by phenol/chloroform and Centricon 100. The cDNAs were
            digested with SalI and NotI enzymes and cloned into
            SalI/NotI site of pSPOR1 plasmid vector. The DH10B E.
            coli host was transformed with the ligation mixture by the
            standard chemical method. The average insert size is about
            3.2 kb. The library was constructed by Yulan Piao."
        101 a 95 c 116 g 173 t
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RESULT 37
AK046781 2833 bp mRNA linear HTC 05-DEC-2002
LOCUS Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN
DEFINITION full-length enriched library, clone:B830005D03 product:LIBG-LIKE
PROTEIN (FRAGMENT) homolog [Mus musculus], full insert sequence.
ACCESSION AK046781 GI:26338356
VERSION AK046781.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Pletschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staab, P., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarini, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.
and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL of 60,770 full-length cDNAs
MEDLINE Nature 420, 563-573 (2002)
PUBMED 11217851
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

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Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Ictani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

source

1. 2833  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:HB30005D03"  
/db\_xref="taxon:10090"  
/clone="B93005D03"  
/tissue\_type="medulla oblongata"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="10 days neonate"  
10. 11299  
/notes="unnamed protein product; LIIB-LIKE PROTEIN (FRAGMENT) homolog [Mus musculus] (SPR1Q99PH1, evidence: FASTQ, 100%ID, 97.9%length, match=1296) putative"

## CDS

/codon\_start=1  
/protein\_id="EAC32864.1"  
/db\_xref="GI:26338357"  
/translations="MSGNHPPEIRPGSFGLSKLWYMSQVSLIERNAPDFGLASVELNLANNLSLPHLPLRYLVHLLHNPWNCDDILMLWLRIEYPTNCTCGRCHAPMEGRVLYVEDQAPFCSAFFIMDAPRDLNIDSDRMALKCRTPMSSVKWLLNGVLSASRHPRLSVLADGTLNFSVLIDTGVTCTMTWAGNSAYLNVLSAELTNPSTFTTIVTTEISPEIDTRKXFPFTSTGYOPATYSTVLIOTRVPKQVPESTDTKMTSLDENVMTKIIIGCFVAVILLAAWLLVFTKLKREHQORS TVTAARTVEIIQVDEIPAPAAATAAPSGVSGEAVVLTTHDINTNTYKPAHGA HTWENSIGNSLHPTVTITSEPTIIQHTKDKVQETQI"

## BASE COUNT

791 a 649 c 685 g 708 t

## ORIGIN

Query Match 7.6%; Score 165; DB 11; Length 2833;  
Best Local Similarity 100.0%; Pred. No. 1.1e-69;  
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1860 CATGACCATATTAACACACCTCAACACACAGCAGCATGGGCCACCTGGACAGAAAC 1919  
1141 CATGACCATATTAACACACCTCAACACACAGCAGCATGGGCCACCTGGACAGAAAC 1200

2Y 1920 AGCTGGGGAACCTCTGCAACCCACAGTCAACATATCTCTGAACCTTATATTCAG 1979  
1201 AGCTGGGGAACCTCTGCAACCCACAGTCAACATATCTCTGAACCTTATATTCAG 1260

2Y 1980 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 2024  
1261 ACCATACCAAGGACAGGTACAGGAACCTCAATATGACTCCCC 1305

## RESULT 38

BQ368354/c  
LOCUS BQ368354 283 bp mRNA linear EST 21-MAY-2002  
DEFINITION PK3-GN0501-160501-003-f04 GN0501 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BQ368354  
VERSION BQ368354.1 GI:21043868  
EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 283)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, P. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&L2=PM3-GN0501-160501-003-f04&t3=2001-05-16&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 17  
High quality sequence stop: 264.

## FEATURES

source

1. 283  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="GN0501"  
/notes="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning PCR products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## BASE COUNT

55 a 74 c 76 g 77 t

## ORIGIN

Query Match 7.1%; Score 155; DB 13; Length 283;  
Best Local Similarity 100.0%; Pred. No. 9.4e-65;  
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1633 CCAGATCATCTGGCTGCTTTGTGGCAGTACTCTGCTAGCTGCGCCCATCTTGATG 1692  
219 CCAAGATCATCTGGCTGCTTTGTGGCAGTACTCTGCTAGCTGCGCCCATCTTGATG 160

QY 1693 TCTTCTATAAACTTCGTAAGCGCACCAGCAGCGAGTACAGTCACAGCGCCCGGACTG 1752  
159 TCTTCTATAAACTTCGTAAGCGCACCAGCAGCGAGTACAGTCACAGCGCCCGGACTG 100

QY 1753 TTGAGATAATCCAGGTGGAGCAAGACATCCAGCA 1787  
29 TTGAGATAATCCAGGTGGAGCAAGACATCCAGCA 65

## RESULT 39

AA224351.1 GI:1844893

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Est.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 150)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krisman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylier, T., Waterston, R. and Wilson, R.  
Waso-NCI human EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL: contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Insert Length: 1183 Std Error: 0.00  
Seq primer: -41m13 fwd, End from Amerham

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FEATURES
source
high quality sequences: 100%
Location/Qualifiers
1. .150
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5424652"
/db_xref="taxon:9606"
/clone="IMAGE:548823"
/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hNT neuron (#937233)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5'
GAATTCGCACGACG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 43 a 25 c 18 g 64 t
ORIGIN
Query Match 6.9%; Score: 150; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 150; Conservative 0; Mismatches 0; Gaps 0;
Qy 2036 ACTTATATATCGAATAGATGCACACACAGCAGCAACTTTTGTACAGTGGGGAGAG 2095

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QY	2096	ACTTTTCTTGTTATATGCTTATATATAAGTCATCGGCTGGTTAAAAAAAACAGATTAT	2155
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QY	2156	ATTAAAAATTTAAAGACAAAAAAGTCAAAAACA	2185
DB	30	ATTAAAAATTTAAAGACAAAAAAGTCAAAAACA	1

RESULT 41  
 BP457723/c  
 LOCUS  
 DEFINITION  
 UI-M-BZ1-bXX-c-06-0-UI.s1 NIH BMAP\_MH12.S1 Mus musculus cDNA clone  
 UI-M-BZ1-bXX-c-06-0-UI 3', mRNA sequence.  
 377 bp mRNA linear EST 01-DEC-2000  
 BP457723

KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 377)

AUTHORS Bernaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PubMed 8889548  
COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NciI site  
and the oligo-dT track served to verify it as a clone from the  
hippocampus tissue cDNA library Preparation: M.B. Soares Lab Clone  
distribution: Researchers may obtain BMAP cDNA clones from RESEARCH  
GENETICS. It should be noted that Bento Soares is generating a  
small number of additional specialized non-redundant arrays of BMAP  
cDNAs whose availability will be considered under appropriate and  
limited collaborative arrangements The following repetitive  
elements were found in this cDNA sequence: 1-42,  
>AT-rich#Low complexity 366-396, >(CAG)n#simple\_repeat  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
source 1..377  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-B21-bkx-C-06-0-UI"  
/dev stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH BMAP MH12 S1"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NIH BMAP MH12 S1 library is a subtracted library derived  
from NIH BMAP MH12. NIH BMAP MH12 is a library derived  
from mouse hippocampus tissue. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at brainest.eng.uiowa.edu.  
TAG\_LIB=NIH BMAP MH12 S1  
TAG\_TISSUE=hippocampus  
TAG\_SEQ=TAGTC"

BASE COUNT 80 a 74 c 98 g 125 t  
ORIGIN  
Query Match 6.3%; Score 138; DB 10; Length 377;  
Best Local Similarity 100.0%; Pred. No. 2.3e-56;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
NY 1887 AACACGACATGGGGCCCACTGGACAGAAAACAGCGCTGGGAACCTCTCTGCACCCCA 1946  
b 243 AACACGACATGGGGCCCACTGGACAGAAAACAGCGCTGGGAACCTCTCTGCACCCCA 184  
y 1947 GTACCACTATCTTGAACTTATATATTCAGACCCATACAGGACAGGTACAGGA 2006  
b 183 GTACCACTATCTTGAACTTATATATTCAGACCCATACAGGACAGGTACAGGA 124  
y 2007 ACTCAATATGACTCCCC 2024  
b 123 ACTCAATATGACTCCCC 106

RESULT 42  
Q340624  
LOCUS BQ340624 300 bp mRNA linear EST 20-MAY-2002  
DEFINITION PMO-NN0258-220501-001-f05 NN0258 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BQ340624

VERSION BQ340624.1 GI:21001705  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PubMed 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-NN0258-  
220501-001-f05&t3=2001-05-22&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 19  
High quality sequence stop: 254.  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev stage="Adult"  
/clone\_lib="NN0258"  
/notes="Organ: nervous normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 56 a 96 c 71 g 77 t  
ORIGIN  
Query Match 6.1%; Score 134; DB 13; Length 300;  
Best Local Similarity 99.5%; Pred. No. 2.1e-54;  
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 878 CCACATAAAGCTCTCTCTTTGGCCCATGACCTTTTACCCGCTGAGGTACTGGTGA 937  
Db 55 CCACATAAAGCTCTCTCTTTGGCCCATGACCTTTTACCCGCTGAGGTACTGGTGA 114  
QY 938 GTTGCACTACACACACACCCCTTGGAACTGTGATCTGTGACATTCCTGGCTAGCCTGGTG 997  
Db 115 GTTGCACTACACACACACCCCTTGGAACTGTGATCTGTGACATTCCTGGCTAGCCTGGTG 174  
QY 998 GCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCTCCCATGCA 1057  
Db 175 GCCTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCTCCCATGCA 234  
QY 1058 CATGC 1062  
Db 235 CATGC 239

RESULT 43  
AW521479/c

LOCUS  
DEFINITION UI-R-B00-agn-e-06-0-UI.s1 si UI-R-B00 Rattus norvegicus cDNA clone  
ACCESSION AWS21479 283 bp mRNA linear EST 06-MAR-2000  
VERSION UI-R-B00-agn-e-06-0-UI 3', mRNA sequence.  
KEYWORDS AWS21479.1 GI:7163904  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
REFERENCE 1 (bases 1 to 283)  
AUTHORS Ronaldo, M. P., Lennon, G. and Soares, M. B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized corpus-striatum library cDNA library Preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 1-47,  
>AT rich/Low complexity  
Seq primer: M13 Forward  
POLYA=yes.

FEATURES  
source  
1..283  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-B00-agn-e-06-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-B00"  
/note="Vector: pTVT3D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; The library  
(UI-R-B00) is a subtracted library derived from a mixture  
of the following tissues: thalamus, cerebellum,  
hypothalamus, medulla, pons, midbrain, cerebral  
corpus striatum and hippocampus. For a detailed  
description of the library from which this clone was  
derived, please visit our web site at  
rateg.eng.uiowa.edu. The subtraction has been previously  
described in (Ronaldo, Lennon and Soares, Genome Research  
6:791-806, 1996)  
TAG\_LIB=UI-R-B00  
TAG\_TISSUE=corpus-striatum  
TAG\_SEQ=CTAGG"

BASE COUNT 66 a 59 g 115 t  
ORIGIN

Query Match 5.7%; Score 124; DB 9; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.8e-49;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1901 GGCCTACTGACAGAAACAGCTGGGAACTCTCTGCACCCACAGTCACCACTATCTC 1960  
DB 283 GGCCTACTGACAGAAACAGCTGGGAACTCTCTGCACCCACAGTCACCACTATCTC 224  
QY 1961 TGAACCTTATATATTCAGACCCATCAAGGACAGGTACAGGAACCTCAATATGACT 2020

Db 223 TGAACCTTATATATTCAGACCCATCAAGGACAGGTACAGGAACCTCAATATGACT 164  
QY 2021 CCCC 2024  
Db 163 CCCC 160

RESULT 44  
AI568859/c  
LOCUS  
DEFINITION 437 bp mRNA linear EST 12-MAY-1999  
to23b10.x1 NCI\_CGAP\_Ut2 Homo sapiens cDNA clone IMAGE:2179867 3',  
mRNA sequence.  
ACCESSION AI568859  
VERSION AI568859.1 GI:4532233  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 437)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaubs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 288)  
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,  
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maizra,M., Martin,  
,J., Moore,B., Schellenberg,K., Seftoe,M., Tan,P., Theising,B.,  
White,Y., Wyllie,T., Waterston,R. and Wilson,R.  
TITLE WashU-NCI human EST Project  
JOURNAL Unpublished  
COMMENT Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNLM ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 1183 Std Error: 0.00  
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ORGANISM

REFERENCE  
AUTHORS  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Itoh,M., Ito,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Izawa,M., Kadota,K., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Kiyosawa,H., Kojima,Y., Kondo,S., Koyama,S., Nakamura,M., Oda,H., Okazaki,Y., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saigo,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,I., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshioka,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished

TITLE  
JOURNAL  
COMMENT  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.go.jp/  
URL: http://genome.scc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsumai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.  
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GAGGAGAGAGATCCACGACTCTTTTCTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGATTCGATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a

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REFERENCE 1 (bases 1 to 256)  
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirozane,T., Inctani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Nunasaki,R., Okazaki,Y., Okido,T., Saio,R., Sakai,C., Sakai,K., Sakazume,N., Sasakawa,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,H., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura.T., et al. 2001)

JOURNAL  
COMMENT  
Unpublished  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.go.jp/  
URL: http://genome.scc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Itoh,M., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
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RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
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cap-trapper. Second strand cDNA was prepared with the
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Job time : 4180 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

DN nucleic - nucleic search, using sw model

Run on: February 6, 2004, 00:12:53 ; Search time 156 Seconds  
(without alignments)  
6182.193 Million cell updates/sec

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Searched: 569978 seqs, 220691566 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	29	1.3	984	4	US-09-996-243-465 Sequence 465, App
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8	20	0.9	1748	4	US-09-996-243-464 Sequence 33, Appl
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110 17 0.8 725 4 US-09-059-625-55 Sequence 55, Appl  
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149 17 0.8 893 3 US-09-142-320-5 Sequence 5, Appl  
150 17 0.8 893 3 US-09-142-320-6 Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-09-996-243-228  
Sequence 228, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 4; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 121 TCTACCTCAGGCGCAAGTGTGGATTCTGTGTGACGCHTCTGCTGCGGCTCAGCG 180  
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Qy 241 CGCGCCGGGCTCTCCGAGGTCCTCCGAGGTCCTCCGAGGTTTCTCTCGAAACACCGGTTACCTCAACC 300  
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Qy 301 TCATGGAGAACACATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACACCTGG 360  
Db 301 TCATGGAGAACACATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACACCTGG 360  
Qy 361 AGGTCTCTCAGTTTGGGCGAGAACTCCATCCGAGATTCAGTGGGGGCTTTCAACGGCC 420  
Db 361 AGGTCTCTCAGTTTGGGCGAGAACTCCATCCGAGATTCAGTGGGGGCTTTCAACGGCC 420  
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DB 2101 TTCTGTTATATGCTTATATATTAAGTCTATGGCTGTTTAAAGTCTGTTTAAAGTCTGTTTAA 2160  
QY 2161 AATTTAAAGCAAAAGTCAAAACA 2185  
DB 2161 AATTTAAAGCAAAAGTCAAAACA 2185

RESULT 2  
US-09-996-243-251  
Sequence 251, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerttsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690





PRIOR FILING DATE: 1998-06-12  
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PRIOR FILING DATE: 1998-06-26  
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PRIOR APPLICATION NUMBER: 60/091478  
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PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 1.4%; Score 31; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5.7e-05;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1930 ACTCTGCGACCCACAGTCACCACTATCTC 1960  
DB 1 ACTCTGCGACCCACAGTCACCACTATCTC 31

RESULT 4  
US-09-482-273-13  
; Sequence 13, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; CURRENT FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 973  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-482-273-13

Query Match 1.3%; Score 29; DB 4; Length 973;  
Best Local Similarity 100.0%; Pred. No. 0.00045;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 489 TACCTGTCCAAGCTCGGGAGCTCTGGCT 517  
DB 533 TACCTGTCCAAGCTCGGGAGCTCTGGCT 561

RESULT 5  
US-09-482-273-82  
; Sequence 82, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 71 Human Secreted Proteins  
 ; FILE REFERENCE: P203051  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; CURRENT FILING DATE: 2000-01-13  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,921  
 ; EARLIER FILING DATE: 1998-07-15  
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 ; EARLIER FILING DATE: 1998-07-15  
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 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; JS-09-482-273-82

Query Match 1.3% Score 29; DB 4; Length 984;  
 Best Local Similarity 100.0%; Pred. No. 0.00045;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 489 TACCTGTCGAAGCTGCGGAGCTCTGGCT 517  
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 Db 539 TACCTGTCGAAGCTGCGGAGCTCTGGCT 567

RESULT 6

US-09-996-243-465/c  
 ; Sequence 465, Application US/09996243  
 ; Patent No. 6478825

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945  
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PRIOR FILING DATE: 1998-07-01

; PRIOR APPLICATION NUMBER: 60/091519  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 1-2%; Score 26; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.013; 0; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 0;

Qy 1969 ATATAATTCAGACCCATACCAAGGAC 1994  
Db 26 ATATAATTCAGACCCATACCAAGGAC 1

## RESULT 7

US-09-996-243-464  
; Sequence 464, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Gurney, Austin I.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
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; PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091978

PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 0.9%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1845 GTGCTGCCACAAATTCATGA 1864  
1 GTGCTGCCACAAATTCATGA 20

RESULT 8  
US-09-620-312D-712/c

Sequence 712, Application US/09620312D  
Patent No. 6569662

## GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyun  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yunqing  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radjic T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt FL\_genes Version 1.0

SEQ ID NO 712

LENGTH: 1748

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (187)..(1467)

US-09-620-312D-712

Query Match 0.9%; Score 20; DB 4; Length 1748;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

163 CTGCTGCCCTCAGCGGG 182

59 CTGCTGCCCTCAGCGGG 40

RESULT 9

US-09-620-454-33/c

Sequence 33, Application US/09690454

Patent No. 6531447

## GENERAL INFORMATION:

APPLICANT: Steven M. Ruben, et al.

TITLE OF INVENTION: 32 Human Secreted Proteins

FILE REFERENCE: P2006P1  
CURRENT APPLICATION NUMBER: US/09/690,454  
CURRENT FILING DATE: 2000-10-18  
PRIOR APPLICATION NUMBER: 09/189,144  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: 60/044,039  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/048,093  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/048,190  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/050,935  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/048,101  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/048,356  
PRIOR FILING DATE: May 30, 1997  
PRIOR APPLICATION NUMBER: 60/056,250  
PRIOR FILING DATE: August 29, 1997  
PRIOR APPLICATION NUMBER: 60/056,296  
PRIOR FILING DATE: August 29, 1997  
PRIOR APPLICATION NUMBER: 60/056,293  
PRIOR FILING DATE: August 29, 1997  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 33  
LENGTH: 997  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (855)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (881)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (916)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (957)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-690-454-33

Query Match 0.9%; Score 19; DB 4; Length 997;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

826 TTGAGCGGAATGCTTTGA 844

796 TTGAGCGGAATGCTTTGA 778

RESULT 10

US-09-016-434-717/c

Sequence 717, Application US/09016434

Patent No. 6500918

## GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seihamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 717:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: THYMOT02
; LIBRARY: 346874
; US-09-016-434-717

Query Match 0.9%; Score 19; DB 4; Length 1236;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 TTGAGCGGAATGCTTTTGA 844
Db 1088 TTGAGCGGAATGCTTTTGA 1070

RESULT 11
US-08-702-344-27/c
; Sequence 27, Application US/08702344
; Patent No. 5723315
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,344
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
```

```
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-702-344-27

Query Match 0.9%; Score 19; DB 1; Length 1243;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 TTGAGCGGAATGCTTTTGA 844
Db 1081 TTGAGCGGAATGCTTTTGA 1063

RESULT 12
US-08-816-617A-1
; Sequence 1, Application US/08816617A
; Patent No. 6022741
; GENERAL INFORMATION:
; APPLICANT: Ting, Jenny P.-Y.
; APPLICANT: Piskurich, Janet
; TITLE OF INVENTION: No. 6022741el Regulatory Genetic DNA that
; TITLE OF INVENTION: Regulates the Class II Transactivator (CIRTA)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 6022741th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,617A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6678 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-816-617A-1

Query Match 0.9%; Score 19; DB 3; Length 6678;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GTGCACCCACACACCTTGA 99
Db 3191 GTGCACCCACACACCTTGA 3209

RESULT 13
US-09-534-638-1/c
; Sequence 1, Application US/09534638
```



Patent No. 6320038  
 GENERAL INFORMATION:  
 APPLICANT: Panula, Pertti A.J.  
 APPLICANT: Brandt, Annika  
 APPLICANT: Westerlund, Johanna  
 TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof  
 TITLE OF INVENTION: for therapy and diagnosis  
 FILE REFERENCE: 2530-104  
 CURRENT APPLICATION NUMBER: US/09/534,638  
 CURRENT FILING DATE: 2000-03-27  
 EARLIER APPLICATION NUMBER: 09/365755  
 EARLIER FILING DATE: 1999-08-03  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 9840  
 TYPE: DNA  
 ORGANISM: Mouse  
 3-09-534-638-1  
 Query Match 0.9%; Score 19; DB 4; Length 9840;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 80 TGTGCACCAACACCTGG 98  
 |||||  
 7923 TGTGCACCAACACCTGG 7905  
 RESULT 14  
 3-09-820-005-3  
 Sequence 3, Application US/09820005  
 Patent No. 6489149  
 GENERAL INFORMATION:  
 APPLICANT: SHAO, Wei et al  
 TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: CL001198  
 CURRENT APPLICATION NUMBER: US/09/820,005  
 CURRENT FILING DATE: 2001-03-29  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 18853  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(18853)  
 OTHER INFORMATION: n = A,T,C or G  
 3-09-820-005-3  
 Query Match 0.9%; Score 19; DB 4; Length 18853;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 80 TGTGCACCAACACCTGG 98  
 |||||  
 6311 TGTGCACCAACACCTGG 6329  
 RESULT 15  
 3-08-311-731A-131/c  
 Sequence 131, Application US/08311731A  
 Patent No. 6583266  
 GENERAL INFORMATION:  
 APPLICANT: SMITH, DOUGLAS  
 APPLICANT: MAO, JEN-I  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
 TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 STREET: 600 ATLANTIC AVENUE  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/311,731A  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GATES, EDWARD R.  
 REGISTRATION NUMBER: 31,616  
 REFERENCE/DOCKET NUMBER: C0044/7125  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/720-3500  
 TELEFAX: 617/720-2441  
 INFORMATION FOR SEQ ID NO: 131:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 42325 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: MYCOBACTERIUM LEPRAE  
 US-08-311-731A-131  
 Query Match 0.9%; Score 19; DB 4; Length 42325;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1656 GTGGCAGTGACTCTGCTAG 1674  
 |||||  
 35665 GTGGCAGTGACTCTGCTAG 35647  
 Db  
 RESULT 16  
 US-09-735-934A-3/c  
 Sequence 3, Application US/09735934A  
 Patent No. 6372468  
 GENERAL INFORMATION:  
 APPLICANT: LI, Jiayin et al  
 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 FILE REFERENCE: CL000851  
 CURRENT APPLICATION NUMBER: US/09/735,934A  
 CURRENT FILING DATE: 2000-12-14  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 43950  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-735-934A-3  
 Query Match 0.9%; Score 19; DB 4; Length 43950;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 80 TGTGCACCAACACCTGG 98  
 |||||  
 23992 TGTGCACCAACACCTGG 23974  
 Db

```

; SEQ ID NO 6
; LENGTH: 45989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-965-048-6

Query Match      0.9%; Score 19; DB 4; Length 45989;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      80 TGTGCACCAACACCACTGG 98
DB      8049 TGTGCACCAACACCACTGG 8057
|||||
|||||

RESULT 20
US-09-873-404-3/c
; Sequence 3, Application US/09873404
; Patent No. 650656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

Query Match      0.9%; Score 19; DB 4; Length 63588;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      80 TGTGCACCAACACCACTGG 98
DB      62145 TGTGCACCAACACCACTGG 62127
|||||
|||||

RESULT 21
US-09-741-150-3/c
; Sequence 3, Application US/09741150
; Patent No. 6436689
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000968
; CURRENT APPLICATION NUMBER: US/09/741,150
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112132
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

Query Match      0.9%; Score 19; DB 4; Length 112132;

```

Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2y 80 TGTGACACACACCTGG 98  
db 81836 TGTGACACACACCTGG 81818

RESULT 22

US-09-103-840A-2/c  
Sequence 2, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103.840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2 4403765  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c, or g  
US-09-103-840A-2

Query Match 0.9%; Score 19; DB 3; Length 4403765;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 443 GCTGTTGACACACTGGCTG 461  
db 318745 GCTGTTGACACACTGGCTG 318727

RESULT 23

US-09-103-840A-1/c  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103.840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1 4411529  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 0.9%; Score 19; DB 3; Length 4411529;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 443 GCTGTTGACACACTGGCTG 461  
db 318636 GCTGTTGACACACTGGCTG 318618

RESULT 24

US-09-313-294A-3480/c  
Sequence 3480, Application US/09313294A  
Patent No. 6476212  
GENERAL INFORMATION:  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
FILE REFERENCE: PL-0017 US  
CURRENT APPLICATION NUMBER: US/09/313.294A  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 7600  
SOFTWARE: PERL Program  
SEQ ID NO 3480  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6476212 700611693H1  
NAME/KEY: unsure  
LOCATION: 69, 71, 130, 172, 206, 209-210, 234, 246, 248, 253  
OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-3480

Query Match 0.8%; Score 18; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 609 GAGTATATCTCTGAGGGA 626  
Db 194 GAGTATATCTCTGAGGGA 177

RESULT 25

PCT-US94-04361-13/c  
Sequence 13, Application PC/TUS9404361  
GENERAL INFORMATION:  
APPLICANT: Brigham and Women's Hospital  
APPLICANT: 75 Francis Street  
APPLICANT: Boston, MA 02115  
APPLICANT: Bunn, H. Franklin  
APPLICANT: Wen, Danyi  
APPLICANT: Showers, Mark O.  
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced  
TITLE OF INVENTION: Activity  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04361  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/049,802  
FILING DATE: 21-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0627,336PC01

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: both  
PCT-US94-04361-13

Query Match 0.8%; Score 18; DB 5; Length 288;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 CAGCAGCGGAGTACGTC 1736  
DB 210 CAGCAGCGGAGTACGTC 193

RESULT 26  
US-08-147-812-3  
Sequence 3, Application US/08147812  
Patent No. 5766909  
GENERAL INFORMATION:  
APPLICANT: Xie, Qiao-wen  
APPLICANT: Nathan, Carl F.  
APPLICANT: Mumford, Richard A.  
APPLICANT: Calaycay, Jimmy Ramos  
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Merck & Co., Inc.  
STREET: 126 East Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh Centris650  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,812  
FILING DATE: NO. 5766909 Available  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/841,641  
FILING DATE: 02-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 186581A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-147-812-3

Query Match 0.8%; Score 18; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 CAGTGGAGACCCAGGAGA 1446  
DB 95 CAGTGGAGACCCAGGAGA 112

RESULT 27  
US-08-475-844-18  
Sequence 18, Application US/08475844  
Patent No. 5972643  
GENERAL INFORMATION:

APPLICANT: Lobanenkov, Victor V.  
APPLICANT: Reiman, Paul E.  
APPLICANT: Klenova, Elena M.  
APPLICANT: Goodwin, Graham H.  
APPLICANT: Filippova, Galina N.  
APPLICANT: Collins, Steven J.  
TITLE OF INVENTION: CTCF  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Khourie and Crew  
STREET: One Market Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,844  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/261,680  
FILING DATE: 17-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14538A-11-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: homo sapiens  
IMMEDIATE SOURCE: CLONE: E4-14  
FEATURE:  
NAME/KEY: -  
LOCATION: 67..68  
OTHER INFORMATION: /label= exon4/intron4  
OTHER INFORMATION: /note= 'exon 4/intron 4 junction'

US-08-475-844-18  
Query Match 0.8%; Score 18; DB 2; Length 500;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2024 CTCCTCCCAAAACTTAT 2041  
DB 206 CTCCTCCCAAAACTTAT 223

RESULT 28  
PCT-US95-08429-18  
Sequence 18, Application PC/TUS9508429  
GENERAL INFORMATION:

APPLICANT: CTCT  
 TITLE OF INVENTION: CTCT  
 NUMBER OF SEQUENCES: 21  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08429  
 FILING DATE: 15-JUN-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/261,680  
 FILING DATE: 17-JUN-1994  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parmelee, Steven W.  
 REGISTRATION NUMBER: 31,990  
 REFERENCE/DOCKET NUMBER: 1438A-11-1PC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-467-9600  
 TELEFAX: 415-543-5043  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 500 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapiens  
 IMMEDIATE SOURCE:  
 CLONE: B4-14  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 67..68  
 OTHER INFORMATION: /label= exon4/intron4  
 OTHER INFORMATION: /note= "exon 4/intron 4 junction"  
 CT-US95-08429-18

Query Match 0.8%; Score 18; DB 5; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 2024 CTCCTCCCAAACTTAT 2041  
 |||||  
 b 206 CTCCTCCCAAACTTAT 223  
 |||||  
 RESULT 29  
 US-09-328-352-2881  
 Sequence 2881, Application US/09128352  
 Patent No. 6562958  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328,352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 2881  
 LENGTH: 531  
 TYPE: DNA  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-2881  
 Query Match 0.8%; Score 18; DB 4; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1874 CTACAACCTTACAACC 1891

Db 407 CTACAACCTTACAACC 424  
 |||||  
 RESULT 30  
 5482709-5  
 Patent No. 5482709  
 APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,  
 SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;  
 AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.  
 TITLE OF INVENTION: BIMERIC ANTIGENIC COMPOSITION WHICH  
 ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS  
 NUMBER OF SEQUENCES: 10  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/148,432  
 FILING DATE: 08-NOV-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 581,693  
 FILING DATE: 12-SEP-1990  
 APPLICATION NUMBER: 215,162  
 FILING DATE: 05-JUL-1989  
 APPLICATION NUMBER: 746,520  
 FILING DATE: 19-JUN-1985  
 APPLICATION NUMBER: 627,811  
 FILING DATE: 05-JUL-1984  
 SEQ ID NO: 5:  
 LENGTH: 533  
 5482709-5  
 Query Match 0.8%; Score 18; DB 6; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1797 GCAGCAGCAACAGCT 1814  
 |||||  
 Db 145 GCAGCAGCAACAGCT 162  
 |||||  
 RESULT 31  
 5273901-6  
 Patent No. 5273901  
 APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,  
 SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;  
 AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.  
 TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS  
 SPOOROITE 21.5 KB ANTIGEN, AC-6B  
 NUMBER OF SEQUENCES: 11  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/581,693  
 FILING DATE: 12-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 215,162  
 FILING DATE: 05-JUL-1988  
 APPLICATION NUMBER: 746,520  
 FILING DATE: 19-JUN-1985  
 APPLICATION NUMBER: 627,811  
 FILING DATE: 05-JUL-1984  
 SEQ ID NO: 6:  
 LENGTH: 543  
 5273901-6  
 Query Match 0.8%; Score 18; DB 6; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1797 GCAGCAGCAACAGCT 1814  
 |||||  
 Db 145 GCAGCAGCAACAGCT 162  
 |||||  
 RESULT 32  
 US-08-609-334-14  
 ; Sequence 14, Application US/08609334

Patent No. 6015663  
GENERAL INFORMATION:  
APPLICANT: Wesley, Ronald D.  
APPLICANT: Mengeling, William L.  
APPLICANT: Clouser, Deborah F.  
APPLICANT: Andreyev, Vladimir G.  
APPLICANT: Vorwald, Ann C.  
APPLICANT: Lager, Kelly M.  
TITLE OF INVENTION: Restriction Enzyme Screen for  
TITLE OF INVENTION: Differentiating Porcine Reproductive and Respiratory  
TITLE OF INVENTION: Syndrome Virus Strains  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis P. Ribando  
STREET: 1815 N. University Street  
CITY: Peoria  
STATE: IL  
COUNTRY: USA  
ZIP: 61604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,334  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ribando, Curtis P.  
REGISTRATION NUMBER: 27,976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 309-681-6513  
TELEFAX: 309-681-6688  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Porcine Reproductive and Respiratory Syndrome  
ORGANISM: Virus  
STRAIN: 41572-2 (NE)  
US-08-609-334-14  
Query Match 0.8%; Score 18; DB 3; Length 603;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1798 CAGCAGCAACAGCAGCTC 1815  
DB 93 CAGCAGCAACAGCAGCTC 110  
RESULT 33  
PCT-US94-04361-25/c  
Sequence 25, Application PC/TUS9404361  
GENERAL INFORMATION:  
APPLICANT: Brigham and Women's Hospital  
APPLICANT: 75 Francis Street  
APPLICANT: Boston, MA 02115  
APPLICANT: Bunn, H. Franklin  
APPLICANT: Wen, Danyi  
APPLICANT: Showers, Mark O.  
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced  
TITLE OF INVENTION: Activity  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04361  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/049,802  
FILING DATE: 21-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0627.336PC01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: single  
TOPOLOGY: both  
PCT-US94-04361-25  
Query Match 0.8%; Score 18; DB 5; Length 687;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1719 CAGCAGCGGAGTACAGTC 1736  
DB 20 CAGCAGCGGAGTACAGTC 3  
RESULT 34  
US-09-107-532A-3104/c  
Sequence 3104, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 3104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8) LOCATION 1...720  
SEQUENCE DESCRIPTION: SEQ ID NO: 3104:  
S-09-107-532A-3104

Query Match 0.8%; Score 18; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 958 CTTGGAACTGTGATTGG 975  
|||||  
b 256 CTTGGAACTGTGATTGG 239

RESULT 35  
US-08-773-368-2/c  
Sequence 2, Application US/08773368  
Patent No. 5856130  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/773,368  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy RJ  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
CLONE: 1599164  
US-08-773-368-2  
Query Match 0.8%; Score 18; DB 2; Length 970;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 428 CCTCAACACCCCTGGAGCT 445  
|||||  
Db 474 CCTCAACACCCCTGGAGCT 457

RESULT 36  
US-09-199-887-2/c.  
Sequence 2, Application US/09199887  
Patent No. 6071874  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/199,887  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/773,368  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy RJ  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: 1599164  
US-09-199-887-2

Query Match 0.8%; Score 18; DB 3; Length 970;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 428 CCTCAACACCCCTGGAGCT 445  
|||||  
Db 474 CCTCAACACCCCTGGAGCT 457

RESULT 37  
US-09-252-991A-10559/c  
Sequence 10559, Application US/09252991A  
Patent No. 6551795



```

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10559
LENGTH: 1119
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10559

Query Match 0.8%; Score 18; DB 4; Length 1119;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 GGCCTTCAACGGCGCTGGC 424
DB 673 GGCCTTCAACGGCGCTGGC 656

RESULT 38
US-09-620-312D-936/C
Sequence 936, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FLgenes Version 1.0
SEQ ID NO 936
LENGTH: 1248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (279)...(932)
US-09-620-312D-936

Query Match 0.8%; Score 18; DB 4; Length 1248;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 341 CGCCACCTCCACCACT 358
DB 334 CGCCACCTCCACCACT 317

RESULT 39
US-08-588-113-1
Sequence 1, Application US/08588113
Patent No. 5710003
GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588.113
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TUU-1652
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 55..1186
US-08-588-113-1

Query Match 0.8%; Score 18; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TCATCGCTGGACTGG 591
DB 581 TCATCGCTGGACTGG 596

RESULT 40
US-09-252-991A-10301
Sequence 10301, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

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PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 10301  
LENGTH: 1425  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10301

Query Match 0.8% Score 18; DB 4; Length 1425;  
Best Local Similarity 100.0%; Pred. No. 73; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0

y 407 GGCCTTCAACGGCTGGC 424  
|||||  
b 858 GGCCTTCAACGGCTGGC 875  
|||||

RESULT 41  
S-09-620-312D-764/c  
Sequence 764, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aigong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yungqing  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radcoje T.  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PL\_FL\_genes Version 1.0  
SEQ ID NO 764  
LENGTH: 1960  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (511)...(1311)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1960)  
OTHER INFORMATION: n = a,t,c or g  
US-09-620-312D-764

Query Match 0.8% Score 18; DB 4; Length 1960;  
Best Local Similarity 100.0%; Pred. No. 72; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0

y 428 CCTCAACCCCTGGAGCT 445  
|||||  
b 973 CCTCAACCCCTGGAGCT 956  
|||||

RESULT 42

US-09-252-991A-10499  
Sequence 10499, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 10499  
LENGTH: 1986  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10499

Query Match 0.8% Score 18; DB 4; Length 1986;  
Best Local Similarity 100.0%; Pred. No. 72; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0

Qy 407 GGCCTTCAACGGCTGGC 424  
|||||  
Db 454 GGCCTTCAACGGCTGGC 471  
|||||

RESULT 43  
US-09-996-243-500  
Sequence 500, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770

1 PRIOR FILING DATE: 1997-11-24  
2 PRIOR APPLICATION NUMBER: 60/075945  
3 PRIOR FILING DATE: 1998-02-25  
4 PRIOR APPLICATION NUMBER: 60/078910  
5 PRIOR FILING DATE: 1998-03-20  
6 PRIOR APPLICATION NUMBER: 60/083322  
7 PRIOR FILING DATE: 1998-04-28  
8 PRIOR APPLICATION NUMBER: 60/084600  
9 PRIOR FILING DATE: 1998-05-07  
10 PRIOR APPLICATION NUMBER: 60/087106  
11 PRIOR FILING DATE: 1998-05-28  
12 PRIOR APPLICATION NUMBER: 60/087607  
13 PRIOR FILING DATE: 1998-06-02  
14 PRIOR APPLICATION NUMBER: 60/087609  
15 PRIOR FILING DATE: 1998-06-02  
16 PRIOR APPLICATION NUMBER: 60/087759  
17 PRIOR FILING DATE: 1998-06-02  
18 PRIOR APPLICATION NUMBER: 60/087827  
19 PRIOR FILING DATE: 1998-06-03  
20 PRIOR APPLICATION NUMBER: 60/088021  
21 PRIOR FILING DATE: 1998-06-04  
22 PRIOR APPLICATION NUMBER: 60/088025  
23 PRIOR FILING DATE: 1998-06-04  
24 PRIOR APPLICATION NUMBER: 60/088026  
25 PRIOR FILING DATE: 1998-06-04  
26 PRIOR APPLICATION NUMBER: 60/088028  
27 PRIOR FILING DATE: 1998-06-04  
28 PRIOR APPLICATION NUMBER: 60/088029  
29 PRIOR FILING DATE: 1998-06-04  
30 PRIOR APPLICATION NUMBER: 60/088030  
31 PRIOR FILING DATE: 1998-06-04  
32 PRIOR APPLICATION NUMBER: 60/088033  
33 PRIOR FILING DATE: 1998-06-04  
34 PRIOR APPLICATION NUMBER: 60/088126  
35 PRIOR FILING DATE: 1998-06-04  
36 PRIOR APPLICATION NUMBER: 60/088167  
37 PRIOR FILING DATE: 1998-06-05  
38 PRIOR APPLICATION NUMBER: 60/088202  
39 PRIOR FILING DATE: 1998-06-05  
40 PRIOR APPLICATION NUMBER: 60/088212  
41 PRIOR FILING DATE: 1998-06-05  
42 PRIOR APPLICATION NUMBER: 60/088217  
43 PRIOR FILING DATE: 1998-06-05  
44 PRIOR APPLICATION NUMBER: 60/088655  
45 PRIOR FILING DATE: 1998-06-09  
46 PRIOR APPLICATION NUMBER: 60/088734  
47 PRIOR FILING DATE: 1998-06-10  
48 PRIOR APPLICATION NUMBER: 60/088738  
49 PRIOR FILING DATE: 1998-06-10  
50 PRIOR APPLICATION NUMBER: 60/088742  
51 PRIOR FILING DATE: 1998-06-10  
52 PRIOR APPLICATION NUMBER: 60/088810  
53 PRIOR FILING DATE: 1998-06-10  
54 PRIOR APPLICATION NUMBER: 60/088824  
55 PRIOR FILING DATE: 1998-06-10  
56 PRIOR APPLICATION NUMBER: 60/088826  
57 PRIOR FILING DATE: 1998-06-10  
58 PRIOR APPLICATION NUMBER: 60/088858  
59 PRIOR FILING DATE: 1998-06-11  
60 PRIOR APPLICATION NUMBER: 60/088861  
61 PRIOR FILING DATE: 1998-06-11  
62 PRIOR APPLICATION NUMBER: 60/088876  
63 PRIOR FILING DATE: 1998-06-11  
64 PRIOR APPLICATION NUMBER: 60/089105  
65 PRIOR FILING DATE: 1998-06-12  
66 PRIOR APPLICATION NUMBER: 60/089440  
67 PRIOR FILING DATE: 1998-06-16  
68 PRIOR APPLICATION NUMBER: 60/089512  
69 PRIOR FILING DATE: 1998-06-16  
70 PRIOR APPLICATION NUMBER: 60/089514  
71 PRIOR FILING DATE: 1998-06-16  
72 PRIOR APPLICATION NUMBER: 60/089532  
73 PRIOR FILING DATE: 1998-06-17

74 PRIOR APPLICATION NUMBER: 60/089538  
75 PRIOR FILING DATE: 1998-06-17  
76 PRIOR APPLICATION NUMBER: 60/089598  
77 PRIOR FILING DATE: 1998-06-17  
78 PRIOR APPLICATION NUMBER: 60/089599  
79 PRIOR FILING DATE: 1998-06-17  
80 PRIOR APPLICATION NUMBER: 60/089600  
81 PRIOR FILING DATE: 1998-06-17  
82 PRIOR APPLICATION NUMBER: 60/089653  
83 PRIOR FILING DATE: 1998-06-17  
84 PRIOR APPLICATION NUMBER: 60/089801  
85 PRIOR FILING DATE: 1998-06-18  
86 PRIOR APPLICATION NUMBER: 60/089907  
87 PRIOR FILING DATE: 1998-06-18  
88 PRIOR APPLICATION NUMBER: 60/089908  
89 PRIOR FILING DATE: 1998-06-18  
90 PRIOR APPLICATION NUMBER: 60/089947  
91 PRIOR FILING DATE: 1998-06-19  
92 PRIOR APPLICATION NUMBER: 60/089948  
93 PRIOR FILING DATE: 1998-06-19  
94 PRIOR APPLICATION NUMBER: 60/089952  
95 PRIOR FILING DATE: 1998-06-19  
96 PRIOR APPLICATION NUMBER: 60/090246  
97 PRIOR FILING DATE: 1998-06-22  
98 PRIOR APPLICATION NUMBER: 60/090252  
99 PRIOR FILING DATE: 1998-06-22  
100 PRIOR APPLICATION NUMBER: 60/090254  
101 PRIOR FILING DATE: 1998-06-22  
102 PRIOR APPLICATION NUMBER: 60/090349  
103 PRIOR FILING DATE: 1998-06-23  
104 PRIOR APPLICATION NUMBER: 60/090355  
105 PRIOR FILING DATE: 1998-06-23  
106 PRIOR APPLICATION NUMBER: 60/090429  
107 PRIOR FILING DATE: 1998-06-24  
108 PRIOR APPLICATION NUMBER: 60/090431  
109 PRIOR FILING DATE: 1998-06-24  
110 PRIOR APPLICATION NUMBER: 60/090435  
111 PRIOR FILING DATE: 1998-06-24  
112 PRIOR APPLICATION NUMBER: 60/090444  
113 PRIOR FILING DATE: 1998-06-24  
114 PRIOR APPLICATION NUMBER: 60/090445  
115 PRIOR FILING DATE: 1998-06-24  
116 PRIOR APPLICATION NUMBER: 60/090472  
117 PRIOR FILING DATE: 1998-06-24  
118 PRIOR APPLICATION NUMBER: 60/090535  
119 PRIOR FILING DATE: 1998-06-24  
120 PRIOR APPLICATION NUMBER: 60/090540  
121 PRIOR FILING DATE: 1998-06-24  
122 PRIOR APPLICATION NUMBER: 60/090542  
123 PRIOR FILING DATE: 1998-06-24  
124 PRIOR APPLICATION NUMBER: 60/090557  
125 PRIOR FILING DATE: 1998-06-24  
126 PRIOR APPLICATION NUMBER: 60/090676  
127 PRIOR FILING DATE: 1998-06-25  
128 PRIOR APPLICATION NUMBER: 60/090678  
129 PRIOR FILING DATE: 1998-06-25  
130 PRIOR APPLICATION NUMBER: 60/090690  
131 PRIOR FILING DATE: 1998-06-25  
132 PRIOR APPLICATION NUMBER: 60/090694  
133 PRIOR FILING DATE: 1998-06-25  
134 PRIOR APPLICATION NUMBER: 60/090695  
135 PRIOR FILING DATE: 1998-06-25  
136 PRIOR APPLICATION NUMBER: 60/090696  
137 PRIOR FILING DATE: 1998-06-25  
138 PRIOR APPLICATION NUMBER: 60/090862  
139 PRIOR FILING DATE: 1998-06-26  
140 PRIOR APPLICATION NUMBER: 60/090863  
141 PRIOR FILING DATE: 1998-06-26  
142 PRIOR APPLICATION NUMBER: 60/091360  
143 PRIOR FILING DATE: 1998-07-01  
144 PRIOR APPLICATION NUMBER: 60/091478  
145 PRIOR FILING DATE: 1998-07-02  
146 PRIOR APPLICATION NUMBER: 60/091544

Prior Filing Date: 1998-07-01  
Prior Application Number: 60/091519  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091626  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091633  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091978  
Prior Filing Date: 1998-07-07  
Prior Application Number: 60/091982  
Prior Filing Date: 1998-07-07  
Prior Application Number: 60/092182  
Prior Filing Date: 1998-07-09

Query Match 0.8%; Score 18; DB 4; Length 2906;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 216 AACAGTTCAGCAGGTC 233  
b 974 AACAGTTCAGCAGGTC 991

RESULT 44  
US-08-074-121-4  
Sequence 4, Application US/08074121  
Patent No. 5767362  
GENERAL INFORMATION:  
APPLICANT: Best, Elaine  
APPLICANT: Knauf, Vic C.  
TITLE OF INVENTION: Methods and Compositions for Modulating  
TITLE OF INVENTION: Lipid Content of Plant Tissues  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: California  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,121  
FILING DATE: 08-JUN-1993  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: 05938/043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-5277  
TELEFAX: (415) 854-0875  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3231 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 861..1328  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1349..2695  
PCT-US94-06447-4  
Query Match 0.8%; Score 18; DB 1; Length 3231;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 GGCTTCACAGCGCTGGC 424  
DB 3108 GGCTTCACAGCGCTGGC 3125

RESULT 45  
PCT-US94-06447-4  
Sequence 4, Application PC/TUS9406447  
GENERAL INFORMATION:  
APPLICANT: Calgene, Inc.  
TITLE OF INVENTION: Methods and Compositions for Modulating  
TITLE OF INVENTION: Lipid Content of Plant Tissues  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Well, Gotshal & Manges  
STREET: 2882 Sand Hill Road, Suite 280  
CITY: Menlo Park  
STATE: California  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06447  
FILING DATE: 06-JUN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: CGNE-097/WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 926-6200  
TELEFAX: (415) 854-3713  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3231 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 861..1328  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1349..2695  
PCT-US94-06447-4  
Query Match 0.8%; Score 18; DB 5; Length 3231;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 GGCTTCACAGCGCTGGC 424  
DB 3108 GGCTTCACAGCGCTGGC 3125

RESULT 46  
US-08-938-291A-2  
Sequence 2, Application US/08938291A  
Patent No. 6117673  
GENERAL INFORMATION:  
APPLICANT: Lev, Sima  
APPLICANT: Florman, Gregory D.  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: RDB PROTEINS AND RELATED

Prior Filing Date: 1998-07-01  
Prior Application Number: 60/091519  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091626  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091633  
Prior Filing Date: 1998-07-02  
Prior Application Number: 60/091978  
Prior Filing Date: 1998-07-07  
Prior Application Number: 60/091982  
Prior Filing Date: 1998-07-07  
Prior Application Number: 60/092182  
Prior Filing Date: 1998-07-09

Query Match 0.8%; Score 18; DB 4; Length 2906;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 216 AACAGTTCAGCAGGTC 233  
b 974 AACAGTTCAGCAGGTC 991

RESULT 44  
US-08-074-121-4  
Sequence 4, Application US/08074121  
Patent No. 5767362  
GENERAL INFORMATION:  
APPLICANT: Best, Elaine  
APPLICANT: Knauf, Vic C.  
TITLE OF INVENTION: Methods and Compositions for Modulating  
TITLE OF INVENTION: Lipid Content of Plant Tissues  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: California  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,121  
FILING DATE: 08-JUN-1993  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: 05938/043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-5277  
TELEFAX: (415) 854-0875  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3231 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 861..1328  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1349..2695  
US-08-074-121-4  
Query Match 0.8%; Score 18; DB 1; Length 3231;

TITLE OF INVENTION: PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,291A  
FILING DATE: September 26, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,337  
FILING DATE: October 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 228/172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4190 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-938-291A-2

Query Match 0.8%; Score 18; DB 3; Length 4190;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGAGGAGCTGGAGATG 731  
Db 2523 CTGGAGGAGCTGGAGATG 2540

RESULT 47  
US-09-589-619-2  
Sequence 2, Application US/09589619  
Patent No. 6576442  
GENERAL INFORMATION:  
APPLICANT: Lev, Sima  
Plowman, Gregory D.  
Schlessinger, Joseph  
TITLE OF INVENTION: RDBG PROTEINS AND RELATED  
PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/589,619  
FILING DATE: 07-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,291  
FILING DATE: September 26, 1997  
APPLICATION NUMBER: 60/027,337  
FILING DATE: October 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 228/172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4190 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-589-619-2

Query Match 0.8%; Score 18; DB 4; Length 4190;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGAGGAGCTGGAGATG 731  
Db 2523 CTGGAGGAGCTGGAGATG 2540

RESULT 48  
US-09-552-950-2  
Sequence 2, Application US/09552950  
Patent No. 6541248  
GENERAL INFORMATION:  
APPLICANT: Oxford Biomedica (UK) Limited  
TITLE OF INVENTION: Anti-Viral Vectors  
FILE REFERENCE: 674524-2004  
CURRENT APPLICATION NUMBER: US/09/552,950  
CURRENT FILING DATE: 2000-04-20  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: gagpol-SYNGp - codon  
OTHER INFORMATION: optimised gagpol sequence  
US-09-552-950-2

Query Match 0.8%; Score 18; DB 4; Length 4307;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1830 GGTGAGGGGGCAGTAGTG 1847  
Db 4173 GGTGAGGGGGCAGTAGTG 4190

RESULT 49  
US-09-392-812A-3  
Sequence 3, Application US/09392812A  
Patent No. 6537778  
GENERAL INFORMATION:  
APPLICANT: Zuker, Charles S.  
APPLICANT: Walker, Richard G.  
APPLICANT: Willingham, Aaron

APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: A Eukaryotic Mechanosensory Transduction Channel  
FILE REFERENCE: 02307E-097600US  
CURRENT APPLICATION NUMBER: US/09/392,812A  
CURRENT FILING DATE: 1999-09-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 6156  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: nompC cDNA sequence  
JS-09-392-812A-3

Query Match 0.8%; Score 18; DB 4; Length 6156;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 593 GGAGCTCAAGAGCTGGA 610  
|||  
3B 912 GGAGCTCAAGAGCTGGA 929

RESULT 50  
JS-09-552-950-5  
Sequence 5, Application US/99552950  
Patent No. 6541248  
GENERAL INFORMATION:  
APPLICANT: Oxford Biomedica (UK) Limited  
TITLE OF INVENTION: Anti-Viral Vectors  
FILE REFERENCE: 674524-2004  
CURRENT APPLICATION NUMBER: US/09/552,950  
CURRENT FILING DATE: 2000-04-20  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 9772  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: pSYNGP  
JS-09-552-950-5

Query Match 0.8%; Score 18; DB 4; Length 9772;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1830 GGTGAGGGGGCAGTAGTG 1847  
|||  
3B 5280 GGTGAGGGGGCAGTAGTG 5297

Search completed: February 6, 2004, 04:00:19  
Job time : 177 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

run on: February 6, 2004, 02:47:54 ; Search time 2687 Seconds

(without alignments)  
2995.436 Million cell updates/sec

title: US-09-989-279-228

effect score: 2185

sequence: 1 gttcccttcgcagccaaa.....aaagacaaaagtcaaacaa 2185

scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

searched: 2449703 seqs, 1841816367 residues

word size : 10

total number of hits satisfying chosen parameters: 2559074

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Listing first 150 summaries

database :

Published Applications NA:\*\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US05\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US05\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
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- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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ALIGNMENTS

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; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.  
/ APPLICANT: Botstein, David  
/ APPLICANT: Desnoyers, Luc  
/ APPLICANT: Baton, Dan L.  
/ APPLICANT: Ferrara, Napoleone  
/ APPLICANT: Fong, Sherman  
/ APPLICANT: Gerber, Hanspeter  
/ APPLICANT: Gerritsen, Mary E.  
/ APPLICANT: Goddard, Audrey  
/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, J. Christopher  
/ APPLICANT: Gurney, Austin L.  
/ APPLICANT: Kljavin, Ivar J.  
/ APPLICANT: Napier, Mary A.  
/ APPLICANT: Pan, James  
/ APPLICANT: Paoni, Nicholas F.  
/ APPLICANT: Roy, Margaret Ann  
/ APPLICANT: Stewart, Timothy A.  
/ APPLICANT: Tamas, Daniel  
/ APPLICANT: Watanabe, Colin K.  
/ APPLICANT: Williams, P. Mickey  
/ APPLICANT: Wood, William I.  
/ APPLICANT: Zhang, Zemin  
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
/ FILE REFERENCE: P2730P1C63  
/ CURRENT APPLICATION NUMBER: US/09/989,722  
/ CURRENT FILING DATE: 2001-11-19  
/ PRIOR APPLICATION NUMBER: 60/049787  
/ PRIOR FILING DATE: 1997-06-16  
/ PRIOR APPLICATION NUMBER: 60/062250  
/ PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1998-07-09

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Db 421 TGGCCAGGCTCAACACCTCGAGCTGTTCGAACTGGCTGACAGTCAATCCCTAGCGGG 480  
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## RESULT 2

US-09-989-723-228  
; Sequence 228, Application US/09989723  
; Patent No. US2002007202A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geisler, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535



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RESULT 3

S-09-989-279-228

Sequence 228 Application US/03989279

Patent No. US2002072496A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

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 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P27301C56  
 CURRENT APPLICATION NUMBER: US/09/989,279  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/049787  
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QY	121	TCTACTCACCGCGAAGTGTGGATTCTGTGTGAGCCATCGCTGCTGCCCTCAGCCG	180
DB	121	TCTACTCACCGCGAAGTGTGGATTCTGTGTGAGCCATCGCTGCTGCCCTCAGCCG	180
QY	181	GGCCGCCGAACTGCCCTCCCTTTGCTGTCAGTAACTTCCAGTTCAGCAAGTGTGTGCA	240
DB	181	GGCCGCCGAACTGCCCTCCCTTTGCTGTCAGTAACTTCCAGTTCAGCAAGTGTGTGCA	240
QY	241	CGCGCCGGGGCTCTCCGAGTCCCGCAGGTATTCCTCGAACAACCGGTACTCTCAAC	300
DB	241	CGCGCCGGGGCTCTCCGAGTCCCGCAGGTATTCCTCGAACAACCGGTACTCTCAAC	300
QY	301	TCATGGAGAACAACTCCAGTATCCAGCGGACACTTCCGCGACCTCCACCACTGG	360
DB	301	TCATGGAGAACAACTCCAGTATCCAGCGGACACTTCCGCGACCTCCACCACTGG	360
QY	361	AGGTCTCTCAGTTGGCGAGGAACCTCCATCCGCGCAGATTGAGTGGGGGCTTCAACCGCC	420
DB	361	AGGTCTCTCAGTTGGCGAGGAACCTCCATCCGCGCAGATTGAGTGGGGGCTTCAACCGCC	420
QY	421	TGGCAGGCTCAACACCTCGAGCTGTTCGACACTGGCTGACAGTCAATCCCTAGCGGG	480
DB	421	TGGCAGGCTCAACACCTCGAGCTGTTCGACACTGGCTGACAGTCAATCCCTAGCGGG	480
QY	481	CTTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCA	540
DB	481	CTTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCA	540



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Db 1621 TCATGAAGACCAACCAAGTATCATTTGGCTGCTTTGGCACTGCTGCTGCTGCCG 1680  
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Db 1681 CCATGTTGATGCTTCTATTAACCTTCTGAAGCGCACCCAGCAGCGAGTACAGTCAAG 1740  
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Db 1741 CCGCCCGGAGCTTGGAGTATCCAGGTGGAAGAGACATCCAGCAGCAACATCCGAG 1800  
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Qy 1861 ATGACCATTAATTAACCAACACTCAAAACCCAGCAGCATGCGGCGCCACTGGAGAGAAAACA 1920  
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Qy 1921 GCTTGGGGAACCTCTGCAACCCCAAGTCAACATCTCTGAACTTATATATATATTA 1980  
Db 1921 GCTTGGGGAACCTCTGCAACCCCAAGTCAACATCTCTGAACTTATATATATTA 1980  
Qy 1981 CCATACCAAGGACCAAGTACAGGAACTCAATATGACTCCCTCCCAAAACCTTA 2040  
Db 1981 CCATACCAAGGACCAAGTACAGGAACTCAATATGACTCCCTCCCAAAACCTTA 2040  
Qy 2041 TAAATGCAATGCAATGCAACCAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT 2100  
Db 2041 TAAATGCAATGCAATGCAACCAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT 2100  
Qy 2101 TTCTTGTATGCTTATATATTAAGTCTATGAGTGTATGAGTGTATTAATTA 2160  
Db 2101 TTCTTGTATGCTTATATATTAAGTCTATGAGTGTATGAGTGTATTAATTA 2160  
Qy 2161 AATTAAGACAAAGTCAABACA 2185  
Db 2161 AATTAAGACAAAGTCAABACA 2185

## RESULT 4

US-09-989-727-228

; Sequence 228 Application US/09989727

; Patent No. US20020072497A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C65

; CURRENT APPLICATION NUMBER: US/09/989,727

1 CURRENT FILING DATE: 2001-11-19  
2 PRIOR APPLICATION NUMBER: 60/049787  
3 PRIOR FILING DATE: 1997-06-16  
4 PRIOR APPLICATION NUMBER: 60/062250  
5 PRIOR FILING DATE: 1997-10-17  
6 PRIOR APPLICATION NUMBER: 60/065186  
7 PRIOR FILING DATE: 1997-11-12  
8 PRIOR APPLICATION NUMBER: 60/065311  
9 PRIOR FILING DATE: 1997-11-13  
10 PRIOR APPLICATION NUMBER: 60/066770  
11 PRIOR FILING DATE: 1997-11-24  
12 PRIOR APPLICATION NUMBER: 60/075945  
13 PRIOR FILING DATE: 1998-02-25  
14 PRIOR APPLICATION NUMBER: 60/078910  
15 PRIOR FILING DATE: 1998-03-20  
16 PRIOR APPLICATION NUMBER: 60/083322  
17 PRIOR FILING DATE: 1998-04-28  
18 PRIOR APPLICATION NUMBER: 60/084600  
19 PRIOR FILING DATE: 1998-05-07  
20 PRIOR APPLICATION NUMBER: 60/087106  
21 PRIOR FILING DATE: 1998-05-28  
22 PRIOR APPLICATION NUMBER: 60/087607  
23 PRIOR FILING DATE: 1998-06-02  
24 PRIOR APPLICATION NUMBER: 60/087609  
25 PRIOR FILING DATE: 1998-06-02  
26 PRIOR APPLICATION NUMBER: 60/087759  
27 PRIOR FILING DATE: 1998-06-02  
28 PRIOR APPLICATION NUMBER: 60/087827  
29 PRIOR FILING DATE: 1998-06-03  
30 PRIOR APPLICATION NUMBER: 60/088021  
31 PRIOR FILING DATE: 1998-06-04  
32 PRIOR APPLICATION NUMBER: 60/088025  
33 PRIOR FILING DATE: 1998-06-04  
34 PRIOR APPLICATION NUMBER: 60/088026  
35 PRIOR FILING DATE: 1998-06-04  
36 PRIOR APPLICATION NUMBER: 60/088028  
37 PRIOR FILING DATE: 1998-06-04  
38 PRIOR APPLICATION NUMBER: 60/088029  
39 PRIOR FILING DATE: 1998-06-04  
40 PRIOR APPLICATION NUMBER: 60/088030  
41 PRIOR FILING DATE: 1998-06-04  
42 PRIOR APPLICATION NUMBER: 60/088033  
43 PRIOR FILING DATE: 1998-06-04  
44 PRIOR APPLICATION NUMBER: 60/088326  
45 PRIOR FILING DATE: 1998-06-04  
46 PRIOR APPLICATION NUMBER: 60/088167  
47 PRIOR FILING DATE: 1998-06-05  
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105 PRIOR FILING DATE: 1998-06-19  
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107 PRIOR FILING DATE: 1998-06-22  
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141 PRIOR FILING DATE: 1998-06-25  
142 PRIOR APPLICATION NUMBER: 60/090694  
143 PRIOR FILING DATE: 1998-06-25  
144 PRIOR APPLICATION NUMBER: 60/090695  
145 PRIOR FILING DATE: 1998-06-25  
146 PRIOR APPLICATION NUMBER: 60/090696

Prior Filing Date: 1998-06-25  
 Prior Application Number: 60/090862  
 Prior Filing Date: 1998-06-26  
 Prior Application Number: 60/090863  
 Prior Filing Date: 1998-06-26  
 Prior Application Number: 60/091360  
 Prior Filing Date: 1998-07-01  
 Prior Application Number: 60/091478  
 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091544  
 Prior Filing Date: 1998-07-01  
 Prior Application Number: 60/091519  
 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091626  
 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091633  
 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091978  
 Prior Filing Date: 1998-07-07  
 Prior Application Number: 60/091982  
 Prior Filing Date: 1998-07-07  
 Prior Application Number: 60/092182  
 Prior Filing Date: 1998-07-09

Query Match 100.0%; Score 2185; DB 9; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-09-989-731-228  
Sequence 228, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
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## RESULT 6

US-09-989-732-228  
Sequence 228, Application US/09989732

Patent No. US20020123463A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC57

CURRENT APPLICATION NUMBER: US/09/989,732

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481	QY	CCTTTGAATACCTGTCTCAAGCTCGCGGAGCTCTGGGTTGCGAACAAACCCCATCGAAAGCA	540
481	DB		
481	QY	CCTTTGAATACCTGTCTCAAGCTCGCGGAGCTCTGGGTTGCGAACAAACCCCATCGAAAGCA	540
481	DB		
541	QY	TCCCTCTTACGCTTCAACACGGGTGCTCCCTCATGTGCGCTTGACCTTGGGGGAGCTCA	600
541	DB		
541	QY	TCCCTCTTACGCTTCAACACGGGTGCTCCCTCATGTGCGCTTGACCTTGGGGGAGCTCA	600
541	DB		
601	QY	AGAAGCTCGAGTATATCTCTGAGGGAGCTTTTTCAGGGGCTGTTTCAACCTCAAGTATCTGA	660
601	DB		
601	QY	AGAAGCTCGAGTATATCTCTGAGGGAGCTTTTTCAGGGGCTGTTTCAACCTCAAGTATCTGA	660
601	DB		
661	QY	ACTTGGGCATGTGCAACATTAAGACATGCCAATCTCACCCCTCTGTGTGGGCTGTGAGG	720
661	DB		
661	QY	ACTTGGGCATGTGCAACATTAAGACATGCCAATCTCACCCCTCTGTGTGGGCTGTGAGG	720
661	DB		
721	QY	AGCTGGAGATCTCAGGGAACCACTTCCCTGAGATCAGGCTGGCTCCTTCCATGSCCTGA	780
721	DB		
721	QY	AGCTGGAGATCTCAGGGAACCACTTCCCTGAGATCAGGCTGGCTCCTTCCATGSCCTGA	780
721	DB		
781	QY	GCTCCCTCAGAAGCTCTGGTTCATGAACCTCACAGGTCAGCTGTGATGTGAGCGGAATGCTT	840
781	DB		
781	QY	GCTCCCTCAGAAGCTCTGGTTCATGAACCTCACAGGTCAGCTGTGATGTGAGCGGAATGCTT	840
781	DB		
841	QY	TGAGCGGCTCGGCTCACTTGTGGAACTCAACTTGGCCCAATAACACTCTCTCTTTGCG	900
841	DB		
841	QY	TGAGCGGCTCGGCTCACTTGTGGAACTCAACTTGGCCCAATAACACTCTCTCTTTGCG	900
841	DB		
901	QY	CCCATGACCTCTTTTACCCCGCTGAGGTAACCTGTGGAGTTGCACTCPACACCAACACCTT	960
901	DB		
901	QY	CCCATGACCTCTTTTACCCCGCTGAGGTAACCTGTGGAGTTGCACTCPACACCAACACCTT	960
901	DB		

y	2041	TAAATGCAATAGATGCAACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTT	2100
b	2041	TAAATGCAATAGATGCAACAAAGACAGCAACTTTTGTACAGAGTGGGAGAGACTTT	2100
y	2101	TTCTTGTATGCTTATATTAAGTCTATGGCTGTTAAABAAAACAGATTATATAA	2160
b	2101	TTCTTGTATGCTTATATTAAGTCTATGGCTGTTAAABAAAACAGATTATATAA	2160
y	2161	AATTTAAAGACAAAAGTCAAAACA	2185
b	2161	AATTTAAAGACAAAAGTCAAAACA	2185

RESULT 7

S-09-991-073-228  
Sequence 228, Application US/09991073  
Patent No. US2002012576A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C15

CURRENT APPLICATION NUMBER: US/09/991,073

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

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 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089908  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089947

1	QY	1	GTTCCTCTCCGAGCCAAATATCCAGCCGATGGTGAATATGAACTGTGCACACCATGA	60
1	Db	1	GTTCCTCTCCGAGCCAAATATCCAGCCGATGGTGAATATGAACTGTGCACACCATGA	60
61	QY	61	AGCTCTTGTGCGCAGTAACCTGTGCACACCACTGGAATGCATCTCTCTCCCTTCG	120
61	Db	61	AGCTCTTGTGCGCAGTAACCTGTGCACACCACTGGAATGCATCTCTCTCCCTTCG	120
121	QY	121	TCTACCTACAGGCGCAAGTGTGGATTCGTGTGAGCAGCATCGCTGTGCGGCTCAGCG	180
121	Db	121	TCTACCTACAGGCGCAAGTGTGGATTCGTGTGAGCAGCATCGCTGTGCGGCTCAGCG	180
181	QY	181	GGCCCCAGACTGCGCTCCGTTTGTGCTGCGAGTACACAGTTTCAGCAAGTGGTGTGCA	240
181	Db	181	GGCCCCAGACTGCGCTCCGTTTGTGCTGCGAGTACACAGTTTCAGCAAGTGGTGTGCA	240
241	QY	241	CGCGCGGGGCTCTCCAGAGTCCCGCAGGATTCCTCGAACAACCCGCTACCTCAACC	300
241	Db	241	CGCGCGGGGCTCTCCAGAGTCCCGCAGGATTCCTCGAACAACCCGCTACCTCAACC	300
301	QY	301	TCATGGAGAACCAATCCAGATTCAGGCGGAGTTCCTCGAACAACCCGCTACCTCAACC	360
301	Db	301	TCATGGAGAACCAATCCAGATTCAGGCGGAGTTCCTCGAACAACCCGCTACCTCAACC	360
361	QY	361	AGTCTCTGCACTTGGGCGAGAACTCCATCCGCGAGATTCAGTGGGGGCTTCAACGGCC	420
361	Db	361	AGTCTCTGCACTTGGGCGAGAACTCCATCCGCGAGATTCAGTGGGGGCTTCAACGGCC	420
421	QY	421	TGGCGAGCTCAACAGCTGAGCTGTTCGACACTGGCTGACAGTCACTCCCTAGCGGG	480
421	Db	421	TGGCGAGCTCAACAGCTGAGCTGTTCGACACTGGCTGACAGTCACTCCCTAGCGGG	480
481	QY	481	CCTTTGAATACCTGTCCAAGCTCGGGAGCTCTGGCTTCGCAACAACCCATCGAAGCA	540
481	Db	481	CCTTTGAATACCTGTCCAAGCTCGGGAGCTCTGGCTTCGCAACAACCCATCGAAGCA	540
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541	Db	541	TCCCTCTTACGCTTCAACCGGGTGCCTCCCTCATCGGCTGAGCTCCCTAGCGGG	600
601	QY	601	AGAGCTGGAGTATCTCTGAGGGAGCTTTTGAAGGGCTGTTCAACTCAAGTATCTGA	660
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661	QY	661	ACTTGGGAGTGTCAACATTAAGACATGCGCAATCTCAACCCCTCTGGTGGGGCTGAGG	720
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781	QY	781	GCTCCCTCAAGAGCTCTGGGTCAATGAATCTCAAGGTCAGCTGATGAGCGGAATGCTT	840
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841	QY	841	TGAGCGGCTGGCTTCACTTGTGGAACTCAACTTGGCGGACAAATACCTCTCTTTTCG	900
841	Db	841	TGAGCGGCTGGCTTCACTTGTGGAACTCAACTTGGCGGACAAATACCTCTCTTTTCG	900
901	QY	901	CCCATGACCTCTTTACCCCGCTGAGGTACCTGTGTGGAGTTGCACTACACCAACCCCTT	960
901	Db	901	CCCATGACCTCTTTACCCCGCTGAGGTACCTGTGTGGAGTTGCACTACACCAACCCCTT	960
961	QY	961	GGAACTGTGATGTGACATTCCTGTGGCTAGCTGTGGCTGAGAGTATATACCAACCA	1020
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1021	QY	1021	ATTCACCTGTGTGGCGGCTGTCTCATGCTCCCATGCAATCGAGGCGGCTACCTCGTGG	1080
1021	Db	1021	ATTCACCTGTGTGGCGGCTGTCTCATGCTCCCATGCAATCGAGGCGGCTACCTCGTGG	1080

Query Match 100.0%; Score 2185; DB 10; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1081 AGTGGACAGGCTCTCTCCAGTCTCTGCCCCCTTCATCATGAGCGCACTCGAGACC 1140  
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1141 TCACATTTCTGAGGTCGATGCGAGCAATTAAGTCTGGACTCCCTATGCTCTCGG 1200  
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1201 TGAAGTGGTGTCTGCCCCAATGCGAGTGTCTAGCCACGCTCTCCGCCCCCAAGGATCT 1260  
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1321 ACACATGATGTGTGACCAATGTTGAGGAACTCCCAAGCTCTGCGCTACCTCAATGTGA 1380  
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1441 CGGAGTCTCGCTGAGGACACCAACGCGAAGTACAAAGCTGTCTTACCACTCCACTG 1500  
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1501 GTTACACGCGGATATPACCACTCTACCAAGCTGTCTTACCACTCCACTG 1560  
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1921 GCTTGGGAACTCTCTGACCCCAAGTACCACTATCTCTGAACTTATATAATTCAGA 1980  
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2041 TAAATGCAATAGATGACACCAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT 2100  
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2101 TTCTTGTATATGCTTATATTAAGTCTATGCGCTGGTTTAAAAAACAAGATATATAA 2160  
2161 AATTTAAAGACAAAAGTCAAAACA 2185

DB 2161 AATTTAAAGACAAAAGTCAAAACA 2185  
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US-09-990-442-228  
; Sequence 228, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609  
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; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
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; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088028

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PRIOR APPLICATION NUMBER:	60/0903419
PRIOR FILING DATE:	1998-06-23
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PRIOR APPLICATION NUMBER:	60/0919826
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PRIOR APPLICATION NUMBER:	60/0921826
PRIOR FILING DATE:	1998-07-09

Best	Local Similarity	100.0%	Pred. No. 0;

[illegible]

121 TCTACCTCAGCGCAAGTGTGGATTCTGTGACGCCATCGCTGCTCGCCTCAGCG 180  
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301 TCATGAGAACAACTCCAGATGATTCAGGCGGACCTTCGCGCACCTCCAGCACTGG 360  
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361 AGGTCTCTGAGTGGGCAAGAACTCCATCCGCGAGATTGAGGTGGGGCTTCAACGGCC 420  
361 AGGTCTCTGAGTGGGCAAGAACTCCATCCGCGAGATTGAGGTGGGGCTTCAACGGCC 420  
421 TGGCGAGCTCAACACCTTGGAGCTGTTCGACAACTGGCTGACGTATCCCTAGCGGG 480  
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1981 CCATATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
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2161 AATTTAAAGCAAAAGTCAAAACA 2185

RESULT 9  
US-09-991-163-228  
; Sequence 228, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P273021C17  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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Db 301 TCATGGAGACACATCCAGATGATCCAGGCGGACAGCTTCCGCGACCTCCACACCTGG 360  
Qy 361 AGGTCTCTGACAGTTGGGACAGAACTCCATCCGCGAGATTGAGGTGGGGGCTTCAAGCGCC 420  
Db 361 AGGTCTCTGACAGTTGGGACAGAACTCCATCCGCGAGATTGAGGTGGGGGCTTCAAGCGCC 420  
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 QY 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGCTTT 2100  
 Db 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGCTTT 2100  
 QY 2101 TTCTGTATATGCTTATATTAATTAAGTCTATGGCTGTTTAAABAAACAGATTATATAA 2160  
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RESULT 10

JS-09-993-604-228

Sequence 228, Application US/09993604

Patent No. US20020137075A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

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 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P27301C25  
 CURRENT APPLICATION NUMBER: US/09/993,604  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	181	GGCCCCAGAACTGCCCTCCCTTTGCTGTCGAGTAACCACTTCCAGCAAGGTGTGTGCA	240
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Qy	241	CGCGCGGGGGCTCTCCGAGTCCGCGAGGGTATTCCCTCGAACACCGGTACTCTCAACC	300
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Qy	301	TCATGGAGAAACAATCCAGATGATCAGGGCCGACACTTCCGGCCACTCCACCACTGG	360
Db	301	TCATGGAGAAACAATCCAGATGATCAGGGCCGACACTTCCGGCCACTCCACCACTGG	360
Qy	361	AGGTCCTGCACTTGGGCGAGGAATCCCATCCGGGAGATGAGGTGGGGGCTTCAACGGCC	420
Db	361	AGGTCCTGCACTTGGGCGAGGAATCCCATCCGGGAGATGAGGTGGGGGCTTCAACGGCC	420

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## RESULT 11

US-09-990-456-228  
; Sequence 228, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2b 61 AGCTCTTGTGACAGTAATGTGCACACACACACCTGGAATGCCATCTGCTCCCGTTG 120  
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2b 121 TCTACCTCAOOGGGAAGTGTGAAATTTGTGTGACGCCATCGCTGCTGACCGG 180  
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2y 241 CGCGCCGGGGCTCTCCGAGTCCCGCAGAGGTATTCCTCGAAACCCGTTCAACC 300  
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2y 301 TCATGGAGAACATTCAGATGATCCAGGCGGACACTTCGCGCACTCCACCACTGG 360  
2b 301 TCATGGAGAACATTCAGATGATCCAGGCGGACACTTCGCGCACTCCACCACTGG 360  
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1621 TCATGAAGACCAAGATCATCATTTGGTCTTTTGGCACTGACTCTGCTAGCTGCGG 1680  
1621 TCATGAAGACCAAGATCATCATTTGGTCTTTTGGCACTGACTCTGCTAGCTGCGG 1680  
1681 CCATGTTGATGTTCTCTATAAATCTCGTAAGCGGCACCCAGCAGCGGAGTACAGTCAAG 1740  
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2101 TTCTGTATATGCTTATATATTAAAGTCTATGGGCTGGTTTAAAAAAGAGATTATATTAA 2160  
2161 AATTTAAAGACAAAAGTCAAAACA 2185  
2161 AATTTAAAGACAAAAGTCAAAACA 2185

## RESULT 12

S-09-989-721-228

Sequence 228, Application US/09989721

Patent No. US20020142961A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C55

CURRENT APPLICATION NUMBER: US/09/989, 721  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
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PRIOR FILING DATE: 1997-11-13  
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 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;  
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QY	61	AGCTCTTTGGCAGGTAACTGTGACCAACACACTGGAATGCCATCTCTCCGTTGG	120
DB	61	AGCTCTTTGGCAGGTAACTGTGACCAACACACTGGAATGCCATCTCTCCGTTGG	120
QY	121	TCCTACTCAGCGGCGAAGTGTGGATTCTGTCTGAGCCATCGTCTGCCCTCAGCGG	180
DB	121	TCCTACTCAGCGGCGAAGTGTGGATTCTGTCTGAGCCATCGTCTGCCCTCAGCGG	180
QY	181	GGCCCCAGAACTGCCCTCCGTTTGTCTGTCAGTAACAGTTTCAGCAAGTGTGTGCA	240
DB	181	GGCCCCAGAACTGCCCTCCGTTTGTCTGTCAGTAACAGTTTCAGCAAGTGTGTGCA	240
QY	241	CGCGCGGGGGCTCTCCGAGGTCCGCGAGGTATTCCTCGAACACCGGTACCTCAAC	300
DB	241	CGCGCGGGGGCTCTCTCCGAGGTCCGCGAGGTATTCCTCGAACACCGGTACCTCAAC	300
QY	301	TCATGGAGAACAAATCCAGATGATCCAGGCGCGACACTTCCGCGCACTCCACCCCTGG	360
DB	301	TCATGGAGAACAAATCCAGATGATCCAGGCGCGACACTTCCGCGCACTCCACCCCTGG	360
QY	361	AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATGAGTGGGGGGCTTCAACGGCC	420
DB	361	AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATGAGTGGGGGGCTTCAACGGCC	420
QY	421	TGGCCAGCTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
DB	421	TGGCCAGCTCAACACCTCGAGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
QY	481	CTTTTGAATACCTGTTCAGCTGCGGGAGCTCTGGCTTCGCAACAAACCCCATCGAAGCA	540
DB	481	CTTTTGAATACCTGTTCAGCTGCGGGAGCTCTGGCTTCGCAACAAACCCCATCGAAGCA	540
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DB	541	TCCTCTCTTACGCTTCAACCGGCTGCCCTCCCTCATCGCTGAGCTTGGGGAGGTCA	600
QY	601	AGAAGCTGAGTATATCTCTGAGGAGGCTTTTGGGGGCTTTCACCTCAAGTATCTGA	660
DB	601	AGAAGCTGAGTATATCTCTGAGGAGGCTTTTGGGGGCTTTCACCTCAAGTATCTGA	660

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1861 ATGACCATATTAACCTTCAACACCTTCAAAACCGACATCGGGGGCCACTGGGACAGAAACA 1920  
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1921 GCTGGGGAATCTCTGCAACCCACAGTCAACCTATCTCTGAACCTTATATATTAATTCAGA 1980  
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1981 CCATACCGAGACAGGTACAGGAACTCAAAATATGATCTCCCTCCCGCCAAAACCTTA 2040  
2041 TAAATGCAATAGATGACACCAAGACAGCACTTTTGTACAGAGTGGGGAGAGACTTT 2100  
2041 TAAATGCAATAGATGACACCAAGACAGCACTTTTGTACAGAGTGGGGAGAGACTTT 2100  
2101 TTCTGTATATGCTTATATTAAGTCTATGGCTGGTTAAAAAACAAGATTTATTA 2160  
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2161 AATTTAAAGACAAAAGTCAAAACA 2185  
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## RESULT 13

US-09-992-598-228  
; Sequence 228, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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142 PRIOR APPLICATION NUMBER: 60/090863  
143 PRIOR FILING DATE: 1998-06-26  
144 PRIOR APPLICATION NUMBER: 60/091360  
145 PRIOR FILING DATE: 1998-07-01  
146 PRIOR APPLICATION NUMBER: 60/091478



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Db 1921 GCCTGGGGAACCTCTGACACCCCAAGTCACCATCTCTGAACTTATATATTTCAGA 1980  
Qy 1981 CCCATACCAAGGACAGGTACAGGAACTCAAAATAGTACTCCCTCCCCCAAAAACTTA 2040  
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Qy 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGTGGGAGAGACTTT 2100  
Db 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGTGGGAGAGACTTT 2100  
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Qy 2161 AATTTAAAGACAAAAGTCARACA 2185  
Db 2161 AATTTAAAGACAAAAGTCARACA 2185

RESULT 14

US-09-989-293A-228

Sequence 228, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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QY 241 CGGCGCGGGGCTCTCCGAGGTCCGCGAGGTATTCCTCGAACAACCCGCTACCTCAACC 300  
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RESULT 15

US-09-989-735-228  
 ; Sequence 228, Application US/09989735  
 ; Publication No. US20020193299A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
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 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
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 ; CURRENT FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: 60/049787  
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54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091544
56	PRIOR FILING DATE: 1998-07-01
57	PRIOR APPLICATION NUMBER: 60/091519
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091626
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091633
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091978
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/091982
66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 2185;	DB 10;	Length 2185;
Best Local Similarity	100.0%;	Pred. No. 0;		

		Matches	2185;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	GTCTCTCTTCCGAGCCAAATCCAGCGATGGTGAATTATGAACGTGCCACCATGA	60								
DB	1	GTCTCTCTTCCGAGCCAAATCCAGCGATGGTGAATTATGAACGTGCCACCATGA	60								
QY	61	AGCTCTTGTGGCAGTAACTGTGCACACACACACCTGGAAATGCATCTCCCTCG	120								
DB	61	AGCTCTTGTGGCAGTAACTGTGCACACACACACCTGGAAATGCATCTCCCTCG	120								
QY	121	TCTACCTCACGGCGCAAGTGTGATCTGTGTGAGCCATCGTGTGCGGCTCAGCG	180								
DB	121	TCTACCTCACGGCGCAAGTGTGATCTGTGTGAGCCATCGTGTGCGGCTCAGCG	180								
QY	181	GGCCCGAGAACTGCGCTCCCTTGTCTGCTGAGTACAGAGTTCAGAGGTGTGCA	240								
DB	181	GGCCCGAGAACTGCGCTCCCTTGTCTGCTGAGTACAGAGTTCAGAGGTGTGCA	240								
QY	241	CGCGCCGGGCTCTCCGAGGTCCGAGGGTATTCCTCGAAACACCGGTACTCAAC	300								
DB	241	CGCGCCGGGCTCTCCGAGGTCCGAGGGTATTCCTCGAAACACCGGTACTCAAC	300								
QY	301	TCATGGAGAACATCAGATGATCAGGCGGACCTTCGCGCACTCCACCACTGG	360								
DB	301	TCATGGAGAACATCAGATGATCAGGCGGACCTTCGCGCACTCCACCACTGG	360								
QY	361	AGTCTCTGAGTGGGAGGAACTCCATCCGCGAGTGAAGTGGGGCTTCAACGGCC	420								
DB	361	AGTCTCTGAGTGGGAGGAACTCCATCCGCGAGTGAAGTGGGGCTTCAACGGCC	420								
QY	421	TGGCCAGCTCAAACCTCTGAGCTGTGTGACAACTGCTGACAGTCACTCTAGCGGG	480								
DB	421	TGGCCAGCTCAAACCTCTGAGCTGTGTGACAACTGCTGACAGTCACTCTAGCGGG	480								
QY	481	CTTTGGAATACCTCCAGCTGGGAGCTCTGGCTTCGCAACACCCATCGAAGCA	540								
DB	481	CTTTGGAATACCTCCAGCTGGGAGCTCTGGCTTCGCAACACCCATCGAAGCA	540								
QY	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGCTGGAGCTCA	600								
DB	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGCTGGAGCTCA	600								
QY	601	AGAGCTGGAGTATCTGAGGAGCTTTGAGGGCTGTTCAACCTCAAGTACTGA	660								
DB	601	AGAGCTGGAGTATCTGAGGAGCTTTGAGGGCTGTTCAACCTCAAGTACTGA	660								
QY	661	ACTTGGGCTATGCAACATTAAGACATGCCAATCTCACCCCTGGTGGGCTGAGG	720								
DB	661	ACTTGGGCTATGCAACATTAAGACATGCCAATCTCACCCCTGGTGGGCTGAGG	720								
QY	721	AGCTGGAGATGTCAGGAAACATCTCCCTGAGATCAGGCTGCTCCATGGCTGA	780								
DB	721	AGCTGGAGATGTCAGGAAACATCTCCCTGAGATCAGGCTGCTCCATGGCTGA	780								
QY	781	GCTCCCTCAAGAGCTCTGGGTATGAATCTCAGAGTCAAGCTGATGAGCGGAATGCT	840								
DB	781	GCTCCCTCAAGAGCTCTGGGTATGAATCTCAGAGTCAAGCTGATGAGCGGAATGCT	840								
QY	841	TTGACGGCTGGCTTCACTTGTGAACTCAACTTGGGCCCAATAACCTCTCTTTTTC	900								
DB	841	TTGACGGCTGGCTTCACTTGTGAACTCAACTTGGGCCCAATAACCTCTCTTTTTC	900								
QY	901	CCCATGACCTTTTACCCGCTGAGTACCTGGTGGAGTTCATCTACCAACACCTTT	960								
DB	901	CCCATGACCTTTTACCCGCTGAGTACCTGGTGGAGTTCATCTACCAACACCTTT	960								
QY	961	GGAACTGTGATGTGACATCTGTGGCTAGCTGTGGCTTCAGAGTATATACCAACA	1020								
DB	961	GGAACTGTGATGTGACATCTGTGGCTAGCTGTGGCTTCAGAGTATATACCAACA	1020								
QY	1021	ATTCACCTGTGGCTGTGCTCATCTCCATGACATGCGAGCGCTACCTCTGTGG	1080								
DB	1021	ATTCACCTGTGGCTGTGCTCATCTCCATGACATGCGAGCGCTACCTCTGTGG	1080								

QY	1081	AGGTGGACCGAGGCTCTTCCAGTGTCTGCCCTCTTCATCATGAGCGACCTTCGAGAC	1140
DB	1081	AGGTGGACCGAGGCTCTTCCAGTGTCTGCCCTCTTCATCATGAGCGACCTTCGAGAC	1140
QY	1141	TCACATTTCTGAGGTTCGATGCGAGAACTTAAGTGTGGAGCTCCCTTATCTCTCG	1200
DB	1141	TCACATTTCTGAGGTTCGATGCGAGAACTTAAGTGTGGAGCTCCCTTATCTCTCG	1200
QY	1201	TGAAGTGTGTGCTGCCCAATGGGAGAGTGTCTAGCCACGCTCCCGCACCCAGGATCT	1260
DB	1201	TGAAGTGTGTGCTGCCCAATGGGAGAGTGTCTAGCCACGCTCCCGCACCCAGGATCT	1260
QY	1261	CTGTCTCTCAACGAGCGCACTTGAATTTTCCAGCTGTCTTCAGACACTCTGGGTGT	1320
DB	1261	CTGTCTCTCAACGAGCGCACTTGAATTTTCCAGCTGTCTTCAGACACTCTGGGTGT	1320
QY	1321	ACACATGATCTGCTGTGAGCACTTGTTCAGGCAACTCCAAAGCTCTCGGCTACCTCAATGTGA	1380
DB	1321	ACACATGATCTGCTGTGAGCACTTGTTCAGGCAACTCCAAAGCTCTCGGCTACCTCAATGTGA	1380
QY	1381	GCACGCTGTGAGCTTAAACACCTTCCAACTACAGCTTCTTCACACAGTAAACAGTGAACCA	1440
DB	1381	GCACGCTGTGAGCTTAAACACCTTCCAACTACAGCTTCTTCACACAGTAAACAGTGAACCA	1440
QY	1441	CGAGATCTGCTGTGAGCACTTGTTCAGGCAACTCCAAAGCTCTCGGCTACCTCAATGTGA	1500
DB	1441	CGAGATCTGCTGTGAGCACTTGTTCAGGCAACTCCAAAGCTCTCGGCTACCTCAATGTGA	1500
QY	1501	GTTACACCGCGCATATACCACTTACACGCTGTCTTACAGCTACCGTGTGCCCA	1560
DB	1501	GTTACACCGCGCATATACCACTTACACGCTGTCTTACAGCTACCGTGTGCCCA	1560
QY	1561	AGCAGTGGCAGTACCCGCGACAGACCACTGACAGAGTGCAGACAGCTGGATGAAG	1620
DB	1561	AGCAGTGGCAGTACCCGCGACAGACCACTGACAGAGTGCAGACAGCTGGATGAAG	1620
QY	1621	TCATGAAAGCAACAAGATCATGTTGGCTGCTTGTGGCGTGTGCTGTGCTAGCTGCCG	1680
DB	1621	TCATGAAAGCAACAAGATCATGTTGGCTGCTTGTGGCGTGTGCTGTGCTAGCTGCCG	1680
QY	1681	CCATGTTGATGCTCTTAAACTTCTAAGCGGCAACAGCAGCGAGTACAGTCAACAG	1740
DB	1681	CCATGTTGATGCTCTTAAACTTCTAAGCGGCAACAGCAGCGAGTACAGTCAACAG	1740
QY	1741	CCGCGCGAGCTGTGAGATAATCCAGGTGACAGACATFCCAGCAGCAATCCCGAG	1800
DB	1741	CCGCGCGAGCTGTGAGATAATCCAGGTGACAGACATFCCAGCAGCAATCCCGAG	1800
QY	1801	CAGCAACAGCAGCTCCGTCGCGGTATCAGGTGAGGGGCGAGTAGTGTGCCACAAATC	1860
DB	1801	CAGCAACAGCAGCTCCGTCGCGGTATCAGGTGAGGGGCGAGTAGTGTGCCACAAATC	1860
QY	1861	ATGACCATATTAACCAACACCTTCAAAACAGCACAATGGGGCCCACTGGACAGAAAAA	1920
DB	1861	ATGACCATATTAACCAACACCTTCAAAACAGCACAATGGGGCCCACTGGACAGAAAAA	1920
QY	1921	GCCTGGGAGTCTCTGACCCACAGTACACTATCTGAACTTATATATTCAG	1980
DB	1921	GCCTGGGAGTCTCTGACCCACAGTACACTATCTGAACTTATATATTCAG	1980
QY	1981	CCCATACCAAGGACAGGTACAGGAACTCAAAATATGATCTCCCTCCCAAAAAAATTA	2040
DB	1981	CCCATACCAAGGACAGGTACAGGAACTCAAAATATGATCTCCCTCCCAAAAAAATTA	2040
QY	2041	TAAATGCAATAGATGCAACAAAGCAGCAACTTTTGTACAGAGTGGGAGACTTT	2100
DB	2041	TAAATGCAATAGATGCAACAAAGCAGCAACTTTTGTACAGAGTGGGAGACTTT	2100
QY	2101	TTCTGTATATGCTTATATATTAAGTCTATGGCTGTTTAAAAAAGCAGATTATATA	2160
DB	2101	TTCTGTATATGCTTATATATTAAGTCTATGGCTGTTTAAAAAAGCAGATTATATA	2160

NY 2161 AATTAAAGACAAAAGTCAAACA 2185  
|||||  
b 2161 AATTAAAGACAAAAGTCAAACA 2185

## RESULT 16

IS-09-990-444-228  
Sequence 228, Application US/09990444  
Publication No. US20020193300A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC19

CURRENT APPLICATION NUMBER: US/09/990,444

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-05-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-06-10  
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PRIOR APPLICATION NUMBER: 60/088858  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252

1	Prior Filing Date: 1998-06-22	QY	121	TCTACCTCAGCGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGTGCTGCGCCCTCAGCGG	180
1	Prior Application Number: 60/090254	Db	121	TCTACCTCAGCGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGTGCTGCGCCCTCAGCGG	180
1	Prior Filing Date: 1998-06-23	QY	181	GSCTCCAGAACTGCCCCCTCCGTTTGTCTGTGTCAGTAAACAGTTTCCAGCAAGTGTGTGCA	240
1	Prior Application Number: 60/090355	Db	181	GSCTCCAGAACTGCCCCCTCCGTTTGTCTGTGTCAGTAAACAGTTTCCAGCAAGTGTGTGCA	240
1	Prior Filing Date: 1998-06-24	QY	241	CGCGCGGGGCTCTCCGAGTCCCGAGGGTATTCCTCGAACACACCGGTACTCCTCAACC	300
1	Prior Application Number: 60/090431	Db	241	CGCGCGGGGCTCTCCGAGTCCCGAGGGTATTCCTCGAACACACCGGTACTCCTCAACC	300
1	Prior Filing Date: 1998-06-24	QY	301	TCATGGAGAACAACTCCAGATGATCCAGGCGGACACTTCCGCGACCTCCACACCTGG	360
1	Prior Application Number: 60/090435	Db	301	TCATGGAGAACAACTCCAGATGATCCAGGCGGACACTTCCGCGACCTCCACACCTGG	360
1	Prior Filing Date: 1998-06-24	QY	361	AGGCTCTGAGTGGGCGGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGCGC	420
1	Prior Application Number: 60/090444	Db	361	AGGCTCTGAGTGGGCGGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGCGC	420
1	Prior Filing Date: 1998-06-24	QY	421	TGGCGAGCTCAACACCTCGAGCTGTTCCAGCACTGGCTGACAGTCACTCCCTAGCGGG	480
1	Prior Application Number: 60/090540	Db	421	TGGCGAGCTCAACACCTCGAGCTGTTCCAGCACTGGCTGACAGTCACTCCCTAGCGGG	480
1	Prior Filing Date: 1998-06-24	QY	481	CCTTGAATACCTGTCAGAGCTGCGGAGCTCTGGCTTCCGCAACACCCCATCGAAAGCA	540
1	Prior Application Number: 60/090557	Db	481	CCTTGAATACCTGTCAGAGCTGCGGAGCTCTGGCTTCCGCAACACCCCATCGAAAGCA	540
1	Prior Filing Date: 1998-06-25	QY	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGGCTGGAGCTTGGGGAGCTCA	600
1	Prior Application Number: 60/090678	Db	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGGCTGGAGCTTGGGGAGCTCA	600
1	Prior Filing Date: 1998-06-25	QY	601	AGAGCTGGAGTATCTCTGAGGAGCTTTTGAAGGGCTGTTCAACCTCAAGTATCTGA	660
1	Prior Application Number: 60/090690	Db	601	AGAGCTGGAGTATCTCTGAGGAGCTTTTGAAGGGCTGTTCAACCTCAAGTATCTGA	660
1	Prior Filing Date: 1998-06-25	QY	661	ACTTGGGATGTGCAACATTAAGACATGCCATCTCACCCCTGCTGGGGCTGGAGG	720
1	Prior Application Number: 60/090696	Db	661	ACTTGGGATGTGCAACATTAAGACATGCCATCTCACCCCTGCTGGGGCTGGAGG	720
1	Prior Filing Date: 1998-06-25	QY	721	AGCTGGAGATGTCAAGGAACTTCCCTGAGATCAGGCTGGCTCTCTCCATGGGCTGA	780
1	Prior Application Number: 60/090862	Db	721	AGCTGGAGATGTCAAGGAACTTCCCTGAGATCAGGCTGGCTCTCTCCATGGGCTGA	780
1	Prior Filing Date: 1998-07-01	QY	781	GCTCCCTCAGAGCTCTGGGTCACTGAACTCAGGTCAGGCTGATGAGCGGAATGCTT	840
1	Prior Application Number: 60/091478	Db	781	GCTCCCTCAGAGCTCTGGGTCACTGAACTCAGGTCAGGCTGATGAGCGGAATGCTT	840
1	Prior Filing Date: 1998-07-02	QY	841	TTGACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATAAATCTCTCTTTTC	900
1	Prior Application Number: 60/091519	Db	841	TTGACGGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATAAATCTCTCTTTTC	900
1	Prior Filing Date: 1998-07-02	QY	901	CCCATGACCTTTTACCCCGCTGAGGTACCTGGTGGAGTGGATCTACACCAACACCTT	960
1	Prior Application Number: 60/091633	Db	901	CCCATGACCTTTTACCCCGCTGAGGTACCTGGTGGAGTGGATCTACACCAACACCTT	960
1	Prior Filing Date: 1998-07-07	QY	961	GGAATGTGATGTGACATCTGTGGCTAGCTGGTGGCTTCCAGAGTATATACCAACA	1020
1	Prior Application Number: 60/091982	Db	961	GGAATGTGATGTGACATCTGTGGCTAGCTGGTGGCTTCCAGAGTATATACCAACA	1020
1	Prior Filing Date: 1998-07-07	QY	1021	ATTCAACTGCTGCTGGGCTCTCCAGTGTCTCCAGTCACTGAGCGGCTGCTGCTGG	1080
1	Prior Application Number: 60/092182	Db	1021	ATTCAACTGCTGCTGGGCTCTCCAGTGTCTCCAGTCACTGAGCGGCTGCTGCTGG	1080
1	Prior Filing Date: 1998-07-09	QY	1081	AGGTGGACCAAGGCTCTCTCCAGTGTCTCCAGTCACTGAGCGGCTGCTGCTGG	1140
1	Prior Application Number: 60/092182	Db	1081	AGGTGGACCAAGGCTCTCTCCAGTGTCTCCAGTCACTGAGCGGCTGCTGCTGG	1140
1	Prior Filing Date: 1998-07-09	QY	1141	TCAACATTTCTGAGGCTGGAATGCGAGAACTTAAGTGTGGAGTCTCCCTTATCTCCG	1200
1	Prior Application Number: 60/092182	Db	1141	TCAACATTTCTGAGGCTGGAATGCGAGAACTTAAGTGTGGAGTCTCCCTTATCTCCG	1200

Query Match 100.0%; Score 2185; DB 10; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y	1	GTTCTCTTCCGAGCCAAATCCAGCGGATGTGAAATTAAGAGTGGCCACACCATGA	60
3b	1	GTTCTCTTCCGAGCCAAATCCAGCGGATGTGAAATTAAGAGTGGCCACACCATGA	60
2y	61	AGCTCTTGTGCGAGTAACTGTGACCAACACACCTGGAATGCCATCTGCTCCCGTTGG	120
3b	61	AGCTCTTGTGCGAGTAACTGTGACCAACACACCTGGAATGCCATCTGCTCCCGTTGG	120

1201	TGAAGTGGTTGGTCCCAATGGGACAGTGTCTCAGCGACGGCTCCCGCACCCCAAGGATCT	1261
1201	TCAAAGTGGTTGGTCCCAATGGGACAGTGTCTCAGCGACGGCTCCCGCACCCCAAGGATCT	1260
1261	CTGTCTCTCAAAGCAGCGGACCTTGAACATTTTCCCAAGTGTCTCTTTCAGACACATGGGGTGT	1320
1261	CTGTCTCTCAAAGCAGCGGACCTTGAACATTTTCCCAAGTGTCTCTTTCAGACACATGGGGTGT	1320
1321	ACACATGCAATGGTGTGACGCAATGTTGGAGGCAATCTCCAGCGCTCGGCTTACTCAATGTGA	1380
1321	ACACATGCAATGGTGTGACGCAATGTTGGAGGCAATCTCCAGCGCTCGGCTTACTCAATGTGA	1380
1381	GCACGGCTGAGCTTAAACACCTTCCAACTACAGCTTCTTTCACACAGTAAACAGTGGAGACCA	1440
1381	GCACGGCTGAGCTTAAACACCTTCCAACTACAGCTTCTTTCACACAGTAAACAGTGGAGACCA	1440
1441	CGGAGATCTCGCTGAGGACACACGCGAAAGTGAAGAGCTGTTCCTTACACAGTCCACTG	1500
1441	CGGAGATCTCGCTGAGGACACACGCGAAAGTGAAGAGCTGTTCCTTACACAGTCCACTG	1500
1501	GTTTACCAGCGGCATATACCACCTCTACACGGTGTCTCATTCAGAGTACCCTGTGCCCCA	1560
1501	GTTTACCAGCGGCATATACCACCTCTACACGGTGTCTCATTCAGAGTACCCTGTGCCCCA	1560
1561	AGCAGGTGGAGTACCGCGGACAGACACACTGACAAGATGACAGTCAGCGCTGATGAAG	1620
1561	AGCAGGTGGAGTACCGCGGACAGACACACTGACAAGATGACAGTCAGCGCTGATGAAG	1620
1621	TCATGAAGACCAACAGACATCATTTGGTCTCTTTGTGGCAGTGACATCTCTAGCTGCGG	1680
1621	TCATGAAGACCAACAGACATCATTTGGTCTCTTTGTGGCAGTGACATCTCTAGCTGCGG	1680
1681	CCATGTTGATTTGCTTCTATTAACCTTCGTAAGCGGACCCAGCGAGGAGTACAGTCAACAG	1740
1681	CCATGTTGATTTGCTTCTATTAACCTTCGTAAGCGGACCCAGCGAGGAGTACAGTCAACAG	1740
1741	CCGCCCGGACCTGTTGAGATTAATCAGGTGACAGAAACATCCACAGCAGCAACATCCGCGAG	1800
1741	CCGCCCGGACCTGTTGAGATTAATCAGGTGACAGAAACATCCACAGCAGCAACATCCGCGAG	1800
1801	CAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGCGAGTAGTGTCTGCCCACAATTC	1860
1801	CAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGCGAGTAGTGTCTGCCCACAATTC	1860
1861	ATGACCATATTTAATCTACAACACCTTACAAACAGACACATGGGGCCACTGGCAGAGAAACA	1920
1861	ATGACCATATTTAATCTACAACACCTTACAAACAGACACATGGGGCCACTGGCAGAGAAACA	1920
1921	GCCTGGGAACTCTCTGCAACCCACAGTCAACATATCTCTGAACTTATATTAATTCAGA	1980
1921	GCCTGGGAACTCTCTGCAACCCACAGTCAACATATCTCTGAACTTATATTAATTCAGA	1980
1981	CCCATACCAAGGACAGGTACAGAAATCTAAATATGACTCCCTCCGCCCAAAAACTTA	2040
1981	CCCATACCAAGGACAGGTACAGAAATCTAAATATGACTCCCTCCGCCCAAAAACTTA	2040
2041	TAAATGCAATAGATGCACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT	2100
2041	TAAATGCAATAGATGCACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT	2100
2101	TTCTGTATATGCTTATATATTTAGTCTATGGCTGTTTAAAAAACAAGATATATTTAA	2160
2101	TTCTGTATATGCTTATATATTTAGTCTATGGCTGTTTAAAAAACAAGATATATTTAA	2160
2161	AAATTAAGACAAAAAGTCAAAACA	2185
2161	AAATTAAGACAAAAAGTCAAAACA	2185

RESULT 17

3-09-993-181-228

6-09-991-181-228  
Sequence 228, Application US/09991181

Sequence 228, Application US/09/067,300  
Publication No. US20020197615A1

```

1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi J.
3 APPLICANT: Baker, Kevin P.
4 APPLICANT: Botstein, David
5 APPLICANT: Desnoyers, Luc
6 APPLICANT: Eaton, Dan L.
7 APPLICANT: Ferrara, Napoleone
8 APPLICANT: Fong, Sherman
9 APPLICANT: Gerber, Hanspeter
10 APPLICANT: Gerritsen, Mary E.
11 APPLICANT: Goddard, Audrey
12 APPLICANT: Godowski, Paul J.
13 APPLICANT: Grimaldi, J. Christopher
14 APPLICANT: Gurney, Austin L.
15 APPLICANT: Kljavin, Ivar J.
16 APPLICANT: Napier, Mary A.
17 APPLICANT: Pan, James
18 APPLICANT: Pacni, Nicholas F.
19 APPLICANT: Roy, Margaret Ann
20 APPLICANT: Stewart, Timothy A.
21 APPLICANT: Tunas, Daniel
22 APPLICANT: Watanabe, Colin K.
23 APPLICANT: Williams, P. Mickey
24 APPLICANT: Wood, William I.
25 APPLICANT: Zhang, Zemin
26 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
27 TITLE OF INVENTION: Acids Encoding the Same
28 FILE REFERENCE: P2730PIC53
29 CURRENT APPLICATION NUMBER: US/09/991,181
30 CURRENT FILING DATE: 2001-11-16
31 PRIOR APPLICATION NUMBER: 60/049787
32 PRIOR FILING DATE: 1997-06-16
33 PRIOR APPLICATION NUMBER: 60/062250
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71 PRIOR APPLICATION NUMBER: 60/088033
72 PRIOR FILING DATE: 1998-06-04
73 PRIOR APPLICATION NUMBER: 60/088326

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; PRIOR FILING DATE: 1998-06-04  
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;  
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 DB 1 GTTCTCTTTCCGAGCCAAATCCAGCGGATGCTGAATTATGAACGTGCCACCAATGA 60  
 QY 61 AGCTTTGTGCGAGGTAACTGTGACACACACACTGGAAATGCCATCTGCTCCGTTGG 120  
 DB 61 AGCTTTGTGCGAGGTAACTGTGACACACACACTGGAAATGCCATCTGCTCCGTTGG 120  
 QY 121 TCTACTCTACGCGCAAGTGTGGATTCTGTGTGAGCATCGCTGCTGCCGCTTCAGCCG 180  
 DB 121 TCTACTCTACGCGCAAGTGTGGATTCTGTGTGAGCATCGCTGCTGCCGCTTCAGCCG 180  
 QY 181 GCGCCCAAGAACTGCCCTCCGTTTGTCTGTCGATTAACAGTTACAGAGTGTGTGCA 240  
 DB 181 GCGCCCAAGAACTGCCCTCCGTTTGTCTGTCGATTAACAGTTACAGAGTGTGTGCA 240

241 CGCGCGGGGCTCTCCGAGGTCCCGAGGTATTCCTTCGAAACACCGGTACCTCAACC 300  
b CGCGCGGGGCTCTCCGAGGTCCCGAGGTATTCCTTCGAAACACCGGTACCTCAACC 300  
301 TCATGAGAGAAACATCCAGATGATCCAGGCGAGACACTTCGCGACCTCCACCACTGG 360  
b TCATGAGAGAAACATCCAGATGATCCAGGCGAGACACTTCGCGACCTCCACCACTGG 360  
361 AGGTCTGCAATGTTGGGCGAGACTCCATCCGCGAGATTGAGGTGGGGGCTTCAACGGCC 420  
b AGGTCTGCAATGTTGGGCGAGACTCCATCCGCGAGATTGAGGTGGGGGCTTCAACGGCC 420  
421 TGSCCAGGCTCAACACCTTGGAGCTTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG 480  
b TGSCCAGGCTCAACACCTTGGAGCTTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG 480  
481 CCTTTGAATACCTGTTCCAGCTCGGGAGCTCTGGCTTCGCAACAACTCCATCGAAGCA 540  
b CCTTTGAATACCTGTTCCAGCTCGGGAGCTCTGGCTTCGCAACAACTCCATCGAAGCA 540  
541 TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATGCGCTGAGCTTGGGGGAGCTCA 600  
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601 AGAAGCTGGAGTATCTCTGAGGAGCTTTTGGGGGCTTTGAGGGCTTCAAGTATCTGA 660  
b AGAAGCTGGAGTATCTCTGAGGAGCTTTTGGGGGCTTTGAGGGCTTCAAGTATCTGA 660  
661 ACTTGGGCTGTCAGCAATTAAGACATCCCAATCTCAACCCCTGGTGGGGCTGGAGG 720  
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721 AGCTGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTTGGCTTCCATGAGGCTGA 780  
b AGCTGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTTGGCTTCCATGAGGCTGA 780  
781 GCTCCCTCAAGAGCTCTGGTCACTGATCAGCTCAGCTGAGCTGATTCAGCGGAGTCTT 840  
b GCTCCCTCAAGAGCTCTGGTCACTGATCAGCTCAGCTGAGCTGATTCAGCGGAGTCTT 840  
841 TTGACGGGCTGGCTTCACTTGTGAACTCAACTGGGCGGCAATTAACCTCTCTTCTTTC 900  
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901 CCATGACCTTTTACCCCGCTGAGTACCTGGTGGAGTTGATCTACACCAACCCCTT 960  
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961 GGAACCTGATTTGATGACATTTCTGGCTAGCTTGGCTTGGAGTATATACCCACCA 1020  
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1081 AGGTGACACAGGCTCTCTTCCAGTGTCTGGCCCTTCAATGATGACGCACTCGAGACC 1140  
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1141 TCACATTTCTGAGGTGCGATGCGAAGACTTAAGTGTGCGACTCCCTCATGCTCTCGG 1200  
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1201 TGAAGTGTGCTGCGCAATGGGACAGTGTCTGAGCAGCCCTCCCGCAGCCCAAGATCT 1260  
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1321 ACATGTCATGTTGACCAATGTTGGAGGCACTTCCCAAGCCCTCGGCTTACCTCATGTC 1380

Db ACATGTCATGTTGACCAATGTTGGAGGCAACTCCAAAGCCCTCGGCTTACCTCAATGTA 1380  
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Qy CAGCAACAGCTGCTCGCTGCTGATCAGGTTGAGGAGGCTGCTGCTGCTGCTGCTGCT 1860  
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## RESULT 18

US-09-989-730-228  
; Sequence 228, Application US/09989730  
; Publication No. US20020197674A1  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deans, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter



APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C69  
CURRENT APPLICATION NUMBER: US/09/989,730  
CURRENT FILING DATE: 2001-11-20  
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 Prior Filing Date: 1998-07-02  
 Prior Application Number: 60/091978  
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 Prior Application Number: 60/091982  
 Prior Filing Date: 1998-07-07  
 Prior Application Number: 60/092182  
 Prior Filing Date: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 GTTCTCCTTTCCGAGCCAAATCCAGGCGATGGTGAATTATGAACGTCGCCACCATGA 60

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 61 AGCTCTTGTGGCAGGTAACCTGTGCACACACACCTGGAAATGCCATCTGCTCCCGTTTCG 120

121 TCTACCTCAAGCGCAGGTGTGATCTGTGTGACGCAATCTGCTGCCGCTCAGCCG 180  
 121 TCTACCTCAAGCGCAGGTGTGATCTGTGTGACGCAATCTGCTGCCGCTCAGCCG 180

181 GCGCCAGAACTGCCCTCGTTGCTGTGCAGTAAACAGTTTCAGCAGGTGGTGTGA 240  
 181 GCGCCAGAACTGCCCTCGTTGCTGTGCAGTAAACAGTTTCAGCAGGTGGTGTGA 240

241 CGCGCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACACCCGGTACCTCAACC 300  
 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACACCCGGTACCTCAACC 300

301 TATGAGAACAACTCCAGATATCCAGGCCGACACTTCGCGCACTCCGACCACTGG 360  
 301 TATGAGAACAACTCCAGATATCCAGGCCGACACTTCGCGCACTCCGACCACTGG 360

361 AGTCTCTCAGTTGGGCGAGGAATCCATCCGCGAGATTGAGGTGGGGGCTTTCACACGGCC 420

361 AGGTCTCTGAGTTGGGCGAGGAATCCATCCGCGAGATTGAGGTGGGGGCTTTCACACGGCC 420  
 421 TGGCCAGCCTCAACACCTCTGGAGCTGTTTCGAACAATGGCTGCACAGTCAATCCCTAGCGGG 480  
 421 TGGCCAGCCTCAACACCTCTGGAGCTGTTTCGAACAATGGCTGCACAGTCAATCCCTAGCGGG 480  
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 481 CTTTGAATACCTGTCCAAAGCTGGGAGCTTGGCTTCGCAACAACCCCATCCAAAGCA 540  
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 541 TCCCTCTTTACGCTTCAACCGGGGTGCCCTCCCTCATGCGCTGAGCTTGGGGGAGCTCA 600  
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 601 AGAGCTGAGTATATCTCTGAGGAGCTTTTGAAGGCTGTTTCAACCTCAAGTATCTGA 660  
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 661 ACTTGGGCAATGCAACATTAAGACATGCCCCTCATCCCTGCTGGGGCTGGAGG 720  
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 1381 GCAGGCTGAGTGTAACTCACTCAAGCTTCTTCAACAGTGTAACTGAGAGCA 1440  
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Db 1501 GTTACAGCGGCATATACCACTCTTACACGGTGCTCATTTACAGACTACCGGTGTGCCCA 1560  
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Db 1621 TCATGAAGACACCAAGATCATCTGTGGCTCTTTGTGGCAGTGCATCTCTGTAGTGGCG 1680  
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Db 1681 CCATGTTGATTTCTTCTATATACTTCTGAAGCGGACCGAGCGGAGTACAGTCAAG 1740  
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Db 1801 CAGCAACAGCAGCTCCGCTCGGCTGTATCAGGTGAGGGGGCAGTAGTGTCTGCCCAATTC 1860  
Qy 1861 ATGACCATATTAACCTACACACCTTACAAACAGCAGACATGGGGCCACTGACAGAAAACA 1920  
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Db 1981 CCCATACCAAGACAGGTACAGGAACCTAAATATGACTCCCTCCCTCCCAAAAACCTTA 2040  
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Db 2041 TAAATGCAATAGATGACACAAAGACAGCACTTTTGTACAGGTGGGGAGAGACTTT 2100  
Qy 2101 TCTTGTATATGCTTATATATTAAGTCTATAGTGGCTGTGTTAAAAAACAAGATATTATTA 2160  
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RESULT 19

US-09-990-436-228  
Sequence 228, Application US/09990436  
Publication No. US20020198148A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnovers, Luc
- APPLICANT: Eaton, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Kijavini, Iwar J.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas P.

- APPLICANT: Roy, Margaret Ann
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tamas, Daniel
- APPLICANT: Watanabe, Colin K.
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- APPLICANT: Zhang, Zemin
- TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
- FILE REFERENCE: P2730P1C14
- CURRENT APPLICATION NUMBER: US/09/990,436
- CURRENT FILING DATE: 2001-11-14
- PRIOR APPLICATION NUMBER: 60/049787
- PRIOR FILING DATE: 1997-06-16
- PRIOR APPLICATION NUMBER: 60/062250
- PRIOR FILING DATE: 1997-10-17
- PRIOR APPLICATION NUMBER: 60/065186
- PRIOR FILING DATE: 1997-11-12
- PRIOR APPLICATION NUMBER: 60/065311
- PRIOR FILING DATE: 1997-11-13
- PRIOR APPLICATION NUMBER: 60/066770
- PRIOR FILING DATE: 1997-11-24
- PRIOR APPLICATION NUMBER: 60/075945
- PRIOR FILING DATE: 1998-02-25
- PRIOR APPLICATION NUMBER: 60/078910
- PRIOR FILING DATE: 1998-03-20
- PRIOR APPLICATION NUMBER: 60/083322
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- PRIOR FILING DATE: 1998-06-04
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- PRIOR FILING DATE: 1998-06-09
- PRIOR APPLICATION NUMBER: 60/088734
- PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 10; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCTTTCCGAGCCAAATCCGAGCGATGTGCAATTATGAACGTGCCACACCATGA 60  
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Db 61 AGCTTTGTGGGAGGTACTGTGCAACACCACTGGAATGCCATCTCTCTCCCGTTCC 120  
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Db 121 TCTACTCTACGGCGCAAGTGTGCAATCTGTGTGCAAGCATCGCTGCTCGCGCTCAGCG 180  
Qy 181 GGGCCGAGAACTGCCCTCTCCGAGGTCCCGAGGTATTCCTCGAACCACCGGTACTCAACC 240  
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Qy 241 CGCGCGGGGGCTCTCCGAGGTCCCGAGGTATTCCTCGAACCACCGGTACTCAACC 300  
Db 241 CGCGCGGGGGCTCTCCGAGGTCCCGAGGTATTCCTCGAACCACCGGTACTCAACC 300  
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Qy 361 AGTCTCTGAGTTGGGCAAGGACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420  
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1321 ACATGATGATGGTACCAATTTGAGGCAATCTCAGGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
1321 ACATGATGATGGTACCAATTTGAGGCAATCTCAGGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
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1501 GTTACAGCGGATATACCTCTTACAGGCTGCTTCTTACAGGCTGCTTCTTACAGGCTGCT 1560  
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1801 CAGCAACAGCAGCTCTCTGCGGTGATCAGTCTGAGGGGCGAGTGTCTGCTGCTGCTGCTGCT 1860  
1861 ATGACCATATTAATCAACACCTTACAAACAGCAGATGGGGCCCACTGACAGCAAGAACCA 1920  
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1981 CCCTATCAAGGAAGATGATCAGGAAACTCAATATATGACTTCTGCTGCTGCTGCTGCTGCTG 2040  
2041 TAAATGCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100  
2041 TAAATGCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100  
2101 TCTGTTATATGCTTAT 2160  
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2161 AATTTAAGACAAAGATCAAAACA 2185  
2161 AATTTAAGACAAAGATCAAAACA 2185

## RESULT 20

US-09-993-687-228  
Sequence 228 Application US/09993687  
Publication No. US20020198149A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

1	PRIOR APPLICATION NUMBER: 60/088871
2	PRIOR FILING DATE: 1998-06-11
3	PRIOR APPLICATION NUMBER: 60/089105
4	PRIOR FILING DATE: 1998-06-12
5	PRIOR APPLICATION NUMBER: 60/089440
6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/089512
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13	PRIOR APPLICATION NUMBER: 60/089538
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22	PRIOR FILING DATE: 1998-06-17
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Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 AGCTCTTGTGGCAGTAATCTGACACCAACACCTGGAATGCCATCTCTCCCGTTG 120

QY 121 TCTACTCAGCGCGCAAGTGTGGATCTGTGTGAGCGATCGCTGCTGCGCCTCAGCG 180
DB 121 TCTACTCAGCGCGCAAGTGTGGATCTGTGTGAGCGATCGCTGCTGCGCCTCAGCG 180

QY 181 GSCCCGAGAACTGCCCCCTCCCTTGTCTGTCAGTAACCAAGTTCAGCAAGTGTGCA 240
DB 181 GSCCCGAGAACTGCCCCCTCCCTTGTCTGTCAGTAACCAAGTTCAGCAAGTGTGCA 240

QY 241 CGCGCGCGGCTCTCCGAGTCCGCGAGGTATTCCTCTGAGCAACCCGGTACCTCAAC 300
DB 241 CGCGCGCGGCTCTCCGAGTCCGCGAGGTATTCCTCTGAGCAACCCGGTACCTCAAC 300

QY 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTCGCGCACTCCACCACTGG 360
DB 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTCGCGCACTCCACCACTGG 360

QY 361 AGGTCTGAGTGGGCGAGAACTCCATCCGCGAGTTCAGTGGGGGCTTCAACGGCC 420
DB 361 AGGTCTGAGTGGGCGAGAACTCCATCCGCGAGTTCAGTGGGGGCTTCAACGGCC 420

QY 421 TGGCAGAGCTCAACCTTCCGAGTGTTCGACCACTGCTGACAGTCACTCCAGCGGG 480
DB 421 TGGCAGAGCTCAACCTTCCGAGTGTTCGACCACTGCTGACAGTCACTCCAGCGGG 480

QY 481 CTTTGAATACCTGTCAGAGTTCGAGGAGCTCTGGCTTCGCAACCCCACTCGAAGCA 540
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QY 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATCGCGCTGAGCTTGGGGAGCTCA 600
DB 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATCGCGCTGAGCTTGGGGAGCTCA 600

QY 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTTGGGGGCTCTTCAAGCTCAAGTATCTGA 660
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QY 781 GCTCCCTCAAGAGCTCTGGGTGATGAACTCACAGGTCAGGCTGATGAGCGGAATGCTT 840
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b 1801 CAGCAACAGCAGCTCGTCCGGTGTATCAGGTGAGGGGCGAGTAGTGTGCCCCCAATTC 1860  
Y 1861 ATGACCATATTAACATACACACTACAAACAGCAGCATGGGGCCCACTGGACAGAAACA 1920  
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b 1921 GCTGGGGAACTCTCTGACCCGCCAGCTCACCACCTATCTCTGAACCTTATATATTCAGA 1980  
Y 1981 CCGTACCAAGACAGAGTACAGGAACTCAATATAGTCTCCCTCCCGCCAAAACCTTA 2040  
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Y 2101 TTCTGTATATCTTATATATTAAGTCTATGGCTGGTTAAAGAAAACAGATTATATTA 2160  
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Y 2161 ATTTAAAGCAAAAAGTCAAAA 2185  
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ESULT 21

S-09-989-734-228

Sequence 228, Application US/09989734

Publication No. US20030003531A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC64  
CURRENT APPLICATION NUMBER: US/09/989,734  
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1501 GTTACGACCGGCTATATACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
1561 AGCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
1561 AGCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
1621 TCATGAAGACCAACCAAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
1621 TCATGAAGACCAACCAAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
1681 CCATGTTGATGCTTCTTATATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
1681 CCATGTTGATGCTTCTTATATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
1741 CCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
1741 CCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
1801 CAGCAACAGAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
1801 CAGCAACAGAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
1861 ATGACCATATTAACTACCAACCTTACAAACCAAGCAGATGGGGCCCACTGGACAGAAAACA 1920

Db 1861 ATGACCATATTAACTACCAACCTTACAAACCAAGCAGATGGGGCCCACTGGACAGAAAACA 1920  
Qy 1921 GCTGGGGAACTCTCTGCAACCCCAAGTCAACCACTATCTCTGCAACCTTATATATATCA 1980  
Db 1921 GCTGGGGAACTCTCTGCAACCCCAAGTCAACCACTATCTCTGCAACCTTATATATCA 1980  
Qy 1981 CCATACCAAGGACAGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAACTTA 2040  
Db 1981 CCATACCAAGGACAGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAACTTA 2040  
Qy 2041 TAAATGCAATAGATGCAACAAAGACAGCAACTTTTCTACAGAGTGGGAGAGACTTT 2100  
Db 2041 TAAATGCAATAGATGCAACAAAGACAGCAACTTTTCTACAGAGTGGGAGAGACTTT 2100  
Qy 2101 TTCTGTATATGCTTATATATTAAGTCTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
Db 2101 TTCTGTATATGCTTATATATTAAGTCTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
Qy 2161 AATTAAAGCAAAAGTCAAAACA 2185  
Db 2161 AATTAAAGCAAAAGTCAAAACA 2185

RESULT 22

US-09-997-653-228  
; Sequence 228, Application US/09997653  
; Publication No US20030008297A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavins, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C38  
; CURRENT APPLICATION NUMBER: US/09/997,653  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322

[illegible]

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GTTCTCCTTCGAGCAAAATCCAGGCGATGGTGAATTAATGAACGTGCCACCATGA 60  
b 1 GTTCTCCTTCGAGCAAAATCCAGGCGATGGTGAATTAATGAACGTGCCACCATGA 60

Y 61 AGCTCTGTGGCAGGTAACCTGTGCACACACACCTGGGAATGCCATCTGCTCCGCTTGG 120  
b 61 AGCTCTGTGGCAGGTAACCTGTGCACACACACCTGGGAATGCCATCTGCTCCGCTTGG 120

Y 121 TCTACCTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCCATCGCTGCTGCGCCTCAGCG 180  
b 121 TCTACCTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCCATCGCTGCTGCGCCTCAGCG 180

Y 181 GSCCCAGAACTGCCCTCGTGTGCTGCTGCAAGTAAACAGTTGAGCAAGTGTGCA 240  
b 181 GSCCCAGAACTGCCCTCGTGTGCTGCTGCAAGTAAACAGTTGAGCAAGTGTGCA 240

Y 241 CGCGCGCGGCGCTCTCCGAGGTCCCGCAGGGTATTCCTTCGAAACCGCGGTACCTCAACC 300  
b 241 CGCGCGCGGCGCTCTCCGAGGTCCCGCAGGGTATTCCTTCGAAACCGCGGTACCTCAACC 300

Y 301 TCAATGAGAAACATCAAGATATCCAGGCGCAGACCTTCGCGCACCTCAACCACTGG 360  
b 301 TCAATGAGAAACATCAAGATATCCAGGCGCAGACCTTCGCGCACCTCAACCACTGG 360

Y 361 AGCTCTCGAGTGTGGCAGAACTCCATCCGCGAGATTGAGGTGGGCGCTTCAAGGSCC 420  
b 361 AGCTCTCGAGTGTGGCAGAACTCCATCCGCGAGATTGAGGTGGGCGCTTCAAGGSCC 420

Y 421 TGSCCAGCTCAACACCTTGGAGCTGTTCGAACTGGCTGACATCTCATCTAGCGGG 480  
b 421 TGSCCAGCTCAACACCTTGGAGCTGTTCGAACTGGCTGACATCTCATCTAGCGGG 480

Y 481 CTTTGAATACCTGTCACAGCTGCGGAGCTCTGCTTCCGCAACACCCCATCGAAGCA 540  
b 481 CTTTGAATACCTGTCACAGCTGCGGAGCTCTGCTTCCGCAACACCCCATCGAAGCA 540

Y 541 TCCCTCTTACGCTTCAACCGGGTGCCCTCCTCATGCGCTGGACCTTGGGGAGCTCA 600  
b 541 TCCCTCTTACGCTTCAACCGGGTGCCCTCCTCATGCGCTGGACCTTGGGGAGCTCA 600

Y 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGA 660  
b 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTGAGGGGCTGTTCAACCTCAAGTATCTGA 660

Y 661 ACTTGGGCAATGTGCACAAATTAAGACATGCCCAATCTCAACCCCTGCTGGGGCTGGAG 720  
b 661 ACTTGGGCAATGTGCACAAATTAAGACATGCCCAATCTCAACCCCTGCTGGGGCTGGAG 720

Y 721 AGCTGAGATGTGAGGAACCACTTCCTCTGAGATCAGGCTGCTGCTTCACTGCGCTGA 780  
b 721 AGCTGAGATGTGAGGAACCACTTCCTCTGAGATCAGGCTGCTGCTTCACTGCGCTGA 780

Y 781 GCTCCCTCAAGAGCTCTGGGTCAATGAACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840  
b 781 GCTCCCTCAAGAGCTCTGGGTCAATGAACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 840

Y 841 TTGAGGGCTGCTTCACTTGTGGAACTCAAGTGGGCCCAATTAACCTCTCTTCTTTCG 900  
b 841 TTGAGGGCTGCTTCACTTGTGGAACTCAAGTGGGCCCAATTAACCTCTCTTCTTTCG 900

Y 901 CCCATACCAAGAGAGGTACAGGAACCTCAATATGACTCCCTCCGCCCAAAACCTTA 960

Db 901 CCCATGACCTCTTTACCCGCTCAGGTACTTGGTGGAGTTGATCTACACCAACCCCTT 960

Qy 961 GGAACCTGTGATGTGACATTTCTGTGGCTAGCTAGCTGTGGCTTGGAGATATATACCA 1020

Db 961 GGAACCTGTGATGTGACATTTCTGTGGCTAGCTAGCTGTGGCTTGGAGATATATACCA 1020

Qy 1021 ATTCCACCTGTCTGTGGCTGTGATCTCCATGACATGACATGAGGCGCTTACCTCGTGG 1080

Db 1021 ATTCCACCTGTCTGTGGCTGTGATCTCCATGACATGAGGCGCTTACCTCGTGG 1080

Qy 1081 AGGTGACCAAGGCTCTCTTCCAGTGTCTGCCCCCTTCAATGAGACGACCTCGAGAC 1140

Db 1081 AGGTGACCAAGGCTCTCTTCCAGTGTCTGCCCCCTTCAATGAGACGACCTCGAGAC 1140

Qy 1141 TCAACATTTCTGAGGGTGTGATGGCAGAACTTAAGTGTGGAGTCCCTTATGTCTCTCG 1200

Db 1141 TCAACATTTCTGAGGGTGTGATGGCAGAACTTAAGTGTGGAGTCCCTTATGTCTCTCG 1200

Qy 1201 TGAAGTGTGTGTGCCAATGGGACAGTGTCTCAGCAAGCTTCCGCGCACCAAGATCT 1260

Db 1201 TGAAGTGTGTGTGCCAATGGGACAGTGTCTCAGCAAGCTTCCGCGCACCAAGATCT 1260

Qy 1261 CTGTCTCTCAAGAGCGCACCTTGAACCTTTTCCAGTGTCTTTTCCAGACATGGGGTGT 1320

Db 1261 CTGTCTCTCAAGAGCGCACCTTGAACCTTTTCCAGTGTCTTTTCCAGACATGGGGTGT 1320

Qy 1321 ACATGCTATGTGTGACCAATGTTCAGGCAACTCCAAAGCTTCCGCTTACCTCAATGTGA 1380

Db 1321 ACATGCTATGTGTGACCAATGTTCAGGCAACTCCAAAGCTTCCGCTTACCTCAATGTGA 1380

Qy 1381 GCAAGCTGAGCTTAAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 1440

Db 1381 GCAAGCTGAGCTTAAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 1440

Qy 1441 CGAGATCTCGCTGAGGACAAACCGGAAAGTCAAGCTTCTTACCACTCCAGCTTCACTG 1500

Db 1441 CGAGATCTCGCTGAGGACAAACCGGAAAGTCAAGCTTCTTACCACTCCAGCTTCACTG 1500

Qy 1501 GTTACAGCGCGCATATACCACTTCTTACAGCTTCTTACAGCTTCTTACAGCTTCTTACAG 1560

Db 1501 GTTACAGCGCGCATATACCACTTCTTACAGCTTCTTACAGCTTCTTACAGCTTCTTACAG 1560

Qy 1561 AGCAGTGTGAGTGTGAGGACAGACCTTCAAGATGACAGCTTCAAGCTTCAAGCTTCAAG 1620

Db 1561 AGCAGTGTGAGTGTGAGGACAGACCTTCAAGATGACAGCTTCAAGCTTCAAGCTTCAAG 1620

Qy 1621 TCAATGAAGCAACCAAGATCATCAATTTGGCTGCTTTTGGCAGTGAATCTGCTAGTGG 1680

Db 1621 TCAATGAAGCAACCAAGATCATCAATTTGGCTGCTTTTGGCAGTGAATCTGCTAGTGG 1680

Qy 1681 CCATGTTGATGCTTCTTATTAACCTTGAAGCGCACAGCGGAGTACAGTCAAG 1740

Db 1681 CCATGTTGATGCTTCTTATTAACCTTGAAGCGCACAGCGGAGTACAGTCAAG 1740

Qy 1741 CGCGCGGAGTGTGAGATATCCAGGTGAGGAGACATCCAGCAGCAACATCCGAG 1800

Db 1741 CGCGCGGAGTGTGAGATATCCAGGTGAGGAGACATCCAGCAGCAACATCCGAG 1800

Qy 1801 CAGCAACAGACCTCGTCCGCTGTATCAGGTGAGGCGGAGTGTGCTGCGCAATTC 1860

Db 1801 CAGCAACAGACCTCGTCCGCTGTATCAGGTGAGGCGGAGTGTGCTGCGCAATTC 1860

Qy 1861 ATGACCATTAATTAACATCAACACCTTCAAAACAGCACTTGGGGCGCACCTGGACAGAA 1920

Db 1861 ATGACCATTAATTAACATCAACACCTTCAAAACAGCACTTGGGGCGCACCTGGACAGAA 1920

Qy 1921 GCTGGGGAACCTCTGCAACCGCAAGTCAACATCTCTGAACTTATATTAATTCAGA 1980

Db 1921 GCTGGGGAACCTCTGCAACCGCAAGTCAACATCTCTGAACTTATATTAATTCAGA 1980

Qy 1981 CCCATACCAAGAGAGGTACAGGAACCTCAATATGACTCCCTCCGCCCAAAACCTTA 2040

Db 1981 CCCATACCAAGACAGGTACAGGAACTCAATATGACTCCCTCCCAAAAACTTA 2040  
QY 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT 2100  
Db 2041 TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGATGGGGAGAGACTTT 2100  
QY 2101 TTCTTGATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAACAACATTATATTA 2160  
Db 2101 TTCTTGATATGCTTATATATTAAGTCTATGGCTGGTTAAAAAACAACATTATATTA 2160  
QY 2161 AATTTAAAGACAAAAGTCAAAACA 2185  
Db 2161 AATTTAAAGACAAAAGTCAAAACA 2185

## RESULT 23

JS-09-993-667-228

Sequence 228, Application US/09993667

Publication No. US20030022187A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C4

CURRENT APPLICATION NUMBER: US/09/993.667

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match

100.0%; Score 2185; DB 11; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCTTCCGAGGCCAAATCCAGGCGATGGTGAATTAAGAGCTGCCACCATGA 60  
Db |||||  
Qy 1 GTTCTCTTCCGAGGCCAAATCCAGGCGATGGTGAATTAAGAGCTGCCACCATGA 60  
Db |||||  
Qy 61 AGCTCTTGTGGCAGGTAACTGTGCAACACCACTGGAATCCATCTCTGCTCCCGTTGG 120  
Db |||||  
Qy 61 AGCTCTTGTGGCAGGTAACTGTGCAACACCACTGGAATCCATCTCTGCTCCCGTTGG 120  
Db |||||  
Qy 121 TCTACCTCAGCGCGCAAGTGTGAATCTGTGTGACGCCATGCTGTGCTCGCGCTCAGCGG 180  
Db |||||  
Qy 121 TCTACCTCAGCGCGCAAGTGTGAATCTGTGTGACGCCATGCTGTGCTCGCGCTCAGCGG 180  
Db |||||  
Qy 181 GCGCCAGAACTGCGCTCCGTTTGTGTGCAAGTAACCACTTCAAGAGGTGGTGTGCA 240  
Db |||||  
Qy 181 GCGCCAGAACTGCGCTCCGTTTGTGTGCAAGTAACCACTTCAAGAGGTGGTGTGCA 240  
Db |||||  
Qy 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACAACCCGGTACCTCAACC 300  
Db |||||  
Qy 241 CGCGCGGGGCTCTCCGAGGTCCCGAGGGTATTCCTCGAACAACCCGGTACCTCAACC 300  
Db |||||  
Qy 301 TCATGGAGAACACATCCAGATGATCCAGGCGACACCTTCCGCCACCTCCACCTGG 360  
Db |||||  
Qy 301 TCATGGAGAACACATCCAGATGATCCAGGCGACACCTTCCGCCACCTCCACCTGG 360  
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Qy 361 AGTCTCTGCAAGTTGGCAGGAACTCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420  
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Qy 361 AGTCTCTGCAAGTTGGCAGGAACTCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420  
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Qy 421 TGGCGAGCTCAACACGCTGGAGCTGTTGCAACACTGGGCTGACAGTCATCCCTAGCGGG 480  
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Qy 421 TGGCGAGCTCAACACGCTGGAGCTGTTGCAACACTGGGCTGACAGTCATCCCTAGCGGG 480  
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Qy 481 CCTTTGAATACCTGTCCAAAGCTCGGAGCTCTGGCTTCGCAACAAACCCCATCGAAAGCA 540  
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Qy 481 CCTTTGAATACCTGTCCAAAGCTCGGAGCTCTGGCTTCGCAACAAACCCCATCGAAAGCA 540  
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Qy 541 TCGCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGAGCTTGGGGGAGCTCA 600  
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Qy 601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660  
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Qy 661 ACTTGGGCAATGTGCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGGCTGGAGG 720  
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Qy 721 AGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGCTTGA 780  
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Qy 841 TTGACCGGCTGGCTTCACTTGTGGAACCTCACTGGCGCACTGAACTCTCTCTTCTTTCG 900  
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Qy 841 TTGACCGGCTGGCTTCACTTGTGGAACCTCACTGGCGCACTGAACTCTCTCTTCTTTCG 900  
Db |||||  
Qy 901 CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGATCTACACCAACACCTT 960  
Db |||||  
Qy 901 CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGATCTACACCAACACCTT 960  
Db |||||  
Qy 961 GGAAGCTGATTTGACATTTCTGGGTAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020  
Db |||||  
Qy 961 GGAAGCTGATTTGACATTTCTGGGTAGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020  
Db |||||  
Qy 1021 ATTCCACCTGCTGTGGCGCTGCTCATGCTCCCATGCAATGCGAGGCGCTACCTCGTGG 1080  
Db |||||



1021 ATTCCACCTGCTGTGGCGCTCATGCTCCATGTCACATGCGAGGCGGCTACCTCGTGG 1080  
 1081 AGGTGGACGAGCTCTCTTCAGTGTCTGCGCCCTTCATCATGCGAGGCGGCTACCTCGAGCC 1140  
 1081 AGGTGGACGAGCTCTCTTCAGTGTCTGCGCCCTTCATCATGCGAGGCGGCTACCTCGAGCC 1140  
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QY 2161 AATTAAAGACAAAGCTCAAAACA 2185  
 DB 2161 AATTAAAGACAAAGCTCAAAACA 2185  
 RESULT 24  
 US-09-997-428-228  
 ; Sequence 228, Application US/09997428  
 ; Publication No. US20030027162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: Matanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P273051C44  
 ; CURRENT APPLICATION NUMBER: US/09/997,428  
 ; CURRENT FILING DATE: 2001-11-15  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR FILING DATE: 1998-06-22

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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCTTTCCGAGCCAAATCCAGCGATGTGAATTATGAACGTGCCACACCATGA 60  
Db 1 GTTCTCTTTCCGAGCCAAATCCAGCGATGTGAATTATGAACGTGCCACACCATGA 60  
Qy 61 AGCTCTTGTGCAGTAACTGTGCACACCACTGGAATGCATCTGTCCCTG 120

Db 61 AGCTCTGTGTGAGAGTAAGTGTGACCAACCACTGGAAATGCGATCTCTGCTCCCGTTGG 120  
Qy 121 TCTACTCTCACGCGCAAGTGTGGATTCTGTGTGAGCCATCGTGTGCGCGCTCAGCGG 180  
Db 121 TCTACTCTCACGCGCAAGTGTGGATTCTGTGTGAGCCATCGTGTGCGCGCTCAGCGG 180  
Qy 181 GCGCCGAGAACTGCGCCCTCCGTTGTGTGTGAGTACCAAGTGTGGTGTGCA 240  
Db 181 GCGCCGAGAACTGCGCCCTCCGTTGTGTGTGAGTACCAAGTGTGGTGTGCA 240  
Qy 241 GCGCGCGGGGCTCTCCAGAGTCCGCGAGGCTATTCCCTCGAAACACCGCGTACTCAACC 300  
Db 241 GCGCGCGGGGCTCTCCAGAGTCCGCGAGGCTATTCCCTCGAAACACCGCGTACTCAACC 300  
Qy 301 TCATGGAGAACAACTCAGATGATCCAGGCGGAGACCTTCGCGCACTCTCAACCTG 360  
Db 301 TCATGGAGAACAACTCAGATGATCCAGGCGGAGACCTTCGCGCACTCTCAACCTG 360  
Qy 361 AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATGTAGGTGGGGGCTTCAACGGCC 420  
Db 361 AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATGTAGGTGGGGGCTTCAACGGCC 420  
Qy 421 TGGCCAGGCTCAACACCTGAGGTGTTCGAACTGGCTGACAGTCAATCCCTAGCGGGG 480  
Db 421 TGGCCAGGCTCAACACCTGAGGTGTTCGAACTGGCTGACAGTCAATCCCTAGCGGGG 480  
Qy 481 CCTTTGAATACCTGTCCAGCTGCGGAGCTCTGGCTTCGCAACATGGCTGACAGTCAAT 540  
Db 481 CCTTTGAATACCTGTCCAGCTGCGGAGCTCTGGCTTCGCAACATGGCTGACAGTCAAT 540  
Qy 541 TCCCTCTTACGCTTCAACCGGTTGCGCTCCCTCATGCGGCTGGAATGGGGAGCTCA 600  
Db 541 TCCCTCTTACGCTTCAACCGGTTGCGCTCCCTCATGCGGCTGGAATGGGGAGCTCA 600  
Qy 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTGGGGCTCTTCAACCTCAAGTATCTGA 660  
Db 601 AGAAGCTGGAGTATATCTCTGAGGAGCTTTTGGGGCTCTTCAACCTCAAGTATCTGA 660  
Qy 661 ACTTGGGATGTGCAACATTTAAAGACATGCCAATCTCACCCCCCTGGTGGGGCTGAGG 720  
Db 661 ACTTGGGATGTGCAACATTTAAAGACATGCCAATCTCACCCCCCTGGTGGGGCTGAGG 720  
Qy 721 AGCTGGAGTGTGAGGAACTCTTCTGTGAGTCAAGCTGCTCTTCCATGGGCTGA 780  
Db 721 AGCTGGAGTGTGAGGAACTCTTCTGTGAGTCAAGCTGCTCTTCCATGGGCTGA 780  
Qy 781 GTTCCCTCAAGAGCTCTGGGTCATGAATCAAGCTCAGCTGAGTCAAGCTGAGTCAAT 840  
Db 781 GTTCCCTCAAGAGCTCTGGGTCATGAATCAAGCTCAGCTGAGTCAAGCTGAGTCAAT 840  
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Db 841 TTGAGGGGCTGCTTCACTGTGGAATCAACTTGGGCCCAATTAACCTCTCTTCTTTC 900  
Qy 901 CCGATGACCTCTTACCGCGTGAAGTACCTGGTGGAGTGTGATCTACACCAACACCTT 960  
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Qy 1021 ATTCCACCTGTGTGGCGCTGATGTCCTCCATGACATGGAGGCGCTACCTCGTGG 1080  
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Qy 1081 AGGTGACCCAGGCTCTTCCAGTGTCTGTGGCTTTCATCATGAGGAGCTCGAGACC 1140  
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RESULT 25  
US-09-997-666-228  
; Sequence 228, Application US/09997666

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Qy 1861 ATGACATATTAACTTACAAACCTTCAAAACAGCAGCACTGGGGCCCACTGGNACAGAAACA 1920  
Db 1861 ATGACATATTAACTTACAAACCTTCAAAACAGCAGCACTGGGGCCCACTGGNACAGAAACA 1920  
Qy 1921 GCTTGGGAACTCTCTGCAACCCCAAGTCAACCTATCTCTGAACTTATATAATTGAGA 1980  
Db 1921 GCTTGGGAACTCTCTCTGCAACCCCAAGTCAACCTATCTCTGAACTTATATAATTGAGA 1980  
Qy 1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCGGAAAACTTA 2040  
Db 1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCGGAAAACTTA 2040  
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Db 2101 TTCTTGTATATGCTTATATATTAAGTCTATGGGTGTTAAAAAAGACAGATTATATTA 2160  
Qy 2161 AATTTAAAGACAAAGTCAAAACA 2185  
Db 2161 AATTTAAAGACAAAGTCAAAACA 2185

Publication No. US20030027163A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC42  
CURRENT APPLICATION NUMBER: US/09/997,666  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
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3 PRIOR APPLICATION NUMBER: 60/088167  
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5 PRIOR APPLICATION NUMBER: 60/088202  
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53 PRIOR FILING DATE: 1998-07-09

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## RESULT 26

S-09-990-438-228  
Sequence 228, Application US/09990438  
Publication No. US2003002754A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCES: P2730P1C3  
CURRENT APPLICATION NUMBER: US/09/990,438  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-06-16  
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41 PRIOR APPLICATION NUMBER: 60/091982  
42 PRIOR FILING DATE: 1998-07-07  
43 PRIOR APPLICATION NUMBER: 60/092182  
44 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 GSCCCAGAACTGCCCTTCGCTTTGCTGTCGAGTAACAGTTTACGCAAGGTGTGTGCA 240  
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841 TTGAGGGCTGGCTTCACTTGTGGAACTCACTTGGCCCAATTAACCTCTTCTTTTC 900  
901 CCCATGACCTCTTTACCCCGCTGAGTACCTGGTGGAGTTGATCTACACCAACCCCTT 960  
901 CCCATGACCTCTTTACCCCGCTGAGTACCTGGTGGAGTTGATCTACACCAACCCCTT 960  
961 GGAAGTGAATGTGACATCTCTGGCTAGCTTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020  
961 GGAAGTGAATGTGACATCTCTGGCTAGCTTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020  
1021 ATTCCACCTGTGTGGCCCTGTCTAGCTCCCATGCAATGCGAGCGCTTACCTCGTGG 1080  
1021 ATTCCACCTGTGTGGCCCTGTCTAGCTCCCATGCAATGCGAGCTTACCTCGTGG 1080  
1081 AGGTGGAACGAGGCTCTTCCAGTGTCTGGCCCTTCAATGAGACCACTCGAGACC 1140  
1081 AGGTGGAACGAGGCTCTTCCAGTGTCTGGCCCTTCAATGAGACCACTCGAGACC 1140  
1141 TCACCAATTTCTGAGGCTCGATGGGAGAACTTAAGTTCGAGCTCCCTCTATGCTCCG 1200  
1141 TCACCAATTTCTGAGGCTCGATGGGAGAACTTAAGTTCGAGCTCCCTCTATGCTCCG 1200  
1201 TGAAGTGGTGTGTCGCCAATGGGACAGTGTCTCAGCGAGCTCCCGCCACCAAGGATCT 1260  
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1381 GACGAGCTGATTAACCTTCACTGAGTCTTTCACCACTGAGTACAGTGGAGCA 1440  
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1441 CGGAGATCTCGCTGAGGACACAAAGTCAAGCCTGTTCTTACCACGCTCACTG 1500  
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1501 GTTACAGCGGATATATACCACTCTTACCAAGTCTCACTCAGACTACCGCTGTGCCCA 1560  
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1561 AGCAGTGGAGTATCCCGGACAGACCACTCTGA CAAGTGAAGTGAAGTGAAG 1620  
1621 TCAATGAAGACCAAGATCATCTTGGCTGCTTGTGGAGTGAAGTGAAGTGAAG 1680  
1621 TCAATGAAGACCAAGATCATCTTGGCTGCTTGTGGAGTGAAGTGAAGTGAAG 1680  
1681 CCAATGATGATCTTCTTATAAACTTCCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740  
1681 CCAATGATGATCTTCTTATAAACTTCCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740  
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1741 CGCCCGGATCTTGGAGTAAATCCAGGTTGAGGAGTGAAGTGAAGTGAAGTGAAG 1800  
1801 CAGCAACAGCAGCTCGTCCGCTGATCAGGTGAGGAGTGAAGTGAAGTGAAGTGAAG 1860  
1801 CAGCAACAGCAGCTCGTCCGCTGATCAGGTGAGGAGTGAAGTGAAGTGAAGTGAAG 1860  
1861 ATGACCATTTAATTAACACCTTACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1920  
1861 ATGACCATTTAATTAACACCTTACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1920  
1921 GCTGGGAGTCTCTGACACCCACAGTCAACATCTCTGAACTTATATATATATATATAT 1980  
1921 GCTGGGAGTCTCTGACACCCACAGTCAACATCTCTGAACTTATATATATATATATAT 1980  
1981 CCATATACCAAGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2040  
1981 CCATATACCAAGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2040  
2041 TAAATGCAATGAATGACACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2100  
2041 TAAATGCAATGAATGACACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2100  
2101 TTCTGTATATCTTAT 2160  
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## RESULT 27

US-09-990-562-228

; Sequence 228, Application US/09990562

; Publication No. US20030027985A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Forgy, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C18  
CURRENT APPLICATION NUMBER: US/09/990,562  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
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PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/089598  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
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PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557

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PRIOR FILING DATE: 1998-06-25	Db	601	AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGA	660
PRIOR APPLICATION NUMBER: 60/090695	Qy	661	ACTTGGGATGTCGACATTAAGACATGCCCAATCTCACCCCTCGTGGTGGGCTGGAGG	720
PRIOR FILING DATE: 1998-06-25	Db	661	ACTTGGGATGTCGACATTAAGACATGCCCAATCTCACCCCTCGTGGTGGGCTGGAGG	720
PRIOR APPLICATION NUMBER: 60/090862	Qy	721	AGCTGGAGATGTGAGGAAACACTTCCCTGAGATCAGGCTGGCTCTTCCATGGCTGA	780
PRIOR FILING DATE: 1998-06-26	Db	721	AGCTGGAGATGTGAGGAAACACTTCCCTGAGATCAGGCTGGCTCTTCCATGGCTGA	780
PRIOR APPLICATION NUMBER: 60/091478	Qy	781	GCTCCCTCAAGAGCTCTGGGTGATGAATCAGGTCAGGCTGAGCTGATGAGCGGATGCTT	840
PRIOR FILING DATE: 1998-07-02	Db	781	GCTCCCTCAAGAGCTCTGGGTGATGAATCAGGTCAGGCTGAGCTGATGAGCGGATGCTT	840
PRIOR APPLICATION NUMBER: 60/091544	Qy	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTTCTTTC	900
PRIOR FILING DATE: 1998-07-01	Db	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTTCTTTC	900
PRIOR APPLICATION NUMBER: 60/091519	Qy	901	CCCATGACCTCTTTTACCCCGCTGAGGTACCTGCTGGAGTTCATACACCAACCTT	960
PRIOR FILING DATE: 1998-07-02	Db	901	CCCATGACCTCTTTTACCCCGCTGAGGTACCTGCTGGAGTTCATACACCAACCTT	960
PRIOR APPLICATION NUMBER: 60/091626	Qy	961	GGAACTGTGATGTGACATTTCTGTGCTAGCTGCTGGTTCGAGAGTATATACCCACCA	1020
PRIOR FILING DATE: 1998-07-02	Db	961	GGAACTGTGATGTGACATTTCTGTGCTAGCTGCTGGTTCGAGAGTATATACCCACCA	1020
PRIOR APPLICATION NUMBER: 60/091633	Qy	1021	ATTCCACTCTGTGGCGCTGTCTGCTCCCATGATGAGGAGCGCTACCTCGTG	1080
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PRIOR APPLICATION NUMBER: 60/091633	Qy	1081	AGGTGGACCGAGGCTCTTCCAGTGTCTGCTCCCTTCTCATGAGGAGCGCTGAGAC	1140
PRIOR FILING DATE: 1998-07-02	Db	1081	AGGTGGACCGAGGCTCTTCCAGTGTCTGCTCCCTTCTCATGAGGAGCGCTGAGAC	1140
PRIOR APPLICATION NUMBER: 60/091978	Qy	1141	TCACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGCGACTCCCTCTATGCTCG	1200
PRIOR FILING DATE: 1998-07-07	Db	1141	TCACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGCGACTCCCTCTATGCTCG	1200
PRIOR APPLICATION NUMBER: 60/091982	Qy	1201	TGAAGTGTGCTGCTCCCAATGGGACAGTGTGAGCGCTCCCGCTCCCGCTGAGATCT	1260
PRIOR FILING DATE: 1998-07-07	Db	1201	TGAAGTGTGCTGCTCCCAATGGGACAGTGTGAGCGCTCCCGCTCCCGCTGAGATCT	1260
PRIOR APPLICATION NUMBER: 60/091982	Qy	1261	CTGTCTCAACGACGCGCTTGAACCTTTTCCCACTGTGCTTTCAGACACTTGGGGTGT	1320
PRIOR FILING DATE: 1998-07-07	Db	1261	CTGTCTCAACGACGCGCTTGAACCTTTTCCCACTGTGCTTTCAGACACTTGGGGTGT	1320
PRIOR APPLICATION NUMBER: 60/092182	Qy	1321	ACACATGCTGGTGAACCAATGTTGCGGAACTTCCAAAGCTCTGGCTTACCTCAATGTGA	1380
PRIOR FILING DATE: 1998-07-09	Db	1321	ACACATGCTGGTGAACCAATGTTGCGGAACTTCCAAAGCTCTGGCTTACCTCAATGTGA	1380
PRIOR APPLICATION NUMBER: 60/092182	Qy	1381	GCAGGCTGAGCTTACACCTTCCAACTGAGAGTTCACCAAGTAAAGTGAAGTGA	1440
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PRIOR APPLICATION NUMBER: 60/092182	Qy	1441	CGGAGATCTCGCTGAGGACCAACCGGAAAGTGAAGGCTGTTCACCACTGCTG	1500
PRIOR FILING DATE: 1998-07-09	Db	1441	CGGAGATCTCGCTGAGGACCAACCGGAAAGTGAAGGCTGTTCACCACTGCTG	1500
PRIOR APPLICATION NUMBER: 60/092182	Qy	1501	GTTACAGGCGGATATACCACTTACCACTGCTGCTTACCACTGCTGCTGCTGCTGCTG	1560
PRIOR FILING DATE: 1998-07-09	Db	1501	GTTACAGGCGGATATACCACTTACCACTGCTGCTTACCACTGCTGCTGCTGCTGCTG	1560
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Query Match	100.0%;	Score 2185;	DB 11;	Length 2185;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2185;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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1	GTTCCTCTTCCGAGCCAAATCCAGGCGATGTAATATGAACTGCGACACCATGA	60		
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121	TCTACCTACCGGCGCAAGTGTGATTTCTGTGTCAGGCAATGCTGCTGCTGCTG	180		
121	TCTACCTACCGGCGCAAGTGTGATTTCTGTGTCAGGCAATGCTGCTGCTGCTG	180		
181	GGCCCGAGAACTGCTCCCTGCTTGTGCTGTCAGTAACTGTCAGGAGTGTGCA	240		
181	GGCCCGAGAACTGCTCCCTGCTTGTGCTGTCAGTAACTGTCAGGAGTGTGCA	240		
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241	CGCGCCGGGCGCTCTCCGAGGCTCCGAGGCTATTCCTCGAACACCGGCTCAACC	300		
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361	AGTCTCTGAGTGGGAGGAGTCCATCCGAGAGTGAAGTGGGGGCTTCAACGGGC	420		
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421	TGGCCAGCTCAACACCTGAGAGTGTGCAACCTGGGTGAGTATCTTACCGGG	480		
481	CCTTTGATACCTGTCCAAAGTGGGGAGCTTGGCTTCCGCAACACCCCATCGAAGCA	540		

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 1681 CCATGTTGATGTTCTTCTATTAATCTTCTAAGCGGACAGCGGAGTACAGTCCAG 1740  
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 1861 ATGACCATATTAATCTAACAACACCTTACAAACAGCAGATGGGCGGCACTGACAGAAACA 1920  
 1921 GCCTGGGGAATCTCTGACACCCCACTGACCTATCTCTGAACTTATATTAATTCAGA 1980  
 1921 GCCTGGGGAATCTCTGACACCCCACTGACCTATCTCTGAACTTATATTAATTCAGA 1980  
 1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAACTTA 2040  
 1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAACTTA 2040  
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 2041 TAAATGCAATAGATGACACCAAGACAGCAACTTTTGTACAGTGGGGAGAGACTTT 2100  
 2101 TCTTGTATATGCTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2160  
 2101 TCTTGTATATGCTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2160  
 2161 AATTTAAAGACAAAAGTCAAAACA 2185  
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RESULT 28  
 JS-09-990-711-228  
 ; Sequence 228, Application US/09990711  
 ; Publication No. US2003032023A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Klijavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C2  
 ; CURRENT APPLICATION NUMBER: US/09/990,711  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCTTTTCGAGCCAAATCCAGGCGATGGTGAATTATGAAGCTGCCACACCATGA 60  
Db 1 GTTCTCTTTTCGAGCCAAATCCAGGCGATGGTGAATTATGAAGCTGCCACACCATGA 60

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Db 61 AGCTCTGTGGCAGGTAACTGTGCAACACACACCTGGATGCCATCTCTGCTCCCGTTG 120

Qy 121 TCTACCTCAGCGCGCAAGTGTGGATTCTGTGTGAGCCATGCTGTCCGCTCAGCG 180  
Db 121 TCTACCTCAGCGCGCAAGTGTGGATTCTGTGTGAGCCATGCTGTCCGCTCAGCG 180

Qy 181 GGCCCGAGAACTGCCCTCGTTTGTCTGTGAGTAACAGTTTCAGAGGTGGTGTGCA 240  
Db 181 GGCCCGAGAACTGCCCTCGTTTGTCTGTGAGTAACAGTTTCAGAGGTGGTGTGCA 240

Qy 241 CGCGCGGGGCTCTCGAGGTCCCGAGGTCCCGAGGTATTCCTCGAACACCCGCTACCTCAAC 300  
Db 241 CGCGCGGGGCTCTCGAGGTCCCGAGGTCCCGAGGTATTCCTCGAACACCCGCTACCTCAAC 300

Qy 301 TCATGGAGAACAAATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTGG 360  
Db 301 TCATGGAGAACAAATCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTGG 360

Qy 361 AGTCTCTGCAAGTTGGGAGAACTCCATCCGAGATTCAGGTGGGGGCTTCAACGGCC 420  
Db 361 AGTCTCTGCAAGTTGGGAGAACTCCATCCGAGATTCAGGTGGGGGCTTCAACGGCC 420

Qy 421 TGCCCAAGCTCAAACCTCTGGAGCTTTTGAACAACTGGGTGACAGTTCATCTCAGCGGG 480  
Db 421 TGCCCAAGCTCAAACCTCTGGAGCTTTTGAACAACTGGGTGACAGTTCATCTCAGCGGG 480

Qy 481 CTTTGTGATACCTGTCGAAGCTGGGGGCTCTGGTTCGCAACACCCCTCAGAAAGCA 540  
Db 481 CTTTGTGATACCTGTCGAAGCTGGGGGCTCTGGTTCGCAACACCCCTCAGAAAGCA 540

Qy 541 TCCCTCTTTAGCGCTTCAACCGGGTSCCTCCCTCATGCGCTGAGCTTTGGGGAGCTCA 600  
Db 541 TCCCTCTTTAGCGCTTCAACCGGGTSCCTCCCTCATGCGCTGAGCTTTGGGGAGCTCA 600

Qy 601 AGAGCTGGAGTATATCTCTGAGGGGCTTTTGGGGGCTTTCAGCTCAAGTATCTCA 660  
Db 601 AGAGCTGGAGTATATCTCTGAGGGGCTTTTGGGGGCTTTCAGCTCAAGTATCTCA 660

601 AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGA 560  
661 ACTTGGGCACTGCAACATTAAGACATGCCAAATCTCACCCCTCTGGTGGGCTGGAGG 720  
661 ACTTGGGCACTGCAACATTAAGACATGCCAAATCTCACCCCTCTGGTGGGCTGGAGG 720  
721 AGCTGGAGAGTCAAGGAAACATCTCCCTGAGATCAGGCTGCTCTCCATGGGCTGA 780  
721 AGCTGGAGAGTCAAGGAAACATCTCCCTGAGATCAGGCTGCTCTCCATGGGCTGA 780  
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1561 AGCAGGTGGGATGACCGGACACACCACTGACAGATGACAGACCTGGATGAAG 1620  
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1681 CCATCTTGAATGCTCTTATTAACCTTCTGAGGCGGACACAGGAGTACAGTCAAG 1740  
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Db 1741 CCGCCCGGAGCTGTTGAGATTAATCCAGGTGGAAGAGATCCAGGAGCAACATCCGGAG 1800  
QY 1801 CAGCAACAGGAGCTCCCTCCGGTGTATCAGGTGAGGGGCGAGTGTCTGCCCAATTC 1860  
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QY 1861 ATGACCAATATTAACCTCAACACCTTAACACCTTAACACCTTAACACCTTAACACCTTA 1920  
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QY 1921 GCTTGGGGAATCTCTGCAACCCACACCTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCT 1980  
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QY 1981 CCCATACCAAGGACAGGTACAGGAACTCAAAATATGATCTCCCTCCCGCCCAAAACTTA 2040  
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QY 2161 AATTTAAGACAAAGTCAAAACA 2185  
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RESULT 29

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; Sequence 228, Application US/09989726  
; Publication No. US2003004073A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deaneys, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gezber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Nepier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Weimin  
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; TITLE OF INVENTION: Acids Encoding the Same  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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1	GTCTCTCTTTCCGAGCCAAATCCAGGCGATGGTGAATATGAACTGCGCACCATCA	60
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61	AGCTCTTTGGCAGGTAAGTGTGCACACACACACCTGGAATGCCATCTGCTCCGCTTCG	120
121	TCTACCTTCAGCGCGAGTGGATCTGTGTCAGCCATCGTGTGCGGCTCAGCGC	180
121	TCTACCTTCAGCGCGAGTGGATCTGTGTCAGCCATCGTGTGCGGCTCAGCGC	180
181	GGCCCCAGAACTGCCCTCCGTTTGGCTGTCGAGTAACCAAGTTGACCAAGTGGTGTGA	240
181	GGCCCCAGAACTGCCCTCCGTTTGGCTGTCGAGTAACCAAGTTGACCAAGTGGTGTGA	240
241	CGCGCGGGGGCTCTCGAGTCCGCGAGGGTATTCCTCGAACACCGGTACTCAAC	300
241	CGCGCGGGGGCTCTCGAGTCCGCGAGGGTATTCCTCGAACACCGGTACTCAAC	300
301	TCATGGAGAACACATCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTG	360
301	TCATGGAGAACACATCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTG	360
361	AGGTCCTGAGTTGGCGAGGAATCCATTCGCGGAGATGAGGTGGGGGCTTCAAGGCC	420
361	AGGTCCTGAGTTGGCGAGGAATCCATTCGCGGAGATGAGGTGGGGGCTTCAAGGCC	420
421	TGGCCAGCTCAACACCTGAGGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
421	TGGCCAGCTCAACACCTGAGGCTGTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
481	CTTTTGAATACCTGTCAGGAGTGGGAGCTCTGGCTGCGAACACCCCATCGAAGCA	540
481	CTTTTGAATACCTGTCAGGAGTGGGAGCTCTGGCTGCGAACACCCCATCGAAGCA	540
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661	ACTTGGGCTGTGAACATTAAGCATGCCCATCTCACCCCTCGTGGGGTGGAGG	720
661	ACTTGGGCTGTGAACATTAAGCATGCCCATCTCACCCCTCGTGGGGTGGAGG	720
721	AGCTGGAGTGTGAGGAGCACTTCCCTGAGATCAGGCTGGCTCTTCCATGGGCTGA	780
721	AGCTGGAGTGTGAGGAGCACTTCCCTGAGATCAGGCTGGCTCTTCCATGGGCTGA	780

QY	781	GCTCCCTCAAGAGCTCTGGGTCAATGAACTCAGAGTCAAGCTGATTCAGCGGAATGCTT	840
DB	781	GCTCCCTCAAGAGCTCTGGGTCAATGAACTCAGAGTCAAGCTGATTCAGCGGAATGCTT	840
QY	841	TTGACGGGCTGGCTTCACTTTGGGAACTCAACTTGGCCCAACAATACCTCTCTTTTC	900
DB	841	TTGACGGGCTGGCTTCACTTTGGGAACTCAACTTGGCCCAACAATACCTCTCTTTTC	900
QY	901	CCATGACCTCTTTTACCCGCTGAGGTACTGGTGGAGTTGCATCTACACCAACACCTT	960
DB	901	CCATGACCTCTTTTACCCGCTGAGGTACTGGTGGAGTTGCATCTACACCAACACCTT	960
QY	961	GGAACTGTGATTTGACATTTCTGTGCTAGCTGGTGGCTTTCGAGAGTATATACCCACA	1020
DB	961	GGAACTGTGATTTGACATTTCTGTGCTAGCTGGTGGCTTTCGAGAGTATATACCCACA	1020
QY	1021	ATTCCACTCTGTGGCGCTGTCATGCTCCCATGACATGCGAGGCCCTACCTCGTGG	1080
DB	1021	ATTCCACTCTGTGGCGCTGTCATGCTCCCATGACATGCGAGGCCCTACCTCGTGG	1080
QY	1081	AGGTGGACCAAGGCTCTCTCCAGTGTCTGCCCCCTTCATGATGAGCGACCTCGAGAC	1140
DB	1081	AGGTGGACCAAGGCTCTCTCCAGTGTCTGCCCCCTTCATGATGAGCGACCTCGAGAC	1140
QY	1141	TCACATTTCTGAGGGTCCGATGCGAGACTTAAGTGTGGACTCCCCCTATGCTCTCG	1200
DB	1141	TCACATTTCTGAGGGTCCGATGCGAGACTTAAGTGTGGACTCCCCCTATGCTCTCG	1200
QY	1201	TGAAGTGGTGTCTGCCCAATGGGACAGTGTCTGAGCCACGCTCCCGCCACCCAGATCT	1260
DB	1201	TGAAGTGGTGTCTGCCCAATGGGACAGTGTCTGAGCCACGCTCCCGCCACCCAGATCT	1260
QY	1261	CTGTCTCAAGAGCGGACCTTGAATTTTCCACGCTGCTTTCAGACACTGGGGTGT	1320
DB	1261	CTGTCTCAAGAGCGGACCTTGAATTTTCCACGCTGCTTTCAGACACTGGGGTGT	1320
QY	1321	ACACATGATGTCAGCAATGTTGAGGCAACTCCAGCGCTCCGGCTTACCTCAATGTGA	1380
DB	1321	ACACATGATGTCAGCAATGTTGAGGCAACTCCAGCGCTCCGGCTTACCTCAATGTGA	1380
QY	1381	GCAGGCTGAGCTTAAACCTCCAGCTTACAGCTTCTTCCACAGTAACAGTGGAGACCA	1440
DB	1381	GCAGGCTGAGCTTAAACCTCCAGCTTACAGCTTCTTCCACAGTAACAGTGGAGACCA	1440
QY	1441	CGGAGATCTCCCTGAGGACACAAACGGAAGTACAGGCTGTTCTTACACCTCCACTG	1500
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DB	1561	AGCAGTGGAGTACCCCGACAGACACCACTGACAGATGACAGACAGCTGGATGAAG	1620
QY	1621	TCATGAGACCAACCAAGTATCATTTGGCTTGTGGTGGAGTGAAGTCTGTAGTCTCG	1680
DB	1621	TCATGAGACCAACCAAGTATCATTTGGCTTGTGGTGGAGTGAAGTCTGTAGTCTCG	1680
QY	1681	CCATGTTGATTTGCTTCTATAAACTTCTGTAAGCGCACAGCAGCGAGTACAGTACAG	1740
DB	1681	CCATGTTGATTTGCTTCTATAAACTTCTGTAAGCGCACAGCAGCGAGTACAGTACAG	1740
QY	1741	CCGCCCCGAGCTGTTGAGATAATCCAGGTGGACGAAGACATCCACAGCAACATCCGAG	1800
DB	1741	CCGCCCCGAGCTGTTGAGATAATCCAGGTGGACGAAGACATCCACAGCAACATCCGAG	1800
QY	1801	CAGCAACAGAGCTCTCGTCCGCTGATCAGTGGGGGGGAGTAGTCTGCCCAATTC	1860
DB	1801	CAGCAACAGAGCTCTCGTCCGCTGATCAGTGGGGGGGAGTAGTCTGCCCAATTC	1860



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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2185; DB 11; Length 2185;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCTCCCTTCCGAGCCAAATCCCGAGCGGATGATGATATGACGTGCGACACCTGA 60
DB      1  GTCTCCCTTCCGAGCCAAATCCCGAGCGGATGATGATATGACGTGCGACACCTGA 60

QY      61  AGCTCTTGTGGCAGGTAACTGTGCACCAACCACTTGAATGCCATCTGTCCCGTTGG 120
DB      61  AGCTCTTGTGGCAGGTAACTGTGCACCAACCACTTGAATGCCATCTGTCCCGTTGG 120

QY      121  TCTACTCTACGCGCGCAAGTGTGGATTCTGTGTGAGCCATGCTGTGCGGCTCAGCG 180
DB      121  TCTACTCTACGCGCGCAAGTGTGGATTCTGTGTGAGCCATGCTGTGCGGCTCAGCG 180

QY      181  GGCCCCAGAACTGCCCTCCGTTTCTGTGTGAGTAACCACTTCAAGAGTGTGTGCA 240
DB      181  GGCCCCAGAACTGCCCTCCGTTTCTGTGTGAGTAACCACTTCAAGAGTGTGTGCA 240

QY      241  CGCGCGGGGCTCTCTCGAGGTTCGCGAGGGTATTCCTCTGAAACACCGGTACCTCAACC 300
DB      241  CGCGCGGGGCTCTCTCGAGGTTCGCGAGGGTATTCCTCTGAAACACCGGTACCTCAACC 300

QY      301  TCATGGAGAACAAATCCAGATGATCCAGGCGGACACCTTCCGCGACCTCCACCACTGG 360
DB      301  TCATGGAGAACAAATCCAGATGATCCAGGCGGACACCTTCCGCGACCTCCACCACTGG 360

QY      361  AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420
DB      361  AGGTCTCTGAGTTGGGAGGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAACGGCC 420

QY      421  TGGCCAGCTCAACACCTGAGCTGTTCGACAACTGGCTGACAGTATCCCTAGCGGGG 480
DB      421  TGGCCAGCTCAACACCTGAGCTGTTCGACAACTGGCTGACAGTATCCCTAGCGGGG 480

QY      481  CTTTGAATACCTGTCCAAGCTGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540
DB      481  CTTTGAATACCTGTCCAAGCTGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540

QY      541  TCCCTCTTAGCCTTCAACCGGTGCGCTGCTCATGCGCTGAGCTTGGGGGAGCTCA 600
DB      541  TCCCTCTTAGCCTTCAACCGGTGCGCTTCCCTCATGCGCTGAGCTTGGGGGAGCTCA 600

QY      601  AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660
DB      601  AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGA 660

QY      661  ACTTGGGATGTGCAACATTAAGAGATGCCATCTCAACCCCTGGTGGGCTGAGG 720
DB      661  ACTTGGGATGTGCAACATTAAGAGATGCCATCTCAACCCCTGGTGGGCTGAGG 720

QY      721  AGCTGGAGATGTCAAGGAACCACTTCCCTGAGATCAGGCTTGGCTTCCCTCATGCGCTGA 780
DB      721  AGCTGGAGATGTCAAGGAACCACTTCCCTGAGATCAGGCTTGGCTTCCCTCATGCGCTGA 780

QY      781  GCTCCCTCAAGAACTCTGGGTCAATGAACATCAGGTGACGCTGATTTGAGGGATGCTT 840
DB      781  GCTCCCTCAAGAACTCTGGGTCAATGAACATCAGGTGACGCTGATTTGAGGGATGCTT 840

QY      841  TTGAGGGCTGCTTCACTTGTGGAATCAACTTGGGCGCCACAATACCTCTCTTCTTTC 900
DB      841  TTGAGGGCTGCTTCACTTGTGGAATCAACTTGGGCGCCACAATACCTCTCTTCTTTC 900

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901 CCCATGACCTCTTTACCCCGCTGAGGTACTCTGGTGGAGTTGCATCTACACCAACACCTTT 960  
b CCCATGACCTCTTTACCCCGCTGAGGTACTCTGGTGGAGTTGCATCTACACCAACACCTTT 960  
961 GGAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1020  
b GGAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1020  
1021 ATTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
b ATTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
1081 AGGTGACCAAGGCTCTCTTCCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
b AGGTGACCAAGGCTCTCTTCCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
1141 TCAACATTTCTGAGGCTCGGATGCGACAGAACTTAAGTGTGGAGTCTCCCTCTATGCTCTCG 1200  
b TCAACATTTCTGAGGCTCGGATGCGACAGAACTTAAGTGTGGAGTCTCCCTCTATGCTCTCG 1200  
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b CTGCTCTCAACGACGCTCACTTCACTTTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
1321 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
b ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
1381 GCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
b GCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
1441 CGGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
b CGGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
1501 GTTACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
b GTTACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
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1861 ATGACCATATTAATCAACACCTTACAACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
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1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 2040

Db 1981 CCCATACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCTCCCTCCCTCCCT 2040  
Qy 2041 TAAATGCAATAGAAATGCAACAAACAGACAGCAACTTTTGTACAGAGTGGGAGACATTT 2100  
Db 2041 TAAATGCAATAGAAATGCAACAAACAGACAGCAACTTTTGTACAGAGTGGGAGACATTT 2100  
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Db 2101 TTCTTGTATATGCTTATATATTAAGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
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## RESULT 31

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; Sequence 228, Application US/09990437  
; Publication No. US20030045463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Pong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Nepler, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C49  
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; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787  
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68 PRIOR FILING DATE: 1998-07-07  
69 PRIOR APPLICATION NUMBER: 60/091982  
70 PRIOR FILING DATE: 1998-07-07  
71 PRIOR APPLICATION NUMBER: 60/092182  
72 PRIOR FILING DATE: 1998-07-09

Query Match		100.0%	Score 2185	DB 11	Length 2185		
Best Local Similarity		100.0%	Pred. No. 0				
Matches 2185		Conservative 0	Mismatches 0	Indels 0	Gaps 0		
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2b	1	GTCTCTCTTCCGAGCCAAATCCAGGCGATGGTGAATTATGAACTGTCACACCATCA	60				
2y	61	AGCTCTTGTGCGAGTAACTGTGCACCAACACACCTGGAAATGCATCTGCTCCCGTTGG	120				
2b	61	AGCTCTTGTGCGAGTAACTGTGCACCAACACACCTGGAAATGCATCTGCTCCCGTTGG	120				
2y	121	TCTACCTCAAGCGGCAAGTGTGGAATCTGTGTGACGCATCGCTGTGCGGCTCAGCG	180				
2b	121	TCTACCTCAAGCGGCAAGTGTGGAATCTGTGTGACGCATCGCTGTGCGGCTCAGCG	180				
2y	181	GGCCCCAGAACTGCCCTCCGTTGCTCGTGCAGTAAACAGTTCACAGAGTGTGTGCA	240				
2b	181	GGCCCCAGAACTGCCCTCCGTTGCTCGTGCAGTAAACAGTTCACAGAGTGTGTGCA	240				
2y	241	CGCGCCGGGCGCTCTCCGAGGTCCCGCAGGCTATTCCTCGAAACCCCGGTACCTCAAC	300				
2b	241	CGCGCCGGGCGCTCTCCGAGGTCCCGCAGGCTATTCCTCGAAACCCCGGTACCTCAAC	300				
2y	301	TCATGAGAAACATCCAGATGATTCAGGCGGACACCTTTCGCGACCTCCACACCTGG	360				
2b	301	TCATGAGAAACATCCAGATGATTCAGGCGGACACCTTTCGCGACCTCCACACCTGG	360				
2y	361	AGTTCCTGCAAGTGGGAGGAACTCCATCCGCGAGATTGAGGTGGGGGCTTCAACGGCC	420				
2b	361	AGTTCCTGCAAGTGGGAGGAACTCCATCCGCGAGATTGAGGTGGGGGCTTCAACGGCC	420				
2y	421	TGGCGAGCTCAACACCTCGAGCTGTGTGACAACTGGCTGACAGTCACTCCCTAGCGGG	480				
2b	421	TGGCGAGCTCAACACCTCGAGCTGTGTGACAACTGGCTGACAGTCACTCCCTAGCGGG	480				
2y	481	CTTTGAACTCTGCAAGCTCGGAGCTCTGGCTTCGCAACCTGGCTGACAGTCACTCCCT	540				
2b	481	CTTTGAACTCTGCAAGCTCGGAGCTCTGGCTTCGCAACCTGGCTGACAGTCACTCCCT	540				
2y	541	TCCCTCTTACGCTTCAACCGGCTCCCTCCCTCATGCGCTGAGCTTTGGGGAGCTCA	600				
2b	541	TCCCTCTTACGCTTCAACCGGCTCCCTCCCTCATGCGCTGAGCTTTGGGGAGCTCA	600				
2y	601	AGAGCTGGAGTATATCTGAGGAGGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660				
2b	601	AGAGCTGGAGTATATCTGAGGAGGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660				
2y	661	ACTTGGGCAATGTCACAACTTAAAGACATGCCAAATCTCACCCCTCTGGTGGGCTGGAG	720				
2b	661	ACTTGGGCAATGTCACAACTTAAAGACATGCCAAATCTCACCCCTCTGGTGGGCTGGAG	720				
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2b	721	AGCTGGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTCGCTTCCATGCGCTTGA	780				
2y	781	GCTCCCTCAAGAGCTCTGGGTATCAACTCAACAGTCAAGCTGAGCTGATGAGGGAATGCT	840				
2b	781	GCTCCCTCAAGAGCTCTGGGTATCAACTCAACAGTCAAGCTGAGCTGATGAGGGAATGCT	840				
2y	841	TTGAGCGGCTGGCTTCACTTGTGAACTCAACTTGGCCCAATTAACCTCTCTCTTTCG	900				
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2y	901	CCCATGACCTTTTACCCCGCTGAGTACTCTGGTGGAGTTGATCTACACACACCTTT	960				
2b	901	CCCATGACCTTTTACCCCGCTGAGTACTCTGGTGGAGTTGATCTACACACACCTTT	960				
2y	961	GGAACTGTGATGTGACATCTCTGAGCTAGCTGGTGTGCTTGGAGTATATACCACCA	1020				
2b	961	GGAACTGTGATGTGACATCTCTGAGCTAGCTGGTGTGCTTGGAGTATATACCACCA	1020				
2y	1021	ATTCCACCTGCTGTGCGGCTGTGCTGCCATGCAATGCGAGGCGCTACCTGTGG	1080				

1021	ATTCCACCTGCTGTGCGGCTGTGCTGCCATGCAATGCGAGGCGCTACCTGTGG	1080
1081	AGTGGACCAAGGCTCTCTCCAGTGTCTTCCGCCCTTCAATCATGGAACGCACTTCGAGAC	1140
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1201	TGAAGTGTGCTGCCCAATGCGACAGTGTCTAGCAACGCTCCCGCCACCCCAAGATCT	1260
1201	TGAAGTGTGCTGCCCAATGCGACAGTGTCTAGCAACGCTCCCGCCACCCCAAGATCT	1260
1261	CTGTCTCAACGACGCGACCTTGAACTTTTCCAGTGTGCTTTTTCAGACACTGGGGTGT	1320
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1321	ACACATGATGTGTGACCAATGTTGCAAGGCAACTCCAAACGCTCCGCTACCTCAATGTGA	1380
1321	ACACATGATGTGTGACCAATGTTGCAAGGCAACTCCAAACGCTCCGCTACCTCAATGTGA	1380
1381	GCACGCTGAGCTTTACACCTCCAACTAAGCTTTTTCACCAAGTAAAGTGAAGCA	1440
1381	GCACGCTGAGCTTTACACCTCCAACTAAGCTTTTTCACCAAGTAAAGTGAAGCA	1440
1441	CGGAGATCTCGCTGAGGACACAAACGCGAAAGTACAAAGCTTTTCTACCACTCCACTG	1500
1441	CGGAGATCTCGCTGAGGACACAAACGCGAAAGTACAAAGCTTTTCTACCACTCCACTG	1500
1501	GTACACAGCGGCTATPACCACTCTTACCAACGCTGTCTTCAATTCAGACTACCGGTGCCA	1560
1501	GTACACAGCGGCTATPACCACTCTTACCAACGCTGTCTTCAATTCAGACTACCGGTGCCA	1560
1561	AGCAGGTGGAGTACCGCGGACGACCACTTCACAGAGTTCAGACCGCTCGGATGAAG	1620
1561	AGCAGGTGGAGTACCGCGGACGACCACTTCACAGAGTTCAGACCGCTCGGATGAAG	1620
1621	TCATGAGACCAACAGATCATCATTTGGCTGTCTTGTGGCAGTACTCTGTAGCTGCG	1680
1621	TCATGAGACCAACAGATCATCATTTGGCTGTCTTGTGGCAGTACTCTGTAGCTGCG	1680
1681	CCATGTTGATGTTCTTATAAATTCGTAAGCGGCAACCCAGCGGAGTACAGTCAAG	1740
1681	CCATGTTGATGTTCTTATAAATTCGTAAGCGGCAACCCAGCGGAGTACAGTCAAG	1740
1741	CCGCCCCGAGCTGTGAGATAATCCAGGTGGAAGACATCCAGCAGCAACATCCGAG	1800
1741	CCGCCCCGAGCTGTGAGATAATCCAGGTGGAAGACATCCAGCAGCAACATCCGAG	1800
1801	CAGCAACAGAGCTCTCGTCCGGTGTATCAGGTGAGGGGAGTGTGCTGCCCAAAATTC	1860
1801	CAGCAACAGAGCTCTCGTCCGGTGTATCAGGTGAGGGGAGTGTGCTGCCCAAAATTC	1860
1861	ATGACCATTAATTAACATAACACTCAACACAGCAGCATGCGGCGCCACTGACAGAAACA	1920
1861	ATGACCATTAATTAACATAACACTCAACACAGCAGCATGCGGCGCCACTGACAGAAACA	1920
1921	GCCTGGGGAATCTCTGACACCACTCACTATCTCTGAACTTATATAATTCAGA	1980
1921	GCCTGGGGAATCTCTGACACCACTCACTATCTCTGAACTTATATAATTCAGA	1980
1981	CCCATACAGGACAGGTACAGGAACTCAATATGATCTCCCTCCCTCCCAAAACTTA	2040
1981	CCCATACAGGACAGGTACAGGAACTCAATATGATCTCCCTCCCTCCCAAAACTTA	2040
2041	TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGAGACTTTT	2100
2041	TAAATGCAATAGATGACACAAAGACAGCAACTTTTGTACAGAGTGGGAGACTTTT	2100
2101	TTCTTGTATATGCTTATATATTAATTAAGTCTATGGCTGTGTTAAAAAACAAGATATATA	2160
2101	TTCTTGTATATGCTTATATATTAATTAAGTCTATGGCTGTGTTAAAAAACAAGATATATA	2160

Db 2101 TTCTTGATATGCTTATATATATTAAGTCTATGCGTGGTTAAAAAAGAGATTATATTA 2160

QY 2161 AATTTAAAGACAAAAGTCARAAACA 2185

Db 2161 AATTTAAAGACAAAAGTCARAAACA 2185

RESULT 32

US-09-991-157-228

Sequence 228, Application US/09991157

Publication No. US20030049638A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C51

CURRENT APPLICATION NUMBER: US/09/991,157

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

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 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 b 1 GTTCTCTTCCGAGCCAAATCCCGGCGATGGTGAATTATGAAACGTGGCCACCATGA 60  
 Y 61 AGCTCTTGTGGCAGGTAACCTGTGACCAACCACTGGAATGCCATCTCGCTCCGCTTCG 120

Db	61	AGCTCTTGTGGCAGGTAACCTGTGACCAACCACTGGAATGCCATCTCGCTCCGCTTCG	120
Qy	121	TCTACCTCACGGCGCAAGTGTGATTTCTGTGTGAGCCATCGCTGTGCGGCTCAGCGG	180
Db	121	TCTACCTCACGGCGCAAGTGTGATTTCTGTGTGAGCCATCGCTGTGCGGCTCAGCGG	180
Qy	181	GGCCCCAGAACTGCCCCCTCCGTTTGTGTCAGTAACCAAGTTTCAGAAAGTGGTGTGCA	240
Db	181	GGCCCCAGAACTGCCCCCTCCGTTTGTGTCAGTAACCAAGTTTCAGAAAGTGGTGTGCA	240
Qy	241	CGCGCCGGGGCTCTCGAGGTCGCCGAGGTATTCCTCGAACACCCGCTCAAC	300
Db	241	CGCGCCGGGGCTCTCGAGGTCGCCGAGGTATTCCTCGAACACCCGCTCAAC	300
Qy	301	TCATGAGAAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACTGG	360
Db	301	TCATGAGAAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACTGG	360
Qy	361	AGTCTCTGCAAGTGGGCGAGAACTCCATCCGCGAGATGAGTGGGGGCTTCAAGGGC	420
Db	361	AGTCTCTGCAAGTGGGCGAGAACTCCATCCGCGAGATGAGTGGGGGCTTCAAGGGC	420
Qy	421	TGCGCAGCTCAACACCCCTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
Db	421	TGCGCAGCTCAACACCCCTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
Qy	481	CTTTGAATACCTGTCCAAAGTGGGAGGCTCTGGCTTCGCAACACCCCATCGAAAGCA	540
Db	481	CTTTGAATACCTGTCCAAAGTGGGAGGCTCTGGCTTCGCAACACCCCATCGAAAGCA	540
Qy	541	TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGAGTGGGGGAGCTCA	600
Db	541	TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGGAGTGGGGGAGCTCA	600
Qy	601	AGAGCTGGAGTATATCTCTGAGGAGCTTTTGAGGGGCTGTTTCAACCTCAAGTATCTGA	660
Db	601	AGAGCTGGAGTATATCTCTGAGGAGCTTTTGAGGGGCTGTTTCAACCTCAAGTATCTGA	660
Qy	661	ACTTGGGCTGTGCAACATTAAGACATGCCCAATCTCAACCCCTGCTGGGCTGGAGG	720
Db	661	ACTTGGGCTGTGCAACATTAAGACATGCCCAATCTCAACCCCTGCTGGGCTGGAGG	720
Qy	721	AGCTGGAGATGTCAAGGAAACACTTCCCTGAGATCAGGCTCGCTCTTCCATGGCTGA	780
Db	721	AGCTGGAGATGTCAAGGAAACACTTCCCTGAGATCAGGCTCGCTCTTCCATGGCTGA	780
Qy	781	GCTCCCTCAAGAGCTCTGGCTCATGAATCAGAGCTCAGCTGATGAGCGGATGCTT	840
Db	781	GCTCCCTCAAGAGCTCTGGCTCATGAATCAGAGCTCAGCTGATGAGCGGATGCTT	840
Qy	841	TTGACGGGCTGGCTTCACTTGTGGAATCAACTTGGCCCACTAACTCTCTTCTTTGC	900
Db	841	TTGACGGGCTGGCTTCACTTGTGGAATCAACTTGGCCCACTAACTCTCTTCTTTGC	900
Qy	901	CCATGACCTTTTACCCGCTGAGTACCTGGTGGAGTGTGATCTACACCAACAACCTT	960
Db	901	CCATGACCTTTTACCCGCTGAGTACCTGGTGGAGTGTGATCTACACCAACAACCTT	960
Qy	961	GGAACTGTGATGTGACATTTCTGTGCTAGCTGTGGCTTCGAGAGTATATACCCACA	1020
Db	961	GGAACTGTGATGTGACATTTCTGTGCTAGCTGTGGCTTCGAGAGTATATACCCACA	1020
Qy	1021	ATTCCACCTGCTGTGCGCTGTCTATGCTCCCATGACATGCGAGCGGCTACCTCGTGG	1080
Db	1021	ATTCCACCTGCTGTGCGCTGTCTATGCTCCCATGACATGCGAGCGGCTACCTCGTGG	1080
Qy	1081	AGGTGACAGGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGCAACGACCTCGAGAC	1140
Db	1081	AGGTGACAGGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGCAACGACCTCGAGAC	1140
Qy	1141	TCAACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGCGAGCTCCCTCTATGCTCTCG	1200
Db	1141	TCAACATTTCTGAGGGTGGATGCGAGAACTTAAGTGTGCGAGCTCCCTCTATGCTCTCG	1200



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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AGCTCTTGGGAGGTAACTGTGACACCAACCTGGAATGCCATCTGCTCCGTTCCG	120
Db	61	AGCTCTTGGGAGGTAACTGTGACACCAACCTGGAATGCCATCTGCTCCGTTCCG	120
Qy	121	TCTACCTCAGCGGCAAGTGTGATTTCTGTGACCATGCTGCTCCGCTCAGCG	180
Db	121	TCTACCTCAGCGGCAAGTGTGATTTCTGTGACCATGCTGCTCCGCTCAGCG	180
Qy	181	GGCCCGAAGTCCCTCCCTGCTGTCAGTAAACAGTTCAGCAAGTGTGTCGA	240

Db 181 GGCCCGAGAACTGCGCCCTCCGTTTCTGCTGTGAGTAACCAAGTTGAGCAAGTGTGTGCA 240  
Qy 241 CGCGCGGCGGCTCTCCGAGGTCCCGCGAGGTAATTCCTCGAACAACCCGGTACTCAACC 300  
Db 241 CGCGCGGCGGCTCTCCGAGGTCCCGCGAGGTAATTCCTCGAACAACCCGGTACTCAACC 300  
Qy 301 TCATGGAGAACACATCCAGATGATCCAGGCGGACACCTTCGCCACCTCCACCACTGG 360  
Db 301 TCATGGAGAACACATCCAGATGATCCAGGCGGACACCTTCGCCACCTCCACCACTGG 360  
Qy 361 AGGTCTCGAGTTGGGACAGAACTCCATCCGGCAGATTGAGTGGGGCCCTTCAACGCCC 420  
Db 361 AGGTCTCGAGTTGGGACAGAACTCCATCCGGCAGATTGAGTGGGGCCCTTCAACGCCC 420  
Qy 421 TGGCCAGCCTCAGACCCCTGGAGCTGTTCGACAACTGCTGACAGTCACTCCTTAGCGGG 480  
Db 421 TGGCCAGCCTCAGACCCCTGGAGCTGTTCGACAACTGCTGACAGTCACTCCTTAGCGGG 480  
Qy 481 CTTTGAATACCTGTCCAGCTGCGGGAGCTCTGGCTTCGAAACAACCCCATCGAAAGCA 540  
Db 481 CTTTGAATACCTGTCCAGCTGCGGGAGCTCTGGCTTCGAAACAACCCCATCGAAAGCA 540  
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Db 541 TCCCTCTTACGCTTCAACCGGCTGCTCCTCATGCGGCTGAGCTTGGGGGAGCTCA 600  
Qy 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTTGAGGGCTGTTCAGCTCAAGTATCTGA 660  
Db 601 AGAAGCTGAGTATATCTCTGAGGAGCTTTTGAGGGCTGTTCAGCTCAAGTATCTGA 660  
Qy 661 ACTTGGGCAATGCAACATTAAGACATGCCCAATCTCAACCCCTGGTGGGGTGGAGG 720  
Db 661 ACTTGGGCAATGCAACATTAAGACATGCCCAATCTCAACCCCTGGTGGGGTGGAGG 720  
Qy 721 AGCTGAGATGTCAGGGAACCACTTCCCTGAGTACAGGCTGGCTCTTCCATCGGCTGA 780  
Db 721 AGCTGAGATGTCAGGGAACCACTTCCCTGAGTACAGGCTGGCTCTTCCATCGGCTGA 780  
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Db 781 GTTCCTCAAGAGCTCTGGGTCTATGAACCTCAAGCTCAGCTCAGCTGATGAGCGAATGCTT 840  
Qy 841 TTGAGGGGTGGCTTCACTTGTGGAACTCAACTTGGGCCCACAATAAATCTCTCTCTTTTC 900  
Db 841 TTGAGGGGTGGCTTCACTTGTGGAACTCAACTTGGGCCCACAATAAATCTCTCTCTTTTC 900  
Qy 901 CCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTGCATCTACACCAACCCCTT 960  
Db 901 CCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTGCATCTACACCAACCCCTT 960  
Qy 961 GGAATGTGATGTGACATCTGTGGCTAGCTGTGGCTTGGAGTATATACCAACCA 1020  
Db 961 GGAATGTGATGTGACATCTGTGGCTAGCTGTGGCTTGGAGTATATACCAACCA 1020  
Qy 1021 ATTCCACCTGTGTGGCGCTGTCTATGTCTCCATGACATCGAGGCGCTTACCTCTGG 1080  
Db 1021 ATTCCACCTGTGTGGCGCTGTCTATGTCTCCATGACATCGAGGCGCTTACCTCTGG 1080  
Qy 1081 AGGTGGACGAGGCTCTTTCAGTGTCTGTGCCCCCTTCATCATGAGCGACTCGAGACC 1140  
Db 1081 AGGTGGACGAGGCTCTTTCAGTGTCTGTGCCCCCTTCATCATGAGCGACTCGAGACC 1140  
Qy 1141 TCAACATTTCTGAGGTCGGATGGCAGAACTTAAGTTCGGACTCCCTCTATGTCCTCG 1200  
Db 1141 TCAACATTTCTGAGGTCGGATGGCAGAACTTAAGTTCGGACTCCCTCTATGTCCTCG 1200  
Qy 1201 TGAAGTGTGTGTGCCCAATGGGACAGTGTCTCAGCAGCCTCCCGCCACCAAGGATCT 1260  
Db 1201 TGAAGTGTGTGTGCCCAATGGGACAGTGTCTCAGCAGCCTCCCGCCACCAAGGATCT 1260  
Qy 1261 CTGTCTCAGACGGGCTTGAATCTTCCAGCTGCTCTTCCAGCTGCTCTTCCAGCTGCT 1320  
Db 1261 CTGTCTCAGACGGGCTTGAATCTTCCAGCTGCTCTTCCAGCTGCTCTTCCAGCTGCT 1320

Qy 1321 ACATATGATGTGTGACCAATGTTGAGGCAACTCCAGCGCTCGGCTTACCTCAATGTA 1380  
Db 1321 ACATATGATGTGTGACCAATGTTGAGGCAACTCCAGCGCTCGGCTTACCTCAATGTA 1380  
Qy 1381 GCACGGCTGAGCTTAAACCTCCCACTACAGTCTTCCACACAGTAACTGAGAGCA 1440  
Db 1381 GCACGGCTGAGCTTAAACCTCCCACTACAGTCTTCCACACAGTAACTGAGAGCA 1440  
Qy 1441 CGAGATCTCGCTGAGGACACACCGGAAAGTACAAGCCTGTTCTTACCACTGCTCACTG 1500  
Db 1441 CGAGATCTCGCTGAGGACACACCGGAAAGTACAAGCCTGTTCTTACCACTGCTCACTG 1500  
Qy 1501 GTTACACGCGGACATATACCACTTACCGGCTCTCATTCAGCTTACCTGCTGCCCCA 1560  
Db 1501 GTTACACGCGGACATATACCACTTACCGGCTCTCATTCAGCTTACCTGCTGCCCCA 1560  
Qy 1561 AGCAGTGGCAGTACCCGCGACAGACACCACTGACCAAGATGACAGCCAGCTGGATGAAG 1620  
Db 1561 AGCAGTGGCAGTACCCGCGACAGACACCACTGACCAAGATGACAGCCAGCTGGATGAAG 1620  
Qy 1621 TCATGAGACCACTGAGATCATCTTGGCTGTTTGGGAGTGAAGTCTGCTGCTGCTGCGG 1680  
Db 1621 TCATGAGACCACTGAGATCATCTTGGCTGTTTGGGAGTGAAGTCTGCTGCTGCTGCGG 1680  
Qy 1681 CCATGTTGATGTTCTTCTATAACTTCGTAAGCGCACAGCAGCGAGTACAGTCAAG 1740  
Db 1681 CCATGTTGATGTTCTTCTATAACTTCGTAAGCGCACAGCAGCGAGTACAGTCAAG 1740  
Qy 1741 CGGCGCGAGCTGTTGAGATTAATCCAGTGGAGAGACATCCAGCAGCAACATCCCGAG 1800  
Db 1741 CGGCGCGAGCTGTTGAGATTAATCCAGTGGAGAGACATCCAGCAGCAACATCCCGAG 1800  
Qy 1801 CAGCAACAGCAGCTCCGCTCCGTTATCAGTGTAGGGGGCAGTGTGCTGCCCAATTC 1860  
Db 1801 CAGCAACAGCAGCTCCGCTCCGTTATCAGTGTAGGGGGCAGTGTGCTGCCCAATTC 1860  
Qy 1861 ATGACCATTAATTAACACCTTACAAACCCAGCAATGCGGCGCCACTGGACAGAAACA 1920  
Db 1861 ATGACCATTAATTAACACCTTACAAACCCAGCAATGCGGCGCCACTGGACAGAAACA 1920  
Qy 1921 GCCTGGGAACTCTCTGCACCCCACTGACCACTCTCTGTAACCTTATATATTCAGA 1980  
Db 1921 GCCTGGGAACTCTCTGCACCCCACTGACCACTCTCTGTAACCTTATATATTCAGA 1980  
Qy 1981 CCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCCCTCCCAAAACTTA 2040  
Db 1981 CCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCCCTCCCAAAACTTA 2040  
Qy 2041 TAAATGCAATGAAATGACACAAAGACAGCACTTTGTACAGAGTGGGAGAGCTTT 2100  
Db 2041 TAAATGCAATGAAATGACACAAAGACAGCACTTTGTACAGAGTGGGAGAGCTTT 2100  
Qy 2101 TTTCTGTATATCTTATATATTAAGTCTATGGGCTGTTAAAAAAAACAGATTATATA 2160  
Db 2101 TTTCTGTATATCTTATATATTAAGTCTATGGGCTGTTAAAAAAAACAGATTATATA 2160  
Qy 2161 AATTTAAAGCAAAAAGTCAAAACA 2185  
Db 2161 AATTTAAAGCAAAAAGTCAAAACA 2185

## RESULT 34

US-09-997-573-228  
; Sequence 228, Application US/09997573  
; Publication NO. US20030049682A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Nagier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C45  
CURRENT APPLICATION NUMBER: US/09/997,573  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/085311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445

[illegible]

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1501 GTTACCAAGCGGGATATACCACTCTTACCAAGCGTGTCTATTAGAGTACCTCGTGTGCCA 1560  
1501 GTTACCAAGCGGGATATACCACTCTTACCAAGCGTGTCTATTAGAGTACCTCGTGTGCCA 1560  
1561 AGCAGTGGCGAGTACCGGACAGACACCACTGACAAAGATGACAGACCACTGAGTGAAG 1620  
1561 AGCAGTGGCGAGTACCGGACAGACACCACTGACAAAGATGACAGACCACTGAGTGAAG 1620  
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1621 TCATGAAGACCAACCAAGATCATCATTTGGCTGCTTTGTGGCAGTACTTGTGAGTGGCG 1680  
1681 CCATGTTGATGCTTCTTATAAATTCGTAAGCGGACCAAGCGGAGTACAGTCAAG 1740  
1681 CCATGTTGATGCTTCTTATAAATTCGTAAGCGGACCAAGCGGAGTACAGTCAAG 1740  
1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGACGAGACATCCAGCAGCAACATCCGCGAG 1800  
1741 CCGCCCGGACTGTTGAGATAATCCAGGTGGACGAGACATCCAGCAGCAACATCCGCGAG 1800  
1801 CAGCAACAGAGTCCGTCGGTGTATCAGGTGAGGGGCGAGTGTGCTGCCCAATTC 1860  
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1861 ATGACCATATTAACATAACACCTTACAAACAGCAGCATGGGCGCCACTGGACAGAAACA 1920  
1861 ATGACCATATTAACATAACACCTTACAAACAGCAGCATGGGCGCCACTGGACAGAAACA 1920  
1921 GCCTGGGGAACCTCTGCGACCCCAAGTCAACACTATCTCTGAACCTTATATATTA 1980  
1921 GCCTGGGGAACCTCTGCGACCCCAAGTCAACACTATCTCTGAACCTTATATATTA 1980  
1981 CCATACCAAGACAGGATACAGGAACTCAATATGATCCCTCCGCCCAAAACCTTA 2040  
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2041 TAAATGCAANTAGATGACACAAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTT 2100  
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2101 TTCTGTATATGCTTATATATTAATAGTCTATGCGCTGTTTAAAAAAGACAGATTATTA 2160  
2161 AATTTAAAGACAAAAGTCAAAACA 2185  
2161 AATTTAAAGACAAAAGTCAAAACA 2185

RESULT 35  
S-09-991-172-228  
Sequence 228, Application US/09991172  
Publication No. US20030050457A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurey, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P27301C50  
CURRENT APPLICATION NUMBER: US/09/991,172  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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70	PRIOR APPLICATION NUMBER: 60/090542	
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:	PRIOR APPLICATION NUMBER:	60/091978
:	PRIOR FILING DATE:	1998-07-07
:	PRIOR APPLICATION NUMBER:	60/091982
:	PRIOR FILING DATE:	1998-07-07
:	PRIOR APPLICATION NUMBER:	60/092182
:	PRIOR FILING DATE:	1998-07-09

  

Query Match		100.0%;	Score 2185;	DB 11;	Length 2185;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2185;	Conservative	0;	Mismatches	0;	Indels    0;    Gaps    0;

  

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QY	61	AGCTCTTGTGGCAGGTAACCTGTGCACACCAACACTCGAATGCCATCTGCTCCGGTTCG	120
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QY	181	GGCCCCAGAATCGCCCTCCGTTTGCTGTGCAGGTAAACAGTTTAGAGAGGTGTGTGCA	240
Db	181	GGCCCCAGAATCGCCCTCCGTTTGCTGTGCAGGTAAACAGTTTAGAGAGGTGTGTGCA	240
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Db	241	CGCGCCGGGGCCTCTCCGAGGTCGCCAGGGATTCCCTCGAACACCCGGGTACCTCAACC	300
QY	301	TCATGGAGACAATCCAGATGATCCAGGCTGACACTTTCGGCCCACTCTCCACCACTTGG	360
Db	301	TCATGGAGACAATCCAGATGATCCAGGCTGACACTTTCGGCCCACTCTCCACCACTTGG	360
QY	361	AGGTCTTCAGTGTGGGCAGGAACCTCCATCCGCGAGATTGAGGTGGGGGCCCTTCAAACGCC	420
Db	361	AGGTCTTCAGTGTGGGCAGGAACCTCCATCCGCGAGATTGAGGTGGGGGCCCTTCAAACGCC	420
QY	421	TGGCCAGCCTCAACACACCTTGGAGCTTTTCCAACATGTGCTGACAGTANTCCTAGCGGGG	480
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## RESULT 36

US-09-990-726-228

; Sequence 228, Application US/09990726

; Publication No US20030054359A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

1 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
2 FILE REFERENCE: P2730PIC16  
3 CURRENT APPLICATION NUMBER: US/09/990.726

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 : PRIOR APPLICATION NUMBER: 60/090862  
 : PRIOR FILING DATE: 1998-06-26  
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 : PRIOR APPLICATION NUMBER: 60/091360  
 : PRIOR FILING DATE: 1998-07-01  
 : PRIOR APPLICATION NUMBER: 60/091478  
 : PRIOR FILING DATE: 1998-07-02  
 : PRIOR APPLICATION NUMBER: 60/091544  
 : PRIOR FILING DATE: 1998-07-01  
 : PRIOR APPLICATION NUMBER: 60/091519  
 : PRIOR FILING DATE: 1998-07-02  
 : PRIOR APPLICATION NUMBER: 60/091626  
 : PRIOR FILING DATE: 1998-07-02  
 : PRIOR APPLICATION NUMBER: 60/091633  
 : PRIOR FILING DATE: 1998-07-02  
 : PRIOR APPLICATION NUMBER: 60/091978  
 : PRIOR FILING DATE: 1998-07-07  
 : PRIOR APPLICATION NUMBER: 60/091982  
 : PRIOR FILING DATE: 1998-07-07  
 : PRIOR APPLICATION NUMBER: 60/092182  
 : PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1201 TGAAGTGTGTGCTGCCAATGGGACAGTGTCTCAGCCAGCTCCCGCCACCAAGATCT 1260  
 QY 1261 CTGTCTCTAAACGAGCACTTTTCCCACTTCCCACTGCTGTCTTTCAGACACTGGGGTGT 1320  
 Db 1261 CTGTCTCTAAACGAGCACTTTTCCCACTTCCCACTGCTGTCTTTCAGACACTGGGGTGT 1320  
 QY 1321 ACACATGCTGTGACCAATGTGAGGCAACTCCCAAGCTCGGCTACCTCAATGTGA 1380  
 Db 1321 ACACATGCTGTGACCAATGTGAGGCAACTCCCAAGCTCGGCTACCTCAATGTGA 1380  
 QY 1381 GCACGGCTGAGCTTAAACCTCCAACTACAGCTTCTTCCACAGTAAACAGTGGAGACCA 1440  
 Db 1381 GCACGGCTGAGCTTAAACCTCCAACTACAGCTTCTTCCACAGTAAACAGTGGAGACCA 1440  
 QY 1441 CGGAGATCTGCTGTGAGGACCAACCGGAAAGTACAGCTGTCTTCCACAGTCCACTG 1500  
 Db 1441 CGGAGATCTGCTGTGAGGACCAACCGGAAAGTACAGCTGTCTTCCACAGTCCACTG 1500  
 QY 1501 GTTACCCAGCCGATATACCACTCTTACACGGGTGCTCAATTCAGACTACCCGTGTGCCCA 1560  
 Db 1501 GTTACCCAGCCGATATACCACTCTTACACGGGTGCTCAATTCAGACTACCCGTGTGCCCA 1560  
 QY 1561 AGCAGGTGCGATACCCGCGACAGACCACTGACAAAGATGACAGACCTGTGATGAG 1620  
 Db 1561 AGCAGGTGCGATACCCGCGACAGACCACTGACAAAGATGACAGACCTGTGATGAG 1620  
 QY 1621 TCATGAGACCAACCAAGATCACTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1680  
 Db 1621 TCATGAGACCAACCAAGATCACTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1680  
 QY 1681 CCATGTGTGATTTCTTCTATAAATCTTCTAAGCGGACACAGCAGCGGAGTACAGTCAAG 1740

1681 CCATGTTGATTGCTCTTCTATAAACTTCGTAAGCGGCACCGAGCGGAGTACAGTCACAG 1740  
1741 CCGCCCGGACTGTTGAGATAATCCAGGTGAGGAGGACATCCCGAGGACCAATCCGCGAG 1800  
1742 CCGCCCGGACTGTTGAGATAATCCAGGTGAGGAGGACATCCCGAGGACCAATCCGCGAG 1800  
1801 CAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGAGGAGTAGTGTGCTGCCACAATTC 1860  
1801 CAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGAGGAGTAGTGTGCTGCCACAATTC 1860  
1861 ATGACCATATTAATACATCAACACCTTACAAACCCAGCACATGGGGCCCACTGGACAGAAAAA 1920  
1861 ATGACCATATTAATACATCAACACCTTACAAACCCAGCACATGGGGCCCACTGGACAGAAAAA 1920  
1921 GCCTGGGGAATCTCTGCAACCCCAAGTCACCACTATCTCTGAACTTATATTAATTCAGA 1980  
1921 GCCTGGGGAATCTCTGCAACCCCAAGTCACCACTATCTCTGAACTTATATTAATTCAGA 1980  
1981 CCCATACCAAGGACAGGTACAGGAACCTCAAAATATGACTCCCTCCGCCCAAAAACTTA 2040  
1981 CCCATACCAAGGACAGGTACAGGAACCTCAAAATATGACTCCCTCCGCCCAAAAACTTA 2040  
2041 TAAATGCAATAGATGACACACAAAGACAGCACTTTTGTACAGAGTGGGGAGACTTT 2100  
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## RESULT 37

JS-09-997-559-228  
; Sequence 228, Application US/09997559  
; Publication No. US20030054403A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klijavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C40  
; CURRENT APPLICATION NUMBER: US/09/997,559  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
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; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-06-26

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PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTTCCGAGCCAAATCCAGGCGATGGTGAATATGAACTGACACACCATGA 60  
DB 1 GTTCTCTTTCCGAGCCAAATCCAGGCGATGGTGAATATGAACTGACACACCATGA 60

QY 61 AGCTCTTGTGGCGAGTAACTGTGCAACACACCTGGGAATGCCATCTGCTCCCGTTGG 120  
DB 61 AGCTCTTGTGGCGAGTAACTGTGCAACACACCTGGGAATGCCATCTGCTCCCGTTGG 120

QY 121 TCTACCTCAGCGGCGAGTGTGGAATCTGTGTGCGAGCATCGCTGTGCGGCTCAGCGG 180  
DB 121 TCTACCTCAGCGGCGAGTGTGGAATCTGTGTGCGAGCATCGCTGTGCGGCTCAGCGG 180

QY 181 GGCCCCAGAACTGCCCTCCGTTTGTCTGTGCAATACAGTTTCAGCAAGGTGTGCA 240  
DB 181 GGCCCCAGAACTGCCCTCCGTTTGTCTGTGCAATACAGTTTCAGCAAGGTGTGCA 240

QY 241 CGGCGCGGGGCTCTCGAGGTCCGCGAGGTATTCCTCGAACACCCGGTACCTCAAC 300  
DB 241 CGGCGCGGGGCTCTCGAGGTCCGCGAGGTATTCCTCGAACACCCGGTACCTCAAC 300

QY 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTTCCGCGCACCTCCACCTGG 360  
DB 301 TCATGGAGAAACAATCCAGATGATCCAGGCGGACACCTTTCCGCGCACCTCCACCTGG 360

QY 361 AGTCTCTGCGAGTTGGGCGAGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAAGGCC 420  
DB 361 AGTCTCTGCGAGTTGGGCGAGAACTCCATCCGCGAGATTGAGTGGGGGCTTCAAGGCC 420

QY 421 TGGCGAGCTCAACACCCCTGGAGCTGTTCGACAACTGGCTGACAGTCATCCCTAGCGGGG 480  
DB 421 TGGCGAGCTCAACACCCCTGGAGCTGTTCGACAACTGGCTGACAGTCATCCCTAGCGGGG 480

QY 481 CTTTGAATACCTGTCCAACTGGGAGCTCTGGCTTCGCGAACAAACCCCACTCGAAAGCA 540  
DB 481 CTTTGAATACCTGTCCAACTGGGAGCTCTGGCTTCGCGAACAAACCCCACTCGAAAGCA 540

QY 541 TCCCTCTTACGCTTCAACCCGGTCCCTCCCTCATGCGCTGAGTCTGGGGGAGCTCA 600  
DB 541 TCCCTCTTACGCTTCAACCCGGTCCCTCCCTCATGCGCTGAGTCTGGGGGAGCTCA 600

QY 601 AGAAGCTGGAGTATCTCTGAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGATCTGA 660  
DB 601 AGAAGCTGGAGTATCTCTGAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGATCTGA 660

QY 661 ACTTGGGCGATGCAACATTAAGACATGCCCAATCTCAACCCCTCTGGTGGGGTGGAGG 720  
DB 661 ACTTGGGCGATGCAACATTAAGACATGCCCAATCTCAACCCCTCTGGTGGGGTGGAGG 720

QY 721 AGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTCGGCTCTTCCATGGCCTGA 780  
DB 721 AGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCTCGGCTCTTCCATGGCCTGA 780

Db 721 AGCTGGAGATGTCAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTCCATGGCCCTGA 780  
 Qy 781 GGTCCCTCAAGAGCTCTGGGTGATGAATCACTCAGGTGAGCTGATTCAGCGGAATGCTT 840  
 Db 781 GGTCCCTCAAGAGCTCTGGGTGATGAATCACTCAGGTGAGCTGATTCAGCGGAATGCTT 840  
 Qy 841 TTGAGGGGTGCTTCACTTGTGGAACTCACTTGTGGCCCAATAACTCTCTCTTTTTC 900  
 Db 841 TTGAGGGGTGCTTCACTTGTGGAACTCACTTGTGGCCCAATAACTCTCTCTTTTTC 900  
 Qy 901 CCATGACCTCTTTACCCCGCTGAGGTGAGTCACTTGTGGAGTGCATCTACACCAACCCCTT 960  
 Db 901 CCATGACCTCTTTACCCCGCTGAGGTGAGTGCATCTACACCAACCCCTT 960  
 Qy 961 GGAATGTGATGTGACATCTCTGGCTGAGCTGTGGTGTCTCGAGATATATACCCACCA 1020  
 Db 961 GGAATGTGATGTGACATCTCTGGCTGAGCTGTGGTGTCTCGAGATATATACCCACCA 1020  
 Qy 1021 ATTCCACCTGTGTGGCGCTGTGATGCTGCCATGCGACATCGGAGGCGCTACCTCGTGG 1080  
 Db 1021 ATTCCACCTGTGTGGCGCTGTGATGCTGCCATGCGACATCGGAGGCGCTACCTCGTGG 1080  
 Qy 1081 AGGTGGACAGGCTCTCTTCCAGTGTCTGTGGCTGTGAGCTGTGAGTGTGAGTGTGAGTGT 1140  
 Db 1081 AGGTGGACAGGCTCTCTTCCAGTGTCTGTGGCTGTGAGCTGTGAGTGTGAGTGTGAGTGT 1140  
 Qy 1141 TCAACATTTCTGAGGTGCGATGCGAGAACTTAAGTGTGGACTCCCTCTATGTCCTCG 1200  
 Db 1141 TCAACATTTCTGAGGTGCGATGCGAGAACTTAAGTGTGGACTCCCTCTATGTCCTCG 1200  
 Qy 1201 TGAAGTGTGTGTGCGCCCAATGGGACAGTGTCTCAGCCAGCTCCCGCCACCCCAAGATCT 1260  
 Db 1201 TGAAGTGTGTGTGCGCCCAATGGGACAGTGTCTCAGCCAGCTCCCGCCACCCCAAGATCT 1260  
 Qy 1261 CTGTCTCAACAGCGGCTTGAATTTTCCAGTGTCTTCCAGTGTCTTTCAGACACTGGGTGT 1320  
 Db 1261 CTGTCTCAACAGCGGCTTGAATTTTCCAGTGTCTTCCAGTGTCTTTCAGACACTGGGTGT 1320  
 Qy 1321 ACACATGATGTGATCAATGTTGAGGCAACTCCAGCGCTCGGCTCACTCAATGTGA 1380  
 Db 1321 ACACATGATGTGATCAATGTTGAGGCAACTCCAGCGCTCGGCTCACTCAATGTGA 1380  
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 Db 1441 CGAGATCTGCTGAGGACACAAAGCAAGTACAGCTGTCTTCCAGAGTACAGTGTGAGAC 1500  
 Qy 1501 GTTACAGCGGCTATACCACTCTTACAGGCTGTCTTCACTCACTTACAGCTTACAGCT 1560  
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 Db 1681 CCATGTTGATGCTCTTCTATAACTTGTAGCGGACCCAGCGGAGTACAGTACAG 1740  
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 Db 1741 CGCCCGGAGCTTGTAGATATCCAGGTGAGAGATCCAGAGTACCCAGAGCAATCCCGAG 1800  
 Qy 1801 CAGCAACAGCAGCTCCGCTGTGTATCAGGTGAGGGGAGTGTGTGCTGCCCAATTC 1860  
 Db 1801 CAGCAACAGCAGCTCCGCTGTGTATCAGGTGAGGGGAGTGTGTGCTGCCCAATTC 1860

RESULT 38

US-09-997-601-228  
 ; Sequence 228, Application US/09997601  
 ; Publication No. US20030054404A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas P.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730PIC36  
 ; CURRENT APPLICATION NUMBER: US/09/997,601  
 ; CURRENT FILING DATE: 2001-11-15  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
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 Qy 1921 GCTCGGGGAATCTCTGTCACCCCACTGTCACCTATCTCTGAACCTTATATATATTCAGA 1980  
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 Qy 1981 CCATACCAAGGACAAAGTACAGGAACTCAAAATATGATCTCCCTCCCAAAAACCTTA 2040  
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 Db 2041 TAAATGCAATAGATGACACCAAGAGCAGCAACTTTGTACAGAGTGGGAGAGACTTT 2100  
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7	PRIOR APPLICATION NUMBER: 60/089801	
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12	PRIOR FILING DATE: 1998-06-18	
13	PRIOR APPLICATION NUMBER: 60/089947	
14	PRIOR FILING DATE: 1998-06-19	
15	PRIOR APPLICATION NUMBER: 60/089948	
16	PRIOR FILING DATE: 1998-06-19	
17	PRIOR APPLICATION NUMBER: 60/089952	
18	PRIOR FILING DATE: 1998-06-19	
19	PRIOR APPLICATION NUMBER: 60/090246	
20	PRIOR FILING DATE: 1998-06-22	
21	PRIOR APPLICATION NUMBER: 60/090252	
22	PRIOR FILING DATE: 1998-06-22	
23	PRIOR APPLICATION NUMBER: 60/090254	
24	PRIOR FILING DATE: 1998-06-22	
25	PRIOR APPLICATION NUMBER: 60/090349	
26	PRIOR FILING DATE: 1998-06-23	
27	PRIOR APPLICATION NUMBER: 60/090355	
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29	PRIOR APPLICATION NUMBER: 60/090429	
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32	PRIOR FILING DATE: 1998-06-24	
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34	PRIOR FILING DATE: 1998-06-24	
35	PRIOR APPLICATION NUMBER: 60/090444	
36	PRIOR FILING DATE: 1998-06-24	
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38	PRIOR FILING DATE: 1998-06-24	
39	PRIOR APPLICATION NUMBER: 60/090472	
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53	PRIOR APPLICATION NUMBER: 60/090578	
54	PRIOR FILING DATE: 1998-06-25	
55	PRIOR APPLICATION NUMBER: 60/090696	
56	PRIOR FILING DATE: 1998-06-25	
57	PRIOR APPLICATION NUMBER: 60/090862	
58	PRIOR FILING DATE: 1998-06-26	
59	PRIOR APPLICATION NUMBER: 60/090863	
60	PRIOR FILING DATE: 1998-06-26	
61	PRIOR APPLICATION NUMBER: 60/091360	
62	PRIOR FILING DATE: 1998-07-01	
63	PRIOR APPLICATION NUMBER: 60/091478	
64	PRIOR FILING DATE: 1998-07-02	
65	PRIOR APPLICATION NUMBER: 60/091544	
66	PRIOR FILING DATE: 1998-07-01	
67	PRIOR APPLICATION NUMBER: 60/091519	
68	PRIOR FILING DATE: 1998-07-02	
69	PRIOR APPLICATION NUMBER: 60/091626	

[illegible]



1	Prior Filing Date: 1998-06-18	Query Match	100.0%; Score 2185; DB 11; Length 2185;
2	Prior Application Number: 60/089908	Best Local Similarity	100.0%; Pred. Nc. 0;
3	Prior Filing Date: 1998-06-18	Matches 2185; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
4	Prior Application Number: 60/089947		
5	Prior Filing Date: 1998-06-19		
6	Prior Application Number: 60/089948		
7	Prior Filing Date: 1998-06-19		
8	Prior Application Number: 60/089952		
9	Prior Filing Date: 1998-06-19		
10	Prior Application Number: 60/090246		
11	Prior Filing Date: 1998-06-22		
12	Prior Application Number: 60/090252		
13	Prior Filing Date: 1998-06-22		
14	Prior Application Number: 60/090254		
15	Prior Filing Date: 1998-06-22		
16	Prior Application Number: 60/090349		
17	Prior Filing Date: 1998-06-23		
18	Prior Application Number: 60/090355		
19	Prior Filing Date: 1998-06-23		
20	Prior Application Number: 60/090429		
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22	Prior Application Number: 60/090431		
23	Prior Filing Date: 1998-06-24		
24	Prior Application Number: 60/090435		
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26	Prior Application Number: 60/090444		
27	Prior Filing Date: 1998-06-24		
28	Prior Application Number: 60/090445		
29	Prior Filing Date: 1998-06-24		
30	Prior Application Number: 60/090472		
31	Prior Filing Date: 1998-06-24		
32	Prior Application Number: 60/090335		
33	Prior Filing Date: 1998-06-24		
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35	Prior Filing Date: 1998-06-24		
36	Prior Application Number: 60/090542		
37	Prior Filing Date: 1998-06-24		
38	Prior Application Number: 60/090557		
39	Prior Filing Date: 1998-06-24		
40	Prior Application Number: 60/090676		
41	Prior Filing Date: 1998-06-25		
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43	Prior Filing Date: 1998-06-25		
44	Prior Application Number: 60/090690		
45	Prior Filing Date: 1998-06-25		
46	Prior Application Number: 60/090694		
47	Prior Filing Date: 1998-06-25		
48	Prior Application Number: 60/090695		
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50	Prior Application Number: 60/090696		
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53	Prior Filing Date: 1998-06-26		
54	Prior Application Number: 60/090863		
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56	Prior Application Number: 60/091360		
57	Prior Filing Date: 1998-07-01		
58	Prior Application Number: 60/091478		
59	Prior Filing Date: 1998-07-02		
60	Prior Application Number: 60/091544		
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66	Prior Application Number: 60/091633		
67	Prior Filing Date: 1998-07-02		
68	Prior Application Number: 60/091978		
69	Prior Filing Date: 1998-07-07		
70	Prior Application Number: 60/091982		
71	Prior Filing Date: 1998-07-07		
72	Prior Application Number: 60/092182		
73	Prior Filing Date: 1998-07-09		

  

QY	1	GTCTCTCTTTCCGAGCCAAATCCAGGCGATGTTGAATATGAACTGATGAACTGACACCATGA	60
DB	1	GTCTCTCTTTCCGAGCCAAATCCAGGCGATGTTGAATATGAACTGATGAACTGACACCATGA	60
QY	61	AGCTCTTTGGCAGGTAACTGTGACACCAACACACTGGAAATGCCATCTCTGCTCCGCTTG	120
DB	61	AGCTCTTTGGCAGGTAACTGTGACACCAACACACTGGAAATGCCATCTCTGCTCCGCTTG	120
QY	121	TCTACTCTACGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGTGCGCCCTCAGCCG	180
DB	121	TCTACTCTACGGCGCAAGTGTGGATTCTGTGTGAGCCATCGCTGTGCGCCCTCAGCCG	180
QY	181	GGCCCCAGAACTGCCCTCCGTTTCTGTGCAAGTAAACAGTTGAGCAAGGTGTGTGCA	240
DB	181	GGCCCCAGAACTGCCCTCCGTTTCTGTGCAAGTAAACAGTTGAGCAAGGTGTGTGCA	240
QY	241	CGGCGCGGGCTCTCCGAGGTCCGCGAGGCTATTCCTCGAACACCCGGTACCTCAACC	300
DB	241	CGGCGCGGGCTCTCCGAGGTCCGCGAGGCTATTCCTCGAACACCCGGTACCTCAACC	300
QY	301	TCATGGAGAAACAACTCCAGATGATCCAGGCGCAGACCTTCGCGCACCTCCACCACTGG	360
DB	301	TCATGGAGAAACAACTCCAGATGATCCAGGCGCAGACCTTCGCGCACCTCCACCACTGG	360
QY	361	AGTCTCTGCAAGTTGGCGAGGAACTTCATCCGGCAGATTGAGTGGGGGCTTCAACGCC	420
DB	361	AGTCTCTGCAAGTTGGCGAGGAACTTCATCCGGCAGATTGAGTGGGGGCTTCAACGCC	420
QY	421	TGGCCAGCTCAACACCTTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
DB	421	TGGCCAGCTCAACACCTTGGAGCTGTTTCGACAACTGGCTGACAGTCACTCCCTAGCGGG	480
QY	481	CTTTGAAATACCTGTCCAGCTGCGGGAGCTCTGCGAACTTCGCAACCCCATCGAAAGCA	540
DB	481	CTTTGAAATACCTGTCCAGCTGCGGGAGCTCTGCGAACTTCGCAACCCCATCGAAAGCA	540
QY	541	TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGGCTGAGCTTGGGGAGCTCA	600
DB	541	TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGGCTGAGCTTGGGGAGCTCA	600
QY	601	AGAAGCTGAGTATATCTCTGAGGAGCTTTTGGGGCTGTTCAACTCAAGTATCTGA	660
DB	601	AGAAGCTGAGTATATCTCTGAGGAGCTTTTGGGGCTGTTCAACTCAAGTATCTGA	660
QY	661	ACTTGGGATGTGCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGGCTGGAGG	720
DB	661	ACTTGGGATGTGCAACATTAAGACATGCCCAATCTCACCCCTGCTGGGGCTGGAGG	720
QY	721	AGCTGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTTCACTGGCCCTGA	780
DB	721	AGCTGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTCTTCACTGGCCCTGA	780
QY	781	GCTCCCTCAAGAGCTCTGGGTCACTGAACTCAGCTCAGCTGATGAGCGGATGCTT	840
DB	781	GCTCCCTCAAGAGCTCTGGGTCACTGAACTCAGCTCAGCTGATGAGCGGATGCTT	840
QY	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGGCTCAATAAATCTCTCTTTTGC	900
DB	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGGCTCAATAAATCTCTCTTTTGC	900
QY	901	CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGATCTACACCAACCTT	960
DB	901	CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGATCTACACCAACCTT	960
QY	961	GGAACTGTGATGTGACATTTCTGTGGCTAGCTGCTGGCTTGGAGTATATACCAACA	1020
DB	961	GGAACTGTGATGTGACATTTCTGTGGCTAGCTGCTGGCTTGGAGTATATATACCAACA	1020

1081	Y	ATTCCACCTGCTGTGGCGCGTGTACGTCCCAATGCAATGCGAGGCGCGTACTCTGTGG	1081
1082	b	ATTCCACCTGCTGTGGCGCGTGTACGTCCCAATGCAATGCGAGGCGCGTACTCTGTGG	1082
1083	Y	AGGTGAGCACAGGCGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGGAAGCACTCTGGAGACC	1140
1084	b	AGGTGAGCACAGGCGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGGAAGCACTCTGGAGACC	1140
1141	Y	TCAAACATTTCTGAGGTTCGGATGGCAGAACTTAATGTGTGCACTCCGCCCTATGTCTCTCG	1200
1142	b	TCAAACATTTCTGAGGTTCGGATGGCAGAACTTAATGTGTGCACTCCGCCCTATGTCTCTCG	1200
1201	Y	TGAAGTGTGTCTGCCCAATGCGACAGTGTCTCAGCCACGCTCCCGCCACCCAGAGATCT	1260
1202	b	TGAAGTGTGTCTGCCCAATGCGACAGTGTCTCAGCCACGCTCCCGCCACCCAGAGATCT	1260
1261	Y	CTGTCTCAACGACGGCACCTTTGAACTTTTCCACGTGTCTCTTCAGACACTGGGGTGT	1320
1262	b	CTGTCTCAACGACGGCACCTTTGAACTTTTCCACGTGTCTCTTCAGACACTGGGGTGT	1320
1321	Y	ACACATGTCATGTGCACCAATGTTCAGGCAACCTCCCAACGCTCCGGCTACTCTCAATGTGA	1380
1322	b	ACACATGTCATGTGCACCAATGTTCAGGCAACCTCCCAACGCTCCGGCTACTCTCAATGTGA	1380
1381	Y	GCACGGCTGAGCTTAAACACCTCCAACTACAGCTCTTTCACACACAGTAAACAGTGAAGCA	1440
1382	b	GCACGGCTGAGCTTAAACACCTCCAACTACAGCTCTTTCACACACAGTAAACAGTGAAGCA	1440
1441	Y	CGAGATCTCGCTGAGGACACAAACGCGAAAGTACAGCTGTTCCTACCAAGTGCACCTG	1500
1442	b	CGAGATCTCGCTGAGGACACAAACGCGAAAGTACAGCTGTTCCTACCAAGTGCACCTG	1500
1501	Y	GTTACACAGCGGATATACCACTCTTACCAACGGTGTCTATTACAGCTACCGGTGTGCCCA	1560
1502	b	GTTACACAGCGGATATACCACTCTTACCAACGGTGTCTATTACAGCTACCGGTGTGCCCA	1560
1561	Y	AGCAGTGGCAGTACCGCGACAGACCACTGACAGATGACAGACACAGCTGTGATGAAG	1620
1562	b	AGCAGTGGCAGTACCGCGACAGACCACTGACAGATGACAGACACAGCTGTGATGAAG	1620
1621	Y	TCATGAGACACCCAGATCATCATTTGGCTGTCTTTGTGCGAGTGACTCTGCTAGCTCCCG	1680
1622	b	TCATGAGACACCCAGATCATCATTTGGCTGTCTTTGTGCGAGTGACTCTGCTAGCTCCCG	1680
1681	Y	CCATGTTGATGTCTTCTATAACTTCGTAAAGCGGACAGCAGCGGAGTACAGTCAAG	1740
1682	b	CCATGTTGATGTCTTCTATAACTTCGTAAAGCGGACAGCAGCGGAGTACAGTCAAG	1740
1741	Y	CGCGCGGACTGTGAGATTAATCCAGGTGACAGAGACATCCACAGCAGACATCCGAG	1800
1742	b	CGCGCGGACTGTGAGATTAATCCAGGTGACAGAGACATCCACAGCAGACATCCGAG	1800
1801	Y	CAGCAACAGCAGCTCCCGTGGTGTATCAGGTGAGGGGCGAGTGTGTGCCCAAAATTC	1860
1802	b	CAGCAACAGCAGCTCCCGTGGTGTATCAGGTGAGGGGCGAGTGTGTGCCCAAAATTC	1860
1861	Y	ATGACCATTTACTACACACCTHACAAACGACATGCGGGCGGCTGTGACAGAAACA	1920
1862	b	ATGACCATTTACTACACACCTHACAAACGACATGCGGGCGGCTGTGACAGAAACA	1920
1921	Y	GCCTGGGGAACTCTCTGCACCCACAGTACACACTACTCTCTGAACCTTATATAATTCAGA	1980
1922	b	GCCTGGGGAACTCTCTGCACCCACAGTACACACTACTCTCTGAACCTTATATAATTCAGA	1980
1981	Y	CCCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCTCCCGCAAAACTTAA	2040
1982	b	CCCATACCAAGGACAGGTACAGGAACTCAAAATATGACTCCCTCTCCCGCAAAACTTAA	2040
2041	Y	TAAATGCCATAGAAATGCAACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT	2100
2042	b	TAAATGCCATAGAAATGCAACAAAGACAGCACTTTTGTACAGAGTGGGAGAGACTTT	2100
2101	Y	TTCTTGATATGCTTATATTAATTAAGTCTATGGGCTGGTTTAAAAAAGACAGATTAATAA	2160

RESULT 40

US-09-991-854-228  
: Sequence 228, Application US/09991854

Publication No. US20

1	GENERAL INFORMATION:	
2	APPLICANT: Ashkenazi, Avi J.	
3	APPLICANT: Baker, Kevin P.	
4	APPLICANT: Botstein, David	
5	APPLICANT: Desnoyers, Luc	
6	APPLICANT: Saton, Dan L.	
7	APPLICANT: Ferrara, Napoleone	
8	APPLICANT: Fong, Sherman	
9	APPLICANT: Gerber, Hanspeter	
10	APPLICANT: Gerritsen, Mary E.	
11	APPLICANT: Goddard, Audrey	
12	APPLICANT: Godowski, Paul J.	
13	APPLICANT: Grimaldi, J. Christopher	
14	APPLICANT: Gurney, Austin L.	
15	APPLICANT: Kijavini, Ivar J.	
16	APPLICANT: Napier, Mary A.	
17	APPLICANT: Pan, James	
18	APPLICANT: Paoni, Nicholas F.	
19	APPLICANT: Roy, Margaret Ann	
20	APPLICANT: Stewart, Timothy A.	
21	APPLICANT: Tumas, Daniel	
22	APPLICANT: Watanabe, Colin K.	
23	APPLICANT: Williams, P. Mickey	
24	APPLICANT: Wood, William I.	
25	APPLICANT: Zhang, Zemin	

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C24  
CURRENT APPLICATION NUMBER: US/08/991 854

; CURRENT APPLICATION NUMBER: US/09/9  
 ; CURRENT FILING DATE: 2001-11-14

CURRENT FILING DATE: 2001-11-11  
PRIOR APPLICATION NUMBER: 60/049

PRIOR FILING DATE: 1997-06-16

;; PRIOR FILING DATE: 1337-08-18  
;; PRIOR APPLICATION NUMBER: 60/06

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/06

PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/06

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/07

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/07  
PRIOR FILING DATE: 1998-03-20

; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/083322

PRIOR APPLICATION NUMBER: 80/08  
PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600

;; PRIOR APPLICATION NUMBER: 00/08  
;; PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

;; PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087759

; PRIOR FILING DATE: 1998-06-02  
 ; PRIORITY DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03

PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/08

;; PRIOR APPLICATION NUMBER: 60/088021  
: PRIOR FILING DATE: 1998-06-04

; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/08

;; PRIOR APPLICATION NO:BSK: 60/08802

1	PRIOR APPLICATION NUMBER: 60/090244	
2	PRIOR FILING DATE: 1998-06-22	
3	PRIOR APPLICATION NUMBER: 60/090252	
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5	PRIOR APPLICATION NUMBER: 60/090254	
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7	PRIOR APPLICATION NUMBER: 60/090349	
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9	PRIOR APPLICATION NUMBER: 60/090355	
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12	PRIOR FILING DATE: 1998-06-24	
13	PRIOR APPLICATION NUMBER: 60/090431	
14	PRIOR FILING DATE: 1998-06-24	
15	PRIOR APPLICATION NUMBER: 60/090435	
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17	PRIOR APPLICATION NUMBER: 60/090444	
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19	PRIOR APPLICATION NUMBER: 60/090445	
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51	PRIOR APPLICATION NUMBER: 60/091544	
52	PRIOR FILING DATE: 1998-07-01	
53	PRIOR APPLICATION NUMBER: 60/091519	
54	PRIOR FILING DATE: 1998-07-02	
55	PRIOR APPLICATION NUMBER: 60/091626	
56	PRIOR FILING DATE: 1998-07-02	
57	PRIOR APPLICATION NUMBER: 60/091633	
58	PRIOR FILING DATE: 1998-07-02	
59	PRIOR APPLICATION NUMBER: 60/091978	
60	PRIOR FILING DATE: 1998-07-07	
61	PRIOR APPLICATION NUMBER: 60/091982	
62	PRIOR FILING DATE: 1998-07-07	
63	PRIOR APPLICATION NUMBER: 60/092182	
64	PRIOR FILING DATE: 1998-07-09	

	Query Match	100.0%;	Score 2185;	DB 11;	Length 2185;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2185;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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241 CCGCGCGCGCTCTCGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTCCT 300  
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301 TCATGAGAAACAACTCCAGATGATTCAGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTC 360  
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361 AGGTCCTGAGTGTGGCAAGAACTCCATCCGCGCAATGAGGTCCTCGAGGTCCTCGAGGTC 420  
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421 TGGCAGGTCCTCAACCTCTGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTC 480  
421 TGGCAGGTCCTCAACCTCTGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTCCTCGAGGTC 480  
481 CTTTGAATACCTGTCCAAAGTGTGCGGAGCTCTGCGCTTCGCAACCAACCCATCGAAAGCA 540  
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601 AGAAGTCGAGTATCTCTGAGGAGCTCTGAGGAGCTCTGAGGAGCTCTGAGGAGCTCTG 660  
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781 GCTCCCTCAAGAACTCTGAGTATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 840  
781 GCTCCCTCAAGAACTCTGAGTATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 840  
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1261 CTGTCTCTCAACGAGGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1320  
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1381 GACGGCTGAGTGTGACCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1440  
1381 GACGGCTGAGTGTGACCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1440  
1441 CGAGATCTGCGCTGAGGACCAACGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1500  
1441 CGAGATCTGCGCTGAGGACCAACGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1500  
1501 GTTACAGCGGCAATATACCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1560  
1501 GTTACAGCGGCAATATACCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1560  
1561 AGCAGTGTGAGTGTGAGGACCAACGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1620  
1561 AGCAGTGTGAGTGTGAGGACCAACGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1620  
1621 TCATGAGAACCCACCAAGATCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1680  
1621 TCATGAGAACCCACCAAGATCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1680  
1681 CCATGTTGATGTCTCTGATTAACCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1740  
1681 CCATGTTGATGTCTCTGATTAACCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1740  
1741 CCGCCCGGACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1800  
1741 CCGCCCGGACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1800  
1801 CAGCAACAGCAGTCTCGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1860  
1801 CAGCAACAGCAGTCTCGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1860  
1861 ATGACCATATTAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1920  
1861 ATGACCATATTAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1920  
1921 GCCTGGGAACTCTCTGACCCCAAGTCAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1980  
1921 GCCTGGGAACTCTCTGACCCCAAGTCAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1980  
1981 CCATATCCAGGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2040  
1981 CCATATCCAGGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2040  
2041 TAAATGTCAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2100  
2041 TAAATGTCAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2100  
2101 TTCTGTGTATGCTGTATATTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2160  
2101 TTCTGTGTATGCTGTATATTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2160  
2161 AATTTAAAGCAAAAAGTCAAAACA 2185  
2161 AATTTAAAGCAAAAAGTCAAAACA 2185

RESULT 41



JS-09-997-628-228  
; Sequence 228, Application US/09997628  
; Publication No. US20030059782A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C30  
; CURRENT APPLICATION NUMBER: US/09/997,628  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
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; PRIOR FILING DATE: 1997-11-13  
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; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
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PRIOR FILING DATE: 1998-07-02	
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PRIOR APPLICATION NUMBER: 60/091982	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/092182	
PRIOR FILING DATE: 1998-07-09	

	Query Match	100.0%;	Score 2185;	DB 11;	Length 2185;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2185;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
iy	1	GTTCCTCTTCCGAGCCAAAATCCACGGCGATGGTGAATTATGAACGTGCCACACCATGA	60		
ib	1	GTTCCTCTTCCGAGCCAAAATCCACGGCGATGGTGAATTATGAACGTGCCACACCATGA	60		
iy	61	AGCTCTTTGTGGCAGGTAACTGTGTGCACCAACACCTGTGGAATGCCATCTCTGTCCCGTTCCG	120		
ib	61	AGCTCTTTGTGGCAGGTAACTGTGTGCACCAACACCTGTGGAATGCCATCTCTGTCCCGTTCCG	120		
iy	121	TCTACCTCAGGGCCAGGTGTGGATTCTGTGTGCACCATCGCTGTGCGGCTCAGCG	180		
ib	121	TCTACCTCAGGGCCAGGTGTGGATTCTGTGTGCACCATCGCTGTGCGGCTCAGCG	180		
iy	181	GGCCCCAGAACTGCCCTCCGTTTGCTGTGTGCAGTAACCAAGTTTCAGCAAGGTGGTGTGCA	240		

181	Db		GGCCCCAGAACTGGCCCTCCGTTTGCTCGTGGTAAACAGTTACGAGGTGGTGTGCA	240
241	Qy		CGCGCGGGGCTCTCCGAGGTCCCGCAGGGGTATTCCTCTCGAAACAACCGGTACCTCAACC	300
241	Db		CGCGCGGGGCTCTCCGAGGTCCCGCAGGGTATTCCTCTCGAAACAACCGGTACCTCAACC	300
301	Qy		TCAATGAGAAACAATCAAGATGATCCAGGCCGACAACCTTCGGCCACCTCCACCACTCTGG	360
301	Db		TCAATGAGAAACAATCAAGATGATCCAGGCCGACAACCTTCGGCCACCTCCACCACTCTGG	360
361	Qy		AGGTCTCGAGTTGGCGAGAACTCCATCCGCGAGATTCAGGTGGGGGCTTTCAACGGCC	420
361	Db		AGGTCTCGAGTTGGCGAGAACTCCATCCGCGAGATTCAGGTGGGGGCTTTCAACGGCC	420
421	Qy		TGGCCAGCTCCAAACCCCTGGAGCTGTTTCGAACAATGGCTGACGTCACTCCCTAGGGGG	480
421	Db		TGGCCAGCTCCAAACCCCTGGAGCTGTTTCGAACAATGGCTGACGTCACTCCCTAGGGGG	480
481	Qy		CGTTTGAATACCTGTCCAAAGCTGGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCA	540
481	Db		CGTTTGAATACCTGTCCAAAGCTGGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCA	540
541	Qy		TCCCTCTTACGCCCTTCAACCCGGTGCCTCCCTCATGCGCTGAGACTTGGGGGAGCTCA	600
541	Db		TCCCTCTTACGCCCTTCAACCCGGTGCCTCCCTCATGCGCTGAGACTTGGGGGAGCTCA	600
601	Qy		AGAGCTGGAGTATATCTCTGAGGGAGCTTTGAGGGCTGTTCAACCTCAAGTATCTGA	660
601	Db		AGAGCTGGAGTATATCTCTGAGGGAGCTTTGAGGGCTGTTCAACCTCAAGTATCTGA	660
661	Qy		ACTTGGGCATGTGCAACTTAAGAACAATGCCAAATCTACCCCTCTGGTGGGCTCGAAG	720
661	Db		ACTTGGGCATGTGCAACTTAAGAACAATGCCAAATCTACCCCTCTGGTGGGCTCGAAG	720
721	Qy		AGCTGAGATGTCAGGGAACTCTCCCTGAGATCAGGCTCGCTCTCTTCCATGGGCTCA	780
721	Db		AGCTGAGATGTCAGGGAACTCTCCCTGAGATCAGGCTCGCTCTCTTCCATGGGCTCA	780
781	Qy		GCTCCCTCAAGAGCTCTGGGTCAFGAACTCAACAGGTCAGGCTGATGTGACGGGAATGCTT	840
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841	Qy		TTGACGGGCTGGCTTCACTTGTGGAATCTCACTTGGCCCAATATACCTCTCTCTTTTC	900
841	Db		TTGACGGGCTGGCTTCACTTGTGGAATCTCACTTGGCCCAATATACCTCTCTCTTTTC	900
901	Qy		CCCATGACCTCTTTACCCCGCTGAGGTACTGCTGTGAGTTGATCTTACACCAACACCTT	960
901	Db		CCCATGACCTCTTTACCCCGCTGAGGTACTGCTGTGAGTTGATCTTACACCAACACCTT	960
961	Qy		GGAACTGTGATTTGTGACATTTCTGTGCTAGCTGGCTTCGAGAGTATATACCAACCA	1020
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1021	Qy		ATTCCACTGCTGTGGCGCTGTCAATGCTCCCATGCACATGCGAGGCGCTACTCTGTGG	1080
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1081	Qy		AGGTGACCAAGGCTCTCTCCAGTGTCTGCCCCCTTCAATGGAACGCACTTCGAGAAC	1140
1081	Db		AGGTGGAACAGGCTCTCTTCCAGTGTCTGCCCCCTTCAATGGAACGCACTTCGAGAAC	1140
1141	Qy		TCAACATTTCTGAGGTCGATGGCAGAACTTAAGTGTGGACTCCCTCTATGTCCTCG	1200
1141	Db		TCAACATTTCTGAGGTCGATGGCAGAACTTAAGTGTGGACTCCCTCTATGTCCTCG	1200
1201	Qy		TGAGTGGTTGCTGCCCAATGGGACAGTGTCTCAGCCACGCTCCCGCCACCCCAAGATCT	1260
1201	Db		TGAGTGGTTGCTGCCCAATGGGACAGTGTCTCAGCCACGCTCCCGCCACCCCAAGATCT	1260
1261	Qy		CTGTCTCTCAACGACGGCACTTGAACTTTTCCCACTGTTGCTGCTTTCGACACTTGGGGTGT	1320

b 1261 CTGCTCTCAACGAGCGCACCTTGAACCTTTCCACGCTGCTGCTTTCCAGACACTGGGGTGT 1320  
y 1321 ACACATGCTATGCTGACCAATGCTGAGCACTCCAGCGCTCGGCTACTCTCAATGTGA 1380  
b 1321 ACACATGCTATGCTGACCAATGCTGAGCACTCCAGCGCTCGGCTACTCTCAATGTGA 1380  
y 1381 GCACGCTGAGCTTAACACCTCCACTACAGCTTTTCCACACAGTAACTAGTGGAGACCA 1440  
b 1381 GCACGCTGAGCTTAACACCTCCACTACAGCTTTTCCACACAGTAACTAGTGGAGACCA 1440  
y 1441 CGGAGATCTCGCTGAGGACACACGCGAAAGTAAAGCTGTTCCCTACCAGCTCCACTG 1500  
b 1441 CGGAGATCTCGCTGAGGACACACGCGAAAGTAAAGCTGTTCCCTACCAGCTCCACTG 1500  
y 1501 GTTACACGCGGATATACCACTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
b 1501 GTTACACGCGGATATACCACTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
y 1561 AGCAGTGGCAGTACCGCGGACAGACACCACTGACAGTACAGCAGCAGCTGATGAAG 1620  
b 1561 AGCAGTGGCAGTACCGCGGACAGACACCACTGACAGTACAGCAGCAGCTGATGAAG 1620  
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b 1621 TCATGAAGACCCCAAGATCATCATCTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
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b 1681 CCATGTTGATTTGCTTCTATTAACCTTCTGTAAGCGGACCCAGCAGGAGTACAGTACAG 1740  
y 1741 CGCCCGGACTGTTGAGTATATCCAGTGGGACGAGACATCCCAAGCAGCAGCAGCAGCAG 1800  
b 1741 CGCCCGGACTGTTGAGTATATCCAGTGGGACGAGACATCCCAAGCAGCAGCAGCAGCAG 1800  
y 1801 CAGCAACAGCAGCTCGCTCGGCTGATCATGCTGAGGCGGAGTAGTCTCCCAACATTC 1860  
b 1801 CAGCAACAGCAGCTCGCTCGGCTGATCATGCTGAGGCGGAGTAGTCTCCCAACATTC 1860  
y 1861 ATGACCATATTAATACAACTACAAACCCAGCAGCAGTATGCTGCTGCTGCTGCTGCTGCTG 1920  
b 1861 ATGACCATATTAATACAACTACAAACCCAGCAGCAGTATGCTGCTGCTGCTGCTGCTGCTG 1920  
y 1921 GCTGGGGAACCTCTGCAACCCCAAGTACCACTATCTCTGAACTTATATATATATATATAT 1980  
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b 1981 CCCTACCAAGGACAGGTACAGGAACTCAATATGACTCCCTCCCTCCCAAAAACTTA 2040  
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## RESULT 42

US-09-997-683-228  
; Sequence 228, Application US/09997683  
; Publication No. US20030059783A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS  
FILE REFERENCE: P2730P1C32  
CURRENT APPLICATION NUMBER: US/09/997,683  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE:	1998-06-24

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23	PRIOR APPLICATION NUMBER: 60/090696
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25	PRIOR APPLICATION NUMBER: 60/090862
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28	PRIOR FILING DATE: 1998-06-26
29	PRIOR APPLICATION NUMBER: 60/091360
30	PRIOR FILING DATE: 1998-07-01
31	PRIOR APPLICATION NUMBER: 60/091478
32	PRIOR FILING DATE: 1998-07-02
33	PRIOR APPLICATION NUMBER: 60/091544
34	PRIOR FILING DATE: 1998-07-01
35	PRIOR APPLICATION NUMBER: 60/091519
36	PRIOR FILING DATE: 1998-07-02
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38	PRIOR FILING DATE: 1998-07-02
39	PRIOR APPLICATION NUMBER: 60/091633
40	PRIOR FILING DATE: 1998-07-02
41	PRIOR APPLICATION NUMBER: 60/091978
42	PRIOR FILING DATE: 1998-07-07
43	PRIOR APPLICATION NUMBER: 60/091982
44	PRIOR FILING DATE: 1998-07-07
45	PRIOR APPLICATION NUMBER: 60/092182
46	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%	Score 2185;	DB 11;	Length 2185;
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QY	241	CGCGCGGGGGCTCTCGAGGTCCCGAGGGTATTCCTCTGACACACCCGGTACCTCAACC	300	
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QY	301	TCATGGAGAACAACTCCAGTATCCAGGCGGACACCTTTCGCGCACCTTCCACCACTGG	360	

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RESULT 43

US-09-989-729A-228  
; Sequence 228, Application US/09989729A  
; Publication NO. US2003005983A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.

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2161 AATTTAAAGACAAAAGTCAAAACA 2185  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC59  
CURRENT APPLICATION NUMBER: US/09/989,729A  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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32 PRIOR APPLICATION NUMBER: 60/091978  
33 PRIOR FILING DATE: 1998-07-07  
34 PRIOR APPLICATION NUMBER: 60/091982  
35 PRIOR FILING DATE: 1998-07-07  
36 PRIOR APPLICATION NUMBER: 60/092182  
37 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
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Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1381 GCAAGCTGAGCTTAAACCTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAA 1440  
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Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 GTTCTCTTTCCGAGCCAAATCCAGGCGATGTGTAATATGAACGTGCCACACCATGA 60  
DB 1 GTTCTCTTTCCGAGCCAAATCCAGGCGATGTGTAATATGAACGTGCCACACCATGA 60  
QY 61 AGCTTTGTGGAGGTAATCTGTGCACACACACACCTGGATGCATCTCTCCCTTCG 120  
DB 61 AGCTTTGTGGAGGTAATCTGTGCACACACACACCTGGATGCATCTCTCCCTTCG 120  
QY 121 TCTACCTCAGCGCGCAAGTGTGGATTTCTGTGTGACGCCATCGCTGTGCGGCTCAGCG 180  
DB 121 TCTACCTCAGCGCGCAAGTGTGGATTTCTGTGTGACGCCATCGCTGTGCGGCTCAGCG 180  
QY 181 GGCCCCAGAACTGCCCCCTCCGTTTGTGTGCGAGTAACCGATTTCAGCAAGGTGTGTGA 240  
DB 181 GGCCCCAGAACTGCCCCCTCCGTTTGTGTGCGAGTAACCGATTTCAGCAAGGTGTGTGA 240  
QY 241 CGGCGCGGGGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCCGGTACTCAACC 300  
DB 241 CGGCGCGGGGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCCGGTACTCAACC 300  
QY 301 TCATGGAGAAACAATCCAGATGATCCAGCCGACACCTTCGCCACCTCCACCACTGG 360  
DB 301 TCATGGAGAAACAATCCAGATGATCCAGCCGACACCTTCGCCACCTCCACCACTGG 360  
QY 361 AGGTCTTCGAGTTGGGCGAGAACTCCATCCGCGCAGATTGAGGTGGGGGCTTCAACGGCC 420  
DB 361 AGGTCTTCGAGTTGGGCGAGAACTCCATCCGCGCAGATTGAGGTGGGGGCTTCAACGGCC 420  
QY 421 TGGCAGCCTCAACACACCTTGGAGCTGTTGCAACACTGGCTGACAGTCATCCCTAGGGGG 480  
DB 421 TGGCAGCCTCAACACACCTTGGAGCTGTTGCAACACTGGCTGACAGTCATCCCTAGGGGG 480  
QY 481 CTTTGAATACCTGTCCAGCTGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540  
DB 481 CTTTGAATACCTGTCCAGCTGGGGAGCTCTGGCTTCGCAACACCCCATCGAAAGCA 540  
QY 541 TCCCTCTTACGCTTCAACCGGGTGCCTCCCTCATGCGCCTTGGAGCTTGGGGAGCTCA 600  
DB 541 TCCCTCTTACGCTTCAACCGGGTGCCTCCCTCATGCGCCTTGGAGCTTGGGGAGCTCA 600

601	Y	AGAA	AGCTGGAGTATATCTCTGAGGGAGAGCTTTTGGAGGGGCTGTTTCAACCTCAAGTATCTCGA	660
601	b	AGA	AGCTGGAGTATATCTCTGAGGGAGAGCTTTTGGAGGGGCTGTTTCAACCTCAAGTATCTCGA	660
661	Y	ACTT	GGGCATGTGCAACATTTAAAGACATGCCCAACTCTCAACCCCTGCTGCTGGCTGGAGG	720
661	b	ACTT	GGGCATGTGCAACATTTAAAGACATGCCCAACTCTCAACCCCTGCTGCTGGCTGGAGG	720
721	Y	AGCT	TGGAGATGTTCAGGAAACCACTTCTCTGGAGATCAGGCTTGGCTCTCTTCCATGGGCTCTGA	780
721	b	AGCT	TGGAGATGTTCAGGAAACCACTTCTCTCTGGAGATCAGGCTTGGCTCTCTTCCATGGGCTCTGA	780
781	Y	GCT	CTCCCTCAGAAAGCTCTCGGTCATGAACCTCACAGCTCAGGCTCATTTGACGGAAATGCTT	840
781	b	GCT	CTCCCTCAGAAAGCTCTCGGTCATGAACCTCACAGCTCAGGCTCATTTGACGGAAATGCTT	840
841	Y	TTGA	CGGGCTGGGCTTCACCTTGTGGAACTCAAACTTTGGCCCCAATAAAGCTCTCTCTTTTGC	900
841	b	TTGA	CGGGCTGGGCTTCACCTTGTGGAACTCAAACTTTGGCCCCAATAAAGCTCTCTCTTTTGC	900
901	Y	CCCA	TGACCTTTTACCGCGCTGAGGTACCTGGTGGAGTTGCATCTACACACAAACCCCTT	960
901	b	CCA	TGACCTTTTACCGCGCTGAGGTACCTGGTGGAGTTGCATCTACACACAAACCCCTT	960
961	Y	GGAA	CTGTGATTTGACATTTCTGTGGCTAGCTTGGCTTGGCTTCGAGAGTATATACCCACCA	1020
961	b	GGAA	CTGTGATTTGACATTTCTGTGGCTAGCTTGGCTTGGCTTCGAGAGTATATACCCACCA	1020
1021	Y	ATT	CCACTGCTGTGGCGGCTGTCACTGCTCCCATGCAATCGGAGCGGCTACCTGTGTG	1080
1021	b	ATT	CCACTGCTGTGGCGGCTGTCACTGCTCCCATGCAATCGGAGCGGCTACCTGTGTG	1080
1081	Y	AGT	TGACAGGCGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGAGAGCGACCTCGAGACC	1140
1081	b	AGT	TGACAGGCGCTCTTCCAGTGTCTGTGCCCCCTTCATCATGAGAGCGACCTCGAGACC	1140
1141	Y	TCAA	CATTTCTGAGGCTGGATGGCAGAACTTTAAGTGTGGAGCTTCCCGCTATGTCTCTCG	1200
1141	b	TCAA	CATTTCTGAGGCTGGATGGCAGAACTTTAAGTGTGGAGCTTCCCGCTATGTCTCTCG	1200
1201	Y	TGA	GTGTTGCTGCCCATGAGCAGTGTCTCAGCCAGCGCTCCCGCCACCCAGGAGTCT	1260
1201	b	TGA	GTGTTGCTGCCCATGAGCAGTGTCTCAGCCAGCGCTCCCGCCACCCAGGAGTCT	1260
1261	Y	CTGT	CTCTCAACGAGCGACCTTTTCCACGTGCTGCTTTTCAGACACTGGGGTGT	1320
1261	b	CTGT	CTCTCAACGAGCGACCTTTTCCACGTGCTGCTTTTCAGACACTGGGGTGT	1320
1321	Y	ACAT	ATCATGTTGACGATTTGACGCACTTCCAAAGCTTCCAAAGCTTCCCTCAATGCTGA	1380
1321	b	ACAT	ATCATGTTGACGATTTGACGCACTTCCAAAGCTTCCAAAGCTTCCCTCAATGCTGA	1380
1381	Y	GCAC	GGCTGAGCTTAAACCTCTCAACCTTACAGCTTCTTCCACCAAGTAAACAGTGGAGACCA	1440
1381	b	GCAC	GGCTGAGCTTAAACCTCTCAACCTTACAGCTTCTTCCACCAAGTAAACAGTGGAGACCA	1440
1441	Y	CGGA	GTCTGCTGCTGAGGACACAAACCGGAAAGTACAGCTTGTCTTACCAAGTCTCACTG	1500
1441	b	CGGA	GTCTGCTGCTGAGGACACAAACCGGAAAGTACAGCTTGTCTTACCAAGTCTCACTG	1500
1501	Y	GTT	ACAGCGGATATACCACTCTTACCAAGTGTCTTCAATTCAGACTACCGGTGCGCCA	1560
1501	b	GTT	ACAGCGGATATACCACTCTTACCAAGTGTCTTCAATTCAGACTACCGGTGCGCCA	1560
1561	Y	AGCA	GTGGCAGTACCGGAGACACCACTTGAACAAGTGCAGACGAGCTTGATGAAG	1620
1561	b	AGCA	GTGGCAGTACCGGAGACACCACTTGAACAAGTGCAGACGAGCTTGATGAAG	1620
1621	Y	TCA	TGAAGACCAACAAGTATCATTTGGCTGCTTTGTGGCAGTGACTCTGTAGCTCGG	1680
1621	b	TCAT	TGAAGACCAACAAGTATCATTTGGCTGCTTTGTGGCAGTGACTCTGTAGCTCGG	1680
1681	Y	CCAT	GTGATTTGCTTCTTATAACTTCGTAAAGCGGACCAAGACGGAGTAAAGTACAG	1740

Db	1681	CCAGTGTGATGTCTCTTATAAATCTCGTAGCGGCRCCAGACGCGAGTTCAGTCCACAG	1740
Qy	1741	CCSCCCGGACTGTGAGATAATCCAGGTGGAAGAAGACATCCAGCAGCAACATCCGCAG	1800
Db	1741	CCSCCCGGACTGTGAGATAATCCAGGTGGAAGAAGACATCCAGCAGCAACATCCGCAG	1800
Qy	1801	CAGCAACAGCAGCTCCGTCCGGTGTATCAGTGTAGGGGGCAGTAGTGTCTGCCCACAATTC	1860
Db	1801	CAGCAACAGCAGCTCCGTCCGGTGTATCAGTGTAGGGGGCAGTAGTGTCTGCCCACAATTC	1860
Qy	1861	ATGACCATATTAACTACACACCTCAAAACCCAGCACATGGGGCCCACTGGACAGAAAACA	1920
Db	1861	ATGACCATATTAACTACACACCTCAAAACCCAGCACATGGGGCCCACTGGACAGAAAACA	1920
Qy	1921	GCCTGGGGAACTCTCTGCAACCCACACAGTACCACTATCTCTGAAACCTTATATTAATTCAGA	1980
Db	1921	GCCTGGGGAACTCTCTGCAACCCACACAGTACCACTATCTCTGAAACCTTATATTAATTCAGA	1980
Qy	1981	CCCATACCAAGGACAGGTACAGGAAACTCCAATATGACTCCCTCCGCCCAAAAACTTAA	2040
Db	1981	CCCATACCAAGGACAGGTACAGGAAACTCCAATATGACTCCCTCCGCCCAAAAACTTAA	2040
Qy	2041	TAAATATGCAATAGAAATGACACAAAGAAGACGAACTTTTGTACAGAGTGGGGAGAGACTTT	2100
Db	2041	TAAATATGCAATAGAAATGACACAAAGAAGACGAACTTTTGTACAGAGTGGGGAGAGACTTT	2100
Qy	2101	TTCTCTGTATATGCTTATATTAAGTCTATGGCTGGTTAAAAAAGAACAGATTATATTAA	2160
Db	2101	TTCTCTGTATGCTTATATTAAGTCTATGGCTGGTTAAAAAAGAACAGATTATATTAA	2160
Qy	2161	AAATTTAAAGCAAAAAGTCAAAAACA	2185
Db	2161	AAATTTAAAGCAAAAAGTCAAAAACA	2185

## RESULT 45

RESULT 45

US-09-997-440-228

Sequence 228, Application US/09997440

Publication No. US20030059833A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P273091C31

CURRENT APPLICATION NUMBER: US/09/997,440

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

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Prior Filing Date: 1998-06-26  
Prior Application Number: 60/091360  
Prior Filing Date: 1998-07-01  
Prior Application Number: 60/091478  
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Y 1 GTTCTCTTCCGAGCCAAATCCAGGCGATGGTGAATATGAACTGGCGACACCATGA 60  
b 1 GTTCTCTTCCGAGCCAAATCCAGGCGATGGTGAATATGAACTGGCGACACCATGA 60  
Y 61 AGCTCTTGTGGCAGTAACTGTGCACACCACTGGAAATGCCATCTGCTCCGTTTCG 120  
b 61 AGCTCTTGTGGCAGTAACTGTGCACACCACTGGAAATGCCATCTGCTCCGTTTCG 120  
Y 121 TCTACTCTACCGCGCAAGTGTGGAATCTGTGTGAGCCATGCTGCTGCGCTCAGCG 180  
b 121 TCTACTCTACCGCGCAAGTGTGGAATCTGTGTGAGCCATGCTGCTGCGCTCAGCG 180  
Y 181 GGCCCGAGAACTGCCCTCGTTGCTGTCAGTAACAGATTGAGAGGTGGTGCA 240  
b 181 GGCCCGAGAACTGCCCTCGTTGCTGTCAGTAACAGATTGAGAGGTGGTGCA 240  
Y 241 CGCGCGGGGCTCTCCGAGGTCCGAGGTATTCCTTCGAACCCCGGTACCTCAACC 300  
b 241 CGCGCGGGGCTCTCCGAGGTCCGAGGTATTCCTTCGAACCCCGGTACCTCAACC 300  
Y 301 TCATGAGAACAACTCCAGATATCCAGGCGACCTTCGCGCACTCCACCTGG 360  
b 301 TCATGAGAACAACTCCAGATATCCAGGCGACCTTCGCGCACTCCACCTGG 360  
Y 361 AGTCTCTGAGTTGGGAGGACTCCATCCGAGATTTGAGTGGGGGCTTCAAGGCC 420  
b 361 AGTCTCTGAGTTGGGAGGACTCCATCCGAGATTTGAGTGGGGGCTTCAAGGCC 420  
Y 421 TGGCCAGCTTCAACACCTGGAGCTGTCGACAACTGGCTGACATCTCCCTAGCGGG 480  
b 421 TGGCCAGCTTCAACACCTGGAGCTGTCGACAACTGGCTGACATCTCCCTAGCGGG 480  
Y 481 CTTTGGATACCTGTCAGGAGCTGTCGAGGAGCTTTGAGGGGCTTCAAGTATCTGA 540  
b 481 CTTTGGATACCTGTCAGGAGCTGTCGAGGAGCTTTGAGGGGCTTCAAGTATCTGA 540  
Y 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGAGCTTGGGGAGCTCA 600  
b 541 TCCCTCTTACGCTTCAACCGGGTCCCTCCCTCATGCGCTGAGCTTGGGGAGCTCA 600  
Y 601 AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCACTCAAGTATCTGA 660  
b 601 AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCACTCAAGTATCTGA 660  
Y 661 ACTTGGGATGTCAACATTAAAGACATCCCAATCTCACCCCTGTTGGGGCTGGAGG 720  
b 661 ACTTGGGATGTCAACATTAAAGACATCCCAATCTCACCCCTGTTGGGGCTGGAGG 720  
Y 721 AGCTGGAGATGTGAGGAGACCACTTCCCTGAGATCAGGCTGCTTCCATGSCCTGA 780

721 AGCTGGAGATGTGAGGAGACCACTTCCCTGAGATCAGGCTGCTCCCTCCATGSCCTGA 780  
Y 781 GCTCCCTCAAGAGCTCTGGGTGATGAGTCTCAGGTGAGCTGAGCTGAGGAGTCTT 840  
b 781 GCTCCCTCAAGAGCTCTGGGTGATGAGTCTCAGGTGAGCTGAGCTGAGGAGTCTT 840  
Y 841 TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTTCTTGC 900  
b 841 TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTTCTTGC 900  
Y 901 CCATGAGCTCTTTTACCCGCTGAGGTACTCTGGTGGAGTGTGATCTACACCAACCTT 960  
b 901 CCATGAGCTCTTTTACCCGCTGAGGTACTCTGGTGGAGTGTGATCTACACCAACCTT 960  
Y 961 GGAATGTGATTTGACATCTTGTGGTGGCTTGGTGGCTTGGAGTATATACCCACCA 1020  
b 961 GGAATGTGATTTGACATCTTGTGGTGGCTTGGTGGCTTGGAGTATATACCCACCA 1020  
Y 1021 ATTCCACCTGCTGGCCGCTGCTCATGCTCCATGACATGAGGCGGCTACCTGCTGG 1080  
b 1021 ATTCCACCTGCTGGCCGCTGCTCATGCTCCATGACATGAGGCGGCTACCTGCTGG 1080  
Y 1081 AGGTGAGACGAGGCTCTTCCAGTCTCTGCGCCCTTCCATGATGAGGAGCTCCGAGCC 1140  
b 1081 AGGTGAGACGAGGCTCTTCCAGTCTCTGCGCCCTTCCATGATGAGGAGCTCCGAGCC 1140  
Y 1141 TCAACATTTCTGAGGCTGGATGGCAGAACTTAAAGTGTGGACTCCCTTATGTCTCTCG 1200  
b 1141 TCAACATTTCTGAGGCTGGATGGCAGAACTTAAAGTGTGGACTCCCTTATGTCTCTCG 1200  
Y 1201 TGAAGTGTGCTGCCAATGGGACAGTCTCAGCCAGCTTCCGCGCCACCAAGAGTCT 1260  
b 1201 TGAAGTGTGCTGCCAATGGGACAGTCTCAGCCAGCTTCCGCGCCACCAAGAGTCT 1260  
Y 1261 CTGCTCTCAAGAGGAGCACTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1320  
b 1261 CTGCTCTCAAGAGGAGCACTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1320  
Y 1321 ACATGCTGAGTGGTGGAGCACTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1380  
b 1321 ACATGCTGAGTGGTGGAGCACTTGAACCTTTTCCACAGTGTCTTTCAGACACTGGGGTGT 1380  
Y 1381 GCAGGCTGAGCTTAACTCTCAACTGAGTCTTCCACAGTGTCTTTCAGACACTGGGGTGT 1440  
b 1381 GCAGGCTGAGCTTAACTCTCAACTGAGTCTTCCACAGTGTCTTTCAGACACTGGGGTGT 1440  
Y 1441 CGAGGCTGAGCTTAACTCTCAACTGAGTCTTCCACAGTGTCTTTCAGACACTGGGGTGT 1500  
b 1441 CGAGGCTGAGCTTAACTCTCAACTGAGTCTTCCACAGTGTCTTTCAGACACTGGGGTGT 1500  
Y 1501 GTTACAGGCGGATATACCTCTTACCAAGTGTCTTTCAGACACTGGGGTGTCCCA 1560  
b 1501 GTTACAGGCGGATATACCTCTTACCAAGTGTCTTTCAGACACTGGGGTGTCCCA 1560  
Y 1561 AGCAGGTGGAGTATCCCGGAGACCACTGACAGTGTGAGGAGTGTGAGTGTGAG 1620  
b 1561 AGCAGGTGGAGTATCCCGGAGACCACTGACAGTGTGAGGAGTGTGAGTGTGAG 1620  
Y 1621 TCAAGAGGAGTATCCCGGAGACCACTGACAGTGTGAGGAGTGTGAGTGTGAG 1680  
b 1621 TCAAGAGGAGTATCCCGGAGACCACTGACAGTGTGAGGAGTGTGAGTGTGAG 1680  
Y 1681 CCAATGAGTGTCTTCTTAACTTCTGAGGAGTGTGAGGAGTGTGAGTGTGAG 1740  
b 1681 CCAATGAGTGTCTTCTTAACTTCTGAGGAGTGTGAGGAGTGTGAGTGTGAG 1740  
Y 1741 CGCGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800  
b 1741 CGCGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800  
Y 1801 CAGCAACAGGCTCTGCTGCTGATCAGGTGAGGAGTGTGCTGCTGCTGCTGCTGCT 1860

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Qy	1	GTCTCTCTTCGAGCCAAAATCCGAGCGATGTGAATTATGAACGTGCCACACATGA	60
Db	1	GTCTCTCTTCGAGCCAAAATCCGAGCGATGTGAATTATGAACGTGCCACACATGA	60
Qy	61	AGCTCTTGTGGCAGGTAACTGTGCACCAACCTGGATGCATCTCTCCGCTTCG	120
Db	61	AGCTCTTGTGGCAGGTAACTGTGCACCAACCTGGATGCATCTCTCCGCTTCG	120
Qy	121	TCTACCTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCATCTCTGCTGCGCCTCAGCG	180
Db	121	TCTACCTCAGCGCGCAAGTGTGATTTCTGTGTGCAGCATCTCTGCTGCGCCTCAGCG	180
Qy	181	GGCCCCAGAACTGCCCTCTCCGTTTCTGTGTGCAGTAAACAGTTTCAGCAAGTGTGTGA	240
Db	181	GGCCCCAGAACTGCCCTCTCCGTTTCTGTGTGCAGTAAACAGTTTCAGCAAGTGTGTGA	240
Qy	241	CGCGCGGGGCTCTCCGAGGTCGCGAGGTTATTCCTCGAACACCCGGTACCTCAACC	300
Db	241	CGCGCGGGGCTCTCCGAGGTCGCGAGGTTATTCCTCGAACACCCGGTACCTCAACC	300
Qy	301	TCATGGAGAACAACTCCAGATGATCCAGGCGGACACCTTCGCGCACTCTCAACCTGG	360
Db	301	TCATGGAGAACAACTCCAGATGATCCAGGCGGACACCTTCGCGCACTCTCAACCTGG	360
Qy	361	AGCTCTCTGAGTTGGGCGAGAACTCCATCCGCGAGATGAGGTGGGGGCTTCACGGCC	420
Db	361	AGCTCTCTGAGTTGGGCGAGAACTCCATCCGCGAGATGAGGTGGGGGCTTCACGGCC	420
Qy	421	TGCGCAGCTCAACACCTCGGAGCTCTTCGACAACTGGCTGACAGTATCTCCCTAGCGGG	480
Db	421	TGCGCAGCTCAACACCTCGGAGCTCTTCGACAACTGGCTGACAGTATCTCCCTAGCGGG	480
Qy	481	CTTTGAATACCTGTCCAAAGCTCGGGAGCTCTGGCTTGGCAACACCCCATCGAAGCA	540
Db	481	CTTTGAATACCTGTCCAAAGCTCGGGAGCTCTGGCTTGGCAACACCCCATCGAAGCA	540
Qy	541	TCCCTCTTACGCTTCAACCGGGTCCCTCTCATGGGCTGCACTTGGGGGAGCTCA	600
Db	541	TCCCTCTTACGCTTCAACCGGGTCCCTCTCATGGGCTGCACTTGGGGGAGCTCA	600
Qy	601	AGAGCTGGAGTATATCTCTGAGGGAGCTTTTGGAGGGCTGTTCACCTCAAGTATCTGA	660
Db	601	AGAGCTGGAGTATATCTCTGAGGGAGCTTTTGGAGGGCTGTTCACCTCAAGTATCTGA	660
Qy	661	ACTTGGGCAATGTGCAACATTAAGCATGCCCAATCTCAACCCCTGGTGGGGCTGGAG	720
Db	661	ACTTGGGCAATGTGCAACATTAAGCATGCCCAATCTCAACCCCTGGTGGGGCTGGAG	720
Qy	721	AGCTGGAGATGTGAGGGAACCACTTCCCTGAGATCAGGCTGGCTCTTCTCCATGGCTGA	780
Db	721	AGCTGGAGATGTGAGGGAACCACTTCCCTGAGATCAGGCTGGCTCTTCTCCATGGCTGA	780
Qy	781	GCTCCCTCAAGAGCTCTGGGTGATGAATCTACAGCTCAGCTGATTCAGCGGAATGCTT	840
Db	781	GCTCCCTCAAGAGCTCTGGGTGATGAATCTACAGCTCAGCTGATTCAGCGGAATGCTT	840
Qy	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTCTTTCG	900
Db	841	TTGACGGGCTGGCTTCACTTGTGGAACTCAACTTGGCCCAACAATAACCTCTCTCTTTCG	900





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7	PRIOR FILING DATE: 1998-07-02
7	PRIOR APPLICATION NUMBER: 60/091378
7	PRIOR FILING DATE: 1998-07-07
7	PRIOR APPLICATION NUMBER: 60/091982
7	PRIOR FILING DATE: 1998-07-07
7	PRIOR APPLICATION NUMBER: 60/092182

7 PRIOR PILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
 Best local Similarity 100.0%; Pred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTCTCTTCGAGCCAAATCCAGGCGATGTGAATATGAAGTGCACACCATGA 60  
 DB 1 GTCTCTCTTCGAGCCAAATCCAGGCGATGTGAATATGAAGTGCACACCATGA 60  
 QY 61 AGCTCTTGTGCGAGTAACTGTGACCAACACACCTCGCAATGCCATCTGCTCCGCTTCG 120  
 DB 61 AGCTCTTGTGCGAGTAACTGTGACCAACACACCTCGCAATGCCATCTGCTCCGCTTCG 120  
 QY 121 TCTACTCTCAOGCGCAAGTGTGATTCGTGTGAGCCATCGCTGTGCGGCTCAGCGG 180  
 DB 121 TCTACTCTCAOGCGCAAGTGTGATTCGTGTGAGCCATCGCTGTGCGGCTCAGCGG 180  
 QY 181 GSCCCAGAACTGCCCTCCGCTTGTCTGTGTCAGTAAACCAAGTTCAGCAAGTGTGTGCA 240  
 DB 181 GSCCCAGAACTGCCCTCCGCTTGTCTGTGTCAGTAAACCAAGTTCAGCAAGTGTGTGCA 240  
 QY 241 CGCGCGGCGCTCTCGAGGTCGCGAGGATTCCTCGGACACCGGTAACCTCAAC 300  
 DB 241 CGCGCGGCGCTCTCGAGGTCGCGAGGATTCCTCGGACACCGGTAACCTCAAC 300  
 QY 301 TCATGGAGAACAACTCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTGG 360  
 DB 301 TCATGGAGAACAACTCCAGATGATCCAGGCGGACACCTTCGCGCACCTCCACCACTGG 360  
 QY 361 AGCTCTCTGAGTGGGCGAGGACTCCATCCGCGAGATTGAGTGGGGGCTTCAAGCGCC 420  
 DB 361 AGCTCTCTGAGTGGGCGAGGACTCCATCCGCGAGATTGAGTGGGGGCTTCAAGCGCC 420  
 QY 421 TGGCGAGCTCAACACCTCGAGCTGTTCGACAACTGCTGACAGTCACTCCCTAGCGGGG 480  
 DB 421 TGGCGAGCTCAACACCTCGAGCTGTTCGACAACTGCTGACAGTCACTCCCTAGCGGGG 480  
 QY 481 CCTTTGAATACCTGTCAGGAGCTTTGAGGCGCTTGGCTTCGCAACACCCATCGAAGCA 540  
 DB 481 CCTTTGAATACCTGTCAGGAGCTTTGAGGCGCTTGGCTTCGCAACACCCATCGAAGCA 540  
 QY 541 TCCCTCTTAGCCCTTCAACCGGCTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCA 600  
 DB 541 TCCCTCTTAGCCCTTCAACCGGCTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCA 600  
 QY 601 AGAAGCTGAGTATCTCTCAGGAGCTTTGAGGCGCTTGGCTTCAGCTCAAGTATCTGA 660  
 DB 601 AGAAGCTGAGTATCTCTCAGGAGCTTTGAGGCGCTTGGCTTCAGCTCAAGTATCTGA 660  
 QY 661 ACTTGGGCACTGCAACATTAAGACATGCCCCATCTCACCCCCCTGGTGGGCTGGAGG 720  
 DB 661 ACTTGGGCACTGCAACATTAAGACATGCCCCATCTCACCCCCCTGGTGGGCTGGAGG 720  
 QY 721 AGCTGGAGATGTCAGGAGCACTCTCCTGAGATCAGGCGCTGCTCTTCAATGGCTGA 780  
 DB 721 AGCTGGAGATGTCAGGAGCACTCTCCTGAGATCAGGCGCTGCTCTTCAATGGCTGA 780  
 QY 781 GCTCCTCTCAAGAGCTCTGGGTCATGAACCTCAGAGTCAAGCTGATGAGCGGAATGCTT 840  
 DB 781 GCTCCTCTCAAGAGCTCTGGGTCATGAACCTCAGAGTCAAGCTGATGAGCGGAATGCTT 840  
 QY 841 TTGAGGCGCTGGCTCACTTGTGGAATCTCAACTTGGCGCCACATACCTCTCTCTTTTC 900  
 DB 841 TTGAGGCGCTGGCTCACTTGTGGAATCTCAACTTGGCGCCACATACCTCTCTCTTTTC 900  
 QY 901 CCCATGACCTTTTACCCCGCTGAGGTACCTGTGTGAGTTGCACTCAGACCAACACCTTT 960  
 DB 901 CCCATGACCTTTTACCCCGCTGAGGTACCTGTGTGAGTTGCACTCAGACCAACACCTTT 960  
 QY 961 GGAAGTGTGATGCACTTCTGTGGCTAGCTGTGGCTTTCAGAGTATATACCCCA 1020  
 DB 961 GGAAGTGTGATGCACTTCTGTGGCTAGCTGTGGCTTTCAGAGTATATACCCCA 1020

QY 1021 ATTCCACTGCTGTGCGCTGTCTGCTATGCTCCATGACATCGAGGCGCTTACCTCGTGG 1080  
 DB 1021 ATTCCACTGCTGTGCGCTGTCTGCTATGCTCCATGACATCGAGGCGCTTACCTCGTGG 1080  
 QY 1081 AGTGGACACAGGCTCTCTTCCAGTGTCTGCGCCCTTCAATGATGAGACACCTCGAGCC 1140  
 DB 1081 AGTGGACACAGGCTCTCTTCCAGTGTCTGCGCCCTTCAATGATGAGACACCTCGAGCC 1140  
 QY 1141 TCAACATTTCTGAGGCTCGGATGCGAGAACTTAAAGTGTGCGACTTCCCTATGCTCTCG 1200  
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 QY 1201 TGAAGTGTGCTGCGCAATGSGACAGTGTCTCAGCACAAGCTCCGCGCACCAAGGATCT 1260  
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 QY 1261 CTCTCTCAACACAGGCTCTTAAACTTTTCCAGCTGTCTCTTTCAGACACTGGGGTGT 1320  
 DB 1261 CTCTCTCAACACAGGCTCTTAAACTTTTCCAGCTGTCTCTTTCAGACACTGGGGTGT 1320  
 QY 1321 ACATGCGATGCTGACCAATGTCAGGCACTTCCAAAGCTCCGCGCTTACCTCAATGTGA 1380  
 DB 1321 ACATGCGATGCTGACCAATGTCAGGCACTTCCAAAGCTCCGCGCTTACCTCAATGTGA 1380  
 QY 1381 GCAGGCTGAGCTTAACTTCAACTTCAAGCTTCTTCAACAGTAACTGAGGAGCA 1440  
 DB 1381 GCAGGCTGAGCTTAACTTCAACTTCAAGCTTCTTCAACAGTAACTGAGGAGCA 1440  
 QY 1441 CGGAGTCTCGCTGAGGACACAGCGGAAAGTACAAAGCTTCTTCAACAGTAACTGAGGAG 1500  
 DB 1441 CGGAGTCTCGCTGAGGACACAGCGGAAAGTACAAAGCTTCTTCAACAGTAACTGAGGAG 1500  
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 DB 1621 TCAAGAGACCAACCAAGATCATCTTGTGCTGCTTGTGCGAGTGAAGTGTGCTGCTGCG 1680  
 QY 1681 CCATGTTGATCTCTTCTATTAACCTTCTGTAAGCGGACACAGCGGAGTACAGTCAAG 1740  
 DB 1681 CCATGTTGATCTCTTCTATTAACCTTCTGTAAGCGGACACAGCGGAGTACAGTCAAG 1740  
 QY 1741 CGCCCGGACTGTGAGATTAATCCAGGTGGAAGAGCATCCAGAGCAACATCCGAG 1800  
 DB 1741 CGCCCGGACTGTGAGATTAATCCAGGTGGAAGAGCATCCAGAGCAACATCCGAG 1800  
 QY 1801 CAGCACAGGCTCGCTCGGCTGATCAGGTGAGGCGGAGTGTGCTGCCACAATTC 1860  
 DB 1801 CAGCACAGGCTCGCTCGGCTGATCAGGTGAGGCGGAGTGTGCTGCCACAATTC 1860  
 QY 1861 ATGACCATTAATTAACCAACCTTACAAACAGGACATGAGGCGGCTTGGACAGAAACA 1920  
 DB 1861 ATGACCATTAATTAACCAACCTTACAAACAGGACATGAGGCGGCTTGGACAGAAACA 1920  
 QY 1921 GCTTGGGAACTCTCTGACCCCAAGTCAAGTCACTTCTCTGAACCTTATATATTCAGA 1980  
 DB 1921 GCTTGGGAACTCTCTGACCCCAAGTCAAGTCACTTCTCTGAACCTTATATATTCAGA 1980  
 QY 1981 CCATACCAAGGACAGGATACAGGAACTCAAAATATGACTCCCTCCCGCAAAACTTA 2040  
 DB 1981 CCATACCAAGGACAGGATACAGGAACTCAAAATATGACTCCCTCCCGCAAAACTTA 2040  
 QY 2041 TAAATGCAATGAGTACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGCTTT 2100  
 DB 2041 TAAATGCAATGAGTACACAAAGACAGCACTTTTGTACAGAGTGGGAGAGCTTT 2100

Y 2101 TTCTGTATATGCTTATATATTAAGTCTATGGCTGGTTTAAAAAACAAGATTATATAA 2160  
b 2101 TTCTGTATATGCTTATATATTAAGTCTATGGCTGGTTTAAAAAACAAGATTATATAA 2160  
Y 2161 AATTAAAGCAAAAAGTCAAAACA 2185  
b 2161 AATTAAAGCAAAAAGTCAAAACA 2185

## RESULT 48

S-09-997-542-228  
Sequence 228, Application US/09997542  
Publication No. US20030068647A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pasni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C26  
CURRENT APPLICATION NUMBER: US/09/997,542  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 1 GTTCTCCCTTCGAGCCCAAAATCCAGCGGATGTAATTATGAACGTGCCACACCATGA 60

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DB	61	AGCTCTTGTGGCAGTAACTGTGCACCAACACCTTGGAAATGCCATCTCTGCTCCCGTTGC	120
QY	121	TCTACTCTACCGCGCAAGTGTGGATTCTGTGTGAGCATCGCTGCTGCGCGCTCAGCGG	180
DB	121	TCTACTCTACCGCGCAAGTGTGGATTCTGTGTGAGCATCGCTGCTGCGCGCTCAGCGG	180
QY	181	GGCCCCAGAACTGCCCTCCGTTTGTCTGTGCACTAACCAAGTTTCAGCAAGTGTGTGCA	240
DB	181	GGCCCCAGAACTGCCCTCCGTTTGTCTGTGCACTAACCAAGTTTCAGCAAGTGTGTGCA	240
QY	241	CGCGCGCGGCTCTTCGAGTCCCGCAGGGTATTCCTCGAACCACCGGTACCTCAACC	300
DB	241	CGCGCGCGGCTCTTCGAGTCCCGCAGGGTATTCCTCGAACCACCGGTACCTCAACC	300
QY	301	TCATGGAGAACAAATCCAGATATCCAGGCGGACACCTTCGCGACCTCCACCACTGG	360
DB	301	TCATGGAGAACAAATCCAGATATCCAGGCGGACACCTTCGCGACCTCCACCACTGG	360
QY	361	AGGTCCTTCAGTTGGCGCAGGAACTCCATCCGCGCAGATTGAGTGGGGGCTTCAAAGGCC	420
DB	361	AGGTCCTTCAGTTGGCGCAGGAACTCCATCCGCGCAGATTGAGTGGGGGCTTCAAAGGCC	420
QY	421	TGGCCAGGCTCAACACCTTGGAGCTGTTGCAACACTGGCTGACAGTCACTCCCTAGCGGG	480
DB	421	TGGCCAGGCTCAACACCTTGGAGCTGTTGCAACACTGGCTGACAGTCACTCCCTAGCGGG	480
QY	481	CCTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACCAACCCCATCGAAAGCA	540
DB	481	CCTTTGAATACCTGTCCAAAGCTGCGGAGCTCTGGCTTCGCAACCAACCCCATCGAAAGCA	540
QY	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATCGCGCTGGAGTGGGGGAGCTCA	600
DB	541	TCCCTCTTACGCTTCAACCGGCTGCTCCCTCATCGCGCTGGAGTGGGGGAGCTCA	600
QY	601	AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660
DB	601	AGAGCTGGAGTATCTCTGAGGAGCTTTGAGGGGCTTTCAACCTCAAGTATCTGA	660
QY	661	ACTTGGGATGTGCAACATTAAGACATGCCCAATCTCAACCCCTGGTGGGGGAGCTCA	720
DB	661	ACTTGGGATGTGCAACATTAAGACATGCCCAATCTCAACCCCTGGTGGGGGAGCTCA	720
QY	721	AGCTGGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGGCTGA	780
DB	721	AGCTGGAGATGTGAGGAAACCACTTCCCTGAGATCAGGCTGGCTTCCATGGGCTGA	780
QY	781	GCTCCCTCAAGAACTCTGGGTCACTGAACTCACAGGTCAAGCTGAGTGGGGAATGCTT	840
DB	781	GCTCCCTCAAGAACTCTGGGTCACTGAACTCACAGGTCAAGCTGAGTGGGGAATGCTT	840
QY	841	TTGAGGGCTGGCTTCACTTGTGGAATCAACTTGGCGCCCAATAACTCTCTCTTTTC	900
DB	841	TTGAGGGCTGGCTTCACTTGTGGAATCAACTTGGCGCCCAATAACTCTCTCTTTTC	900
QY	901	CCCATGACCTCTTTTACCCCGCTGAGTACCTGTGGAGTTGCACTTACCAACCAACCTT	960
DB	901	CCCATGACCTCTTTTACCCCGCTGAGTACCTGTGGAGTTGCACTTACCAACCAACCTT	960
QY	961	GGAACTGTGATGTGACATTTCTGTGGCTAGCTGTGGCTTGGAGTATATACCAACCA	1020
DB	961	GGAACTGTGATGTGACATTTCTGTGGCTAGCTGTGGCTTGGAGTATATACCAACCA	1020
QY	1021	ATTCACCTGTGTGGCGGCTGTGCTATGCTCCCATGCAATGCGAGGCGGCTTACCTGTGG	1080
DB	1021	ATTCACCTGTGTGGCGGCTGTGCTATGCTCCCATGCAATGCGAGGCGGCTTACCTGTGG	1080
QY	1081	AGGTGGACCAAGGCTCTTCCAGTGTCTGCGGCTTTCATCATGAGGCGGCTTGGAGCC	1140
DB	1081	AGGTGGACCAAGGCTCTTCCAGTGTCTGCGGCTTTCATCATGAGGCGGCTTGGAGCC	1140

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1141	TCACATTTCTGAGGTCGGATGGCAGAACTTAAAGTGTGGAATCCCCCTATGTCCTCG	1200
1201	TGAAGTGGTGTCTGCCCRAATGGCAGAGTCTCAGCAAGCTCCCGCCACCCCAAGATCT	1260
1201	TGAAGTGGTGTCTGCCCRAATGGCAGAGTCTCAGCAAGCTCCCGCCACCCCAAGATCT	1260
1261	CTGTCTCTCAACGACGGCACCTTTTAACTTTTCCAGTGTCTTTTCCAGACATCTGGGGTGT	1320
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1321	ACACATGCAATGGTGAACCAATGTTGCGGCACTCCACGGCTCGGCTCACTCAATGTCA	1380
1321	ACACATGCAATGGTGAACCAATGTTGCGGCACTCCACGGCTCGGCTCACTCAATGTGA	1380
1381	GCAGGCTGAGCTTAAACACTCCCACTACAGCTTTCTTCCACCACTAGTAACTGGAGACCA	1440
1381	GCAGGCTGAGCTTAAACACTCCCACTACAGCTTTCTTCCACCACTAGTAACTGGAGACCA	1440
1441	CGGAGATCTCGCTTGAGGACAACCGGGAAGTACAGCCTGTTCTTACCAGCTGCCACTG	1500
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1501	GTTTACCAGCGGCATATACCACCTCTACCAAGCTCTCTCACTTCCAGTACCAGCTGTGCCA	1560
1501	GTTTACCAGCGGCATATACCACCTCTACCAAGCTCTCTCACTTCCAGTACCAGCTGTGCCA	1560
1561	AGCAGGTGGCAGTACCGCGACAGACACCTGAAGATGAGCAGACAGAGTGGATGAAG	1620
1561	AGCAGGTGGCAGTACCGCGACAGACACCTGAAGATGAGCAGACAGAGTGGATGAAG	1620
1621	TCATGAAGACCAACCAAGTACATCTGGCTGCTTTGTGGCAGTGACTCTGTAGCTGCCG	1680
1621	TCATGAAGACCAACCAAGTACATCTGGCTGCTTTGTGGCAGTGACTCTGTAGCTGCCG	1680
1681	CCATGTTGATGTCTTCTATAAACTTCGTAAGCGCACCGCGGAGTACAGTCAAG	1740
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1741	CGCGCCGACCTGTGAGATTAATCCAGGTGGAGAGACATCCACGACGACACATCCGACAG	1800
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1801	CAGCAACAGCAGCTCCGCTCGGCTGTATCAGGTGAGGGGCACTAGTGTGCCCAATTC	1860
1861	ATGACCATTAATTAATCAACAACCTTAACACCGACATGCGGCCCACTGGACGAGAAACA	1920
1861	ATGACCATTAATTAATCAACAACCTTAACACCGACATGCGGCCCACTGGACGAGAAACA	1920
1921	GCTTGGGGAATCTCTGACCCCACTGACCACTATCTCTGAACCTTATATAATTCAGA	1980
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1981	CCCATACCAAGGACAGGTAAGAAATCAAAATATGAATCCCTCTCCCAAAAACTTA	2040
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RESULT 49
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; Sequence 228, Application US/09993748
; Publication No. US2003069403A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Tra
; FILE REFERENCE: P2730P1C23
CURRENT APPLICATION NUMBER: US/09/999
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065195
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PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2185; DB 11; Length 2185;  
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Matches 2185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AGCTCTTGCGAGTAACTGTGCACCAACCACTTGAATGCCATCTGCTCCGTTG	120
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## RESULT 50

US-09-980-439-228  
; Sequence 228, Application US/09990439  
; Publication No. US2003007309A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavicius, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C52  
CURRENT APPLICATION NUMBER: US/09/990,439  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/0493787  
PRIOR FILING DATE: 1997-06-16  
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 Job time : 2721 secs

GenCore version 5.1.6  
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DM protein - protein search, using sw model

Run on: February 5, 2004, 15:45:19 ; Search time 47 Seconds  
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2205.286 Million cell updates/sec

Title: US-09-989-279-229

Perfect score: 3440

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Scoring table: BLOSUM62

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3440	100.0	653	21	Human PRO1111 prot
2	3440	100.0	653	21	Membrane-bound pro
3	3440	100.0	653	22	Human SSGPRO331a p
4	3440	100.0	653	22	Human PRO1111 poly
5	3440	100.0	653	22	Human PRO1111 (UNQ
6	3440	100.0	653	24	Human PRO polypept
7	3440	100.0	653	24	Human secreted/tra
8	3440	100.0	653	24	Human secreted and
9	3440	100.0	653	24	Novel human secret

10	3440	100.0	653	24	ABUS9257	Human secreted/tra
11	3440	100.0	653	24	ABUS9406	Novel human secret
12	3440	100.0	653	24	ABUS0541	Human secreted/tra
13	3440	100.0	653	24	ABUS8032	Human PRO polypept
14	3440	100.0	653	24	ABUS8963	Human secreted/tr
15	3440	100.0	653	24	ABUI3923	Human PRO1111 poly
16	3440	100.0	653	24	ABUI0878	Human PRO polypept
17	3431	99.7	653	20	cc359_4 secreted p	Human leucine rich
18	3407	99.0	649	23	ABG98016	Human SLIT protein
19	3407	99.0	694	21	ABZ23033	Human immunoglobul
20	3481	92.5	606	22	AAU18035	Human SLIT protein
21	2951	85.8	590	21	AAZ23034	Human cDNA SEQ ID
22	2888	84.0	553	22	ABBI0349	Human polypeptide
23	2888	84.0	553	23	ABP66936	Human ORPX OR2855
24	2389	69.4	448	21	AAZ23044	Human SLIT protein
25	2312	67.2	441	21	AAZ23044	Human leucine-rich
26	1931	56.1	713	22	AAE13006	Human nervous syst
27	1931	56.1	713	23	ABG97991	Human novel secret
28	1931	56.1	713	23	AAU91335	Human GPCR related
29	1931	56.1	713	24	ABUS2381	Human PRO331 prote
30	1865	54.2	640	20	AAV08100	Novel protein (Cio
31	1865	54.2	640	20	AAW85722	Amino acid sequenc
32	1865	54.2	640	20	AAV13394	Human PRO331 prote
33	1865	54.2	640	21	AAZ24407	Human PRO331 prote
34	1865	54.2	640	21	AAU70673	Human immune respo
35	1865	54.2	640	22	AAU12355	Human PRO331 prote
36	1865	54.2	640	22	AAU08026	Human PRO331 prote
37	1865	54.2	640	22	AAZ80262	Human PRO331 prote
38	1865	54.2	640	22	AAZ85292	Human angiogenesis
39	1865	54.2	640	22	AAZ83089	Novel human secret
40	1865	54.2	640	24	ABU69872	Human PRO polypept
41	1865	54.2	640	24	ABU71495	Human secreted/tra
42	1865	54.2	640	24	ABU71941	Human PRO polypept
43	1865	54.2	640	24	ABU66753	Human secreted/tra
44	1865	54.2	640	24	ABU67029	Human secreted/tra
45	1865	54.2	640	24	ABU67395	Human secreted and
46	1865	54.2	640	24	ABU59334	Novel secreted and
47	1865	54.2	640	24	ABU64549	Human secreted/tra
48	1865	54.2	640	24	ABUS9185	Novel human secret
49	1865	54.2	640	24	ABUS9332	Human secreted/tra
50	1865	54.2	640	24	ABUS9481	Human secreted/tra
51	1865	54.2	640	24	ABU60616	Human PRO polypept
52	1865	54.2	640	24	ABU58107	Human secreted/tr
53	1865	54.2	640	24	ABU59038	Human secreted/tra
54	1865	54.2	640	24	ABU54397	Human secreted/tra
55	1865	54.2	640	24	ABU13998	Human PRO331 polyp
56	1865	54.2	640	24	ABU10953	Human PRO polypept
57	1855	53.9	634	23	ABG97967	Human nervous syst
58	1827.5	53.1	634	23	ABG10522	Human cDNA SEQ ID
59	1466	42.6	281	22	ABU18084	Human immunoglobul
60	1466	42.6	281	22	ABU18084	Human polypeptide
61	1466	42.6	281	23	ABP67109	Human secreted pro
62	1005.5	29.2	295	24	ABR47760	Human secreted pro
63	1003.5	29.2	302	21	AAZ87066	Human gene 3 encod
64	1003.5	29.2	302	22	AAE06043	Human secreted pro
65	1003.5	29.2	302	23	ABG33865	Human secreted pro
66	1003.5	29.2	302	24	ABR48030	Human secreted pro
67	720.5	20.9	224	21	AAZ87135	Human secreted pro
68	720.5	20.9	224	21	AAE06112	Human gene 3 encod
69	720.5	20.9	224	23	ABG33934	Human secreted pro
70	720.5	20.9	224	24	ABR48031	Human secreted pro
71	537	15.6	606	23	AAZ96850	Human NOV4b protei
72	537	15.6	606	23	ABG60230	Human SLIT-3-like
73	537	15.6	606	23	AAU85411	Human protein NOV9
74	526.5	15.3	614	20	AAZ84596	Amino acid sequenc
75	523.5	15.2	620	22	AAZ74705	Human membrane ass
76	522	15.2	606	22	AAZ06799	Human neuronal gui
77	522	15.2	606	23	ABP60969	Novel human protei
78	522	15.2	606	23	ABP60970	Novel human protei
79	518.5	15.1	579	22	AAZ06804	Mature human neuro
80	518	15.1	606	23	AAZ96849	Human NOV4a protei
81	518	15.1	606	23	ABG60229	Human SLIT-3-like
82	518	15.1	606	23	AAU85410	Human protein NOV8

83	518	15.1	606	23	AAU85418	NOV8 allelic varia
84	516.5	15.0	620	20	AAU13357	Amino acid sequenc
85	516.5	15.0	620	20	AAU12333	Human PRO227 polyp
86	516.5	15.0	620	22	AAU80225	Human PRO227 prote
87	516.5	15.0	620	24	ABU69635	Novel human secret
88	516.5	15.0	620	24	ABU71458	Human PRO polypept
89	516.5	15.0	620	24	ABU71904	Human secreted/tra
90	516.5	15.0	620	24	ABU66731	Human PRO polypept
91	516.5	15.0	620	24	ABU67007	Human secreted/tra
92	516.5	15.0	620	24	ABU67358	Human secreted/tra
93	516.5	15.0	620	24	ABU59812	Novel secreted and
94	516.5	15.0	620	24	ABU64512	Human secreted/tra
95	516.5	15.0	620	24	ABU54360	Human secreted/tra
96	513	14.9	578	23	ABU14783	Human immunoglobul
97	506.5	14.7	582	23	ABU80578	Human sbg618691RR
98	494	14.4	592	22	AAU09437	Human LP polypepti
99	494	14.4	592	23	AAU25351	Human novel protei
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101	494	14.4	592	23	AAU79167	Human novel secret
102	494	14.4	592	23	AAU91329	Novel leucine-rich
103	494	14.4	608	23	ABU61770	Human CGSD protein
104	490	14.2	592	24	ABU74693	Human secreted pro
105	462	13.4	1070	23	ABU69674	Human secreted pro
106	451.5	13.1	1077	23	ABU70316	Human NOV30a. Hom
107	451.5	13.1	1093	23	ABU69660	Amino acid sequenc
108	443	12.9	548	22	ABU31161	Sequence used in d
109	438	12.7	1091	18	AAU41641	Murine glial cell
110	438	12.7	1091	20	AAU08099	Mouse LG-1 protei
111	438	12.7	1091	20	AAU08010	Murine LG-1 protei
112	438	12.7	1091	21	AAU97833	Novel human dieno
113	437	12.7	981	22	ABU22633	Novel human dieno
114	433	12.6	1021	22	ABU60162	Drosophila melanog
115	427.5	12.4	1101	20	AAU08008	Human HLIG-1 prote
116	425.5	12.4	716	21	ABU33472	Human PRO1338 prot
117	425.5	12.4	716	22	AAU12427	Human PRO1338 poly
118	425.5	12.4	716	22	ABU27234	Human EXMAD-12 SEQ
119	425.5	12.4	716	22	ABU50965	Human PRO1338 prot
120	425.5	12.4	716	22	ABU57530	Amino acid sequenc
121	425.5	12.4	716	23	ABU95533	Human angiogenesis
122	425.5	12.4	716	23	ABU84927	Human PRO1338 prot
123	425.5	12.4	716	23	AAU83686	Human PRO protein,
124	425.5	12.4	716	24	ABU71431	Human neoplasia in
125	425.5	12.4	716	24	ABU66825	Human PRO polypept
126	425.5	12.4	716	24	ABU67101	Human secreted/tra
127	425.5	12.4	716	24	ABU59906	Novel secreted and
128	423.5	12.3	791	20	AAU08096	Murine glial cell
129	423.5	12.3	825	20	AAU08115	Murine glial cell
130	420	12.2	1119	20	AAU08114	Human PRO326 prote
131	420	12.2	1119	21	AAU70674	Human PRO326 prote
132	420	12.2	1119	22	AAU12347	Human PRO326 polyp
133	420	12.2	1119	22	AAU00827	Human immune respo
134	420	12.2	1119	22	AAU80263	Human PRO326 prote
135	420	12.2	1119	22	AAU48162	Human PRO326 polyp
136	420	12.2	1119	24	ABU59673	Novel human secret
137	420	12.2	1119	24	ABU71496	Human PRO polypept
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139	420	12.2	1119	24	ABU66745	Human PRO polypept
140	420	12.2	1119	24	ABU67021	Human secreted/tra
141	420	12.2	1119	24	ABU67396	Human secreted/tra
142	420	12.2	1119	24	ABU59826	Novel secreted and
143	420	12.2	1119	24	ABU64550	Human secreted/tra
144	420	12.2	1119	24	ABU54398	Human secreted/tra
145	419.5	12.2	1120	20	AAU13395	Amino acid sequenc
146	415.5	12.1	533	22	ABU67511	Amino acid sequenc
147	415	12.1	719	23	ABU43533	Human secreted pro
148	415	12.1	766	22	ABU59826	Amino acid sequenc
149	415	12.1	766	24	ABU19357	NOV8 related prote
150	413.5	12.0	611	21	AAU66643	Membrane-bound pro

ALIGNMENTS

RESULT 1	
AB24073	AB24073 standard; Protein; 653 AA.
XX	XX
AC	AC AAB24073;
XX	XX
DT	DT 29-JAN-2001 (first entry)
XX	XX
DE	DE Human PRO1111 protein sequence SEQ ID NO:46.
XX	XX
KW	KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumorigenesis; identification; cancer; cytostatic; neurotic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastococic disorder; inflammatory disorder; immunologic disorder.
XX	XX
OS	OS Homo sapiens.
XX	XX
PN	PN WO200053755-A2.
XX	XX
PD	PD 14-SEP-2000.
XX	XX
PP	PP 06-JAN-2000; 2000WO-US00376.
XX	XX
PR	PR 08-MAR-1999; 99WO-US05028.
PR	PR 02-JUN-1999; 99WO-US12252.
PR	PR 23-JUN-1999; 99US-0141037.
PR	PR 07-JUL-1999; 99US-0143048.
PR	PR 26-JUL-1999; 99US-0145898.
PR	PR 30-NOV-1999; 99WO-US28313.
PR	PR 20-DEC-1999; 99WO-US30911.
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PA	PA 05-JAN-2000; 2000WO-US00219.
XX	XX (GETH ) GENENTECH INC.
XX	XX
PI	PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI	PI Watanabe CK, Wood WI;
XX	XX
DR	DR WPI; 2000-572270/53.
DR	DR N-PSDB; AAC58383.
XX	XX
PT	PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer -
XX	XX
PS	PS Claim 61; Fig 34; 286pp; English.
XX	XX
CC	CC The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic, carcinomas, sarcomas, glioblastomas, and various disorders such as neuronal, leukaemia and lymphoid malignancies, other disorders such as neuroal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastococic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
CC	CC
XX	XX

## RESULT 2



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01-JUL-1998; 98US-0091358.  
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01-JUL-1998; 98US-0091364.  
01-JUL-1998; 98US-0091444.  
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17-AUG-1998; 98US-0096897.  
18-AUG-1998; 98US-0096949.  
18-AUG-1998; 98US-0096950.  
18-AUG-1998; 98US-0096959.  
18-AUG-1998; 98US-0096960.  
18-AUG-1998; 98US-0097022.  
19-AUG-1998; 98US-0097141.  
20-AUG-1998; 98US-0097218.  
24-AUG-1998; 98US-0097661.  
26-AUG-1998; 98US-0097951.  
26-AUG-1998; 98US-0097952.  
26-AUG-1998; 98US-0097954.  
26-AUG-1998; 98US-0097955.  
26-AUG-1998; 98US-0097971.  
26-AUG-1998; 98US-0097974.  
26-AUG-1998; 98US-0097978.  
26-AUG-1998; 98US-0097979.  
26-AUG-1998; 98US-0097986.  
26-AUG-1998; 98US-0098014.  
31-AUG-1998; 98US-0098525.  
16-SEP-1998; 98US-0100634.  
12-JAN-1999; 99US-0115565.

(GETH ) GENENTECH INC.

Baker X, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;

WPI: 2000-072883/06.  
N-PSDB; AAZ65033.

Membrane-bound proteins and related nucleotide sequences

PS claim 12; Fig 157; 822pp; English.  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIS  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.

XX Sequence 653 AA;

Query Match 100.0%; Score 3440; DB 21; Length 653;  
Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MCLLMQVTVHHTWNAILLPFVYLTAQVWILCAIAAASAGPQNCPSVCSNQPQKVV 60  
Db 1 MCLLMQVTVHHTWNAILLPFVYLTAQVWILCAIAAASAGPQNCPSVCSNQPQKVV 60  
Qy 61 CTRRGISEVPGQIPSNTRYLNLMENNIQMIQADTFPHLHLVQLGNSIRQIEVGFN 120  
Db 61 CTRRGISEVPGQIPSNTRYLNLMENNIQMIQADTFPHLHLVQLGNSIRQIEVGFN 120  
Qy 121 GLASLNTLELFONMLTVTPSGAFEYLSKRLRLRNNDPIPSYAFNRVPSLMRLDGE 180  
Db 121 GLASLNTLELFONMLTVTPSGAFEYLSKRLRLRNNDPIPSYAFNRVPSLMRLDGE 180  
Qy 181 LKLEVISSEGAPEGLFNKYLNLGNCKNPKNPPLVGLSELEMSGNHPEIRPGSFHG 240  
Db 181 LKLEVISSEGAPEGLFNKYLNLGNCKNPKNPPLVGLSELEMSGNHPEIRPGSFHG 240  
Qy 241 LSSKKLWYNSQVSLIBERNAPDGLASIVELNLAHNNLSLPHDLFTPLRYLVELHLHN 300  
Db 241 LSSKKLWYNSQVSLIBERNAPDGLASIVELNLAHNNLSLPHDLFTPLRYLVELHLHN 300  
Qy 301 PWNCDLILWAWLREYIPTNSTCCGCHAPMWRGRLVVEVDQASFOCSAPFMDAPR 360  
Db 301 PWNCDLILWAWLREYIPTNSTCCGCHAPMWRGRLVVEVDQASFOCSAPFMDAPR 360  
Qy 361 DLNISEGRMAELKCTPPMSSVKKLLPNSGTVLSHSHRPRISVLNDGTLAPSHVLLSCTG 420  
Db 361 DLNISEGRMAELKCTPPMSSVKKLLPNSGTVLSHSHRPRISVLNDGTLAPSHVLLSCTG 420  
Qy 421 VYTCMVTVNAGNSASAVLNSTAEINTSNYSFFTVTVETETSPEDTTRKYKVPVPTS 480  
Db 421 VYTCMVTVNAGNSASAVLNSTAEINTSNYSFFTVTVETETSPEDTTRKYKVPVPTS 480  
Qy 481 TGYQPAYTTSITVLITQTRVPKQAVPATDTDDKQVSLDEWMTTKIIIGCFVAVTLLA 540  
Db 481 TGYQPAYTTSITVLITQTRVPKQAVPATDTDDKQVSLDEWMTTKIIIGCFVAVTLLA 540  
Qy 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDI PAATSAATAAPSGVSGEGAVLPT 600  
Db 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDI PAATSAATAAPSGVSGEGAVLPT 600  
Qy 601 IHDHINYNITKPAHGAHWNTENSLNSLHPTVTITISEPYIIQTHTKDKVQETQI 653  
Db 601 IHDHINYNITKPAHGAHWNTENSLNSLHPTVTITISEPYIIQTHTKDKVQETQI 653

RESULT 3

AAE09438

ID AAE09438 standard; Protein; 653 AA.

XX AAE09438;

XX DT 19-NOV-2001 (first entry)  
 XX DE Human sbgPRO331a protein.  
 XX DE  
 XX KW Human; Alzheimer's disease; amyotrophic lateral sclerosis;  
 KW ALS; Zöllinger-Ellison syndrome; immune system disease; schizophrenia;  
 KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;  
 KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;  
 KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;  
 KW sexual disorder; growth abnormality; infection; autoimmune disease;  
 KW rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;  
 KW cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;  
 KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;  
 KW diabetes mellitus; glomerulonephritis; renovascular hypertension;  
 KW cancer; vaccine; gene therapy; sbgPRO331a gene.  
 XX KW Homo sapiens.  
 XX KW WO2000160850-A1.  
 XX PN 23-AUG-2001.  
 XX PD 14-FEB-2001; 2001WO-US04703.  
 XX PF 14-FEB-2000; 2000US-0182172.  
 XX PR 29-FEB-2000; 2000US-0186084.  
 XX PR 18-APR-2000; 2000US-0198583.  
 XX PR 04-OCT-2000; 2000US-0237963.  
 XX PR (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX QX Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 XX WPI; 2001-536566/59.  
 XX N-PSDB; RAD16345.  
 XX NT New secreted and membrane associated polypeptides for treating  
 XX Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual  
 XX disorders, stroke, and asthma -  
 XX Claim 1; Page 56-58; 94pp; English.  
 XX The present sequence is a human sbgPRO331a protein,  
 XX a membrane bound protein of the invention.  
 XX The invention relates to secreted and membrane associated polypeptides  
 XX and nucleic acid molecules encoding such polypeptides. Sequences of the  
 XX invention are useful for treating diseases such as Alzheimer's disease,  
 XX amyotrophic lateral sclerosis (ALS), Zöllinger-Ellison syndrome, diseases  
 XX of the immune system, haematopoietic disease, inflammation, anxiety,  
 XX schizophrenia, feeding disorders, anorexia, depression, social, sexual  
 XX and memory alteration and altered immune response, sleep disorder, learning  
 XX cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment  
 XX of transsexuals, growth abnormalities, obesity, infections, autoimmune  
 XX diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,  
 XX disorders associated with healthy maintenance of gastric mucosa and  
 XX repair of acute and chronic mucosal lesion, lung carcinoma, cerebral  
 XX ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,  
 XX amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,  
 XX congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,  
 XX viral and non-viral hepatitis, type I and type II diabetes mellitus,  
 XX glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic  
 XX paralyses, tendinitis and malignant hyperthermia. Polypeptides of the  
 XX invention are used to identify membrane bound and soluble receptors.  
 XX They are also useful as vaccines for inducing an immunological response  
 XX in a mammal. Polynucleotides of the invention are used in gene therapy.  
 XX They are also valuable for chromosome localisation studies and tissue  
 XX expression studies.  
 XX Sequence 653 AA;

Query Match 100.0%; Score 3440; DB 22; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
 Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLLMQVTVHHHTWNAILLPFVYLTQAQVWILCAALAAASAGPQNCPSVCSNQPSKV 60  
 DB 1 MKLLMQVTVHHHTWNAILLPFVYLTQAQVWILCAALAAASAGPQNCPSVCSNQPSKV 60  
 QY 61 CTRGLSEVPOGIPSNTRYLMNENNIQMIQADTFRLHLHLEVLQGLGNSIRQIEVGA 120  
 DB 61 CTRGLSEVPOGIPSNTRYLMNENNIQMIQADTFRLHLHLEVLQGLGNSIRQIEVGA 120  
 QY 121 GLASLNTLELFDNMLTWIPSGAFYLSKRLRELNRNPIESIPSYAFNRVPSLMRLD 180  
 DB 121 GLASLNTLELFDNMLTWIPSGAFYLSKRLRELNRNPIESIPSYAFNRVPSLMRLD 180  
 QY 181 LKCLEYISSEGAPEGLFNLKYLNLGMCNIKDMFNLTPLVGLFEELMSGNHPEIRPS 240  
 DB 181 LKCLEYISSEGAPEGLFNLKYLNLGMCNIKDMFNLTPLVGLFEELMSGNHPEIRPS 240  
 QY 241 LSSLEKLLWMSQVSLITERNAFDGLASLVELNLAAHNLSSLPHDLFTPLRYLVEL 300  
 DB 241 LSSLEKLLWMSQVSLITERNAFDGLASLVELNLAAHNLSSLPHDLFTPLRYLVEL 300  
 QY 301 FWCDCDILAWMLRBYIPTNSTCCGRCHAPMGRGYLVEDVDQASFOCSADPMDAPR 360  
 DB 301 FWCDCDILAWMLRBYIPTNSTCCGRCHAPMGRGYLVEDVDQASFOCSADPMDAPR 360  
 QY 361 DLNTSEGRMAELKCTPPMSVKWLLPNGTVLHSHSRHPRISVLNDGTLNFSHYLS 420  
 DB 361 DLNTSEGRMAELKCTPPMSVKWLLPNGTVLHSHSRHPRISVLNDGTLNFSHYLS 420  
 QY 421 VYTCWNTNVAAGNSAYLVNSTAEALNTSNYSPTTIVTVEITISPEDTTRKYPVPT 480  
 DB 421 VYTCWNTNVAAGNSAYLVNSTAEALNTSNYSPTTIVTVEITISPEDTTRKYPVPT 480  
 QY 481 TGYOPAVTSTTVLIQTRVPKQVAVPATDTDKMOTSLDEVMTTKIIIGCFVAVTLL 540  
 DB 481 TGYOPAVTSTTVLIQTRVPKQVAVPATDTDKMOTSLDEVMTTKIIIGCFVAVTLL 540  
 QY 541 AAMLIVFYKLRKHQQRSTVTAARTVEIIQVDEDIQAATSAATAAPSGVSGAVLPT 600  
 DB 541 AAMLIVFYKLRKHQQRSTVTAARTVEIIQVDEDIQAATSAATAAPSGVSGAVLPT 600  
 QY 601 IHDHINTYTKPARGAHTWNTSGLNSLHPTVTVTISSEPIYIIQTHKDKVQETQI 653  
 DB 601 IHDHINTYTKPARGAHTWNTSGLNSLHPTVTVTISSEPIYIIQTHKDKVQETQI 653

RESULT 4  
 AAU12390  
 ID AAU12390 standard; Protein; 653 AA.  
 XX AC AAU12390;

DT 24-OCT-2001 (first entry)

XX Human PRO1111 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIa; gene therapy.

XX Homo sapiens.

XX WO200140466-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99MO-US28534.  
PR 02-DEC-1999; 99MO-US28551.  
PR 02-DEC-1999; 99MO-US28564.  
PR 02-DEC-1999; 99MO-US28565.  
PR 09-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99MO-US30095.  
PR 20-DEC-1999; 99MO-US30911.  
PR 20-DEC-1999; 99MO-US30999.  
PR 30-DEC-1999; 99MO-US32243.  
PR 06-JAN-2000; 2000MO-US00277.  
PR 06-JAN-2000; 2000MO-US00376.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04342.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 24-FEB-2000; 2000MO-US05004.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 20-MAR-2000; 2000MO-US07377.  
PR 21-MAR-2000; 2000MO-US07532.  
PR 30-MAR-2000; 2000MO-US08439.  
PR 17-MAY-2000; 2000MO-US13705.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 10-NOV-2000; 2000MO-US30873.  
XX (GETH ) GENENTECH INC.  
XX Baker K2, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen MB, Goddard A, Godowski RJ, Gurney AL, Sherwood S;  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;  
XX MPI; 2001-408281/43.  
XX N-PSDB; AAS21462.  
XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
XX other PRO polypeptides, link bioactive molecules to cells expressing  
XX PRO polypeptides, and detect the presence of mammalian tumours e.g.  
XX lung, breast, prostate, cervical  
XX Claim 12; Fig 438; 813pp; English.  
XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
XX PRO polypeptides. The PRO polypeptides are useful to detect other  
XX PRO polypeptides, to link bioactive molecules to cells expressing  
XX PRO polypeptides, to modulate biological activities of cells expressing  
XX PRO polypeptides, and to detect the presence of mammalian lung, colon,  
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO  
XX polypeptide expression in a cell sample to that in a control sample.  
XX Some of the 275 sequences are also useful to stimulate the release of  
XX tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
XX proliferation or differentiation of chondrocytes, the proliferation or  
XX gene expression in pericyte cells, the release of proteoglycans from  
XX cartilage, the proliferation of inner ear utricular supporting cells or  
XX of T-lymphocytes, the release of a cytokine from peripheral blood  
XX monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
XX the PRO polypeptides may modulate glucose or free fatty acid uptake by  
XX skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide  
XX to factor VIIA. The PRO polypeptides can be used in assays to identify  
XX molecules involved in binding interactions. The polynucleotides encoding  
XX PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
XX transgenic or knock out animals and can be used in gene therapy.  
XX Sequence 653 AA;  
XX Query Match 100.0%; Score 3440; DB 22; Length 653;  
XX Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
XX Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MKLLQVTVVHHHTNAILLPVLVTAQWILCAIAAASAGFQNCPSVCSCNQFSKV 60  
XX 1 MKLLQVTVVHHHTNAILLPVLVTAQWILCAIAAASAGFQNCPSVCSCNQFSKV 60

QY 61 CTRRGLSEVPQGPENTRYLNLMMENNIQMIQADTFRLHLHLLEVQLGRNSIRQIEVGAFN 120  
DB 61 CTRRGLSEVPQGPENTRYLNLMMENNIQMIQADTFRLHLHLLEVQLGRNSIRQIEVGAFN 120  
QY 121 GLASLNTLLEFDNWLTVIPSGAFVYLSKLRRLRNPIESIPSYAFNRVPSLWRLDGE 180  
DB 121 GLASLNTLLEFDNWLTVIPSGAFVYLSKLRRLRNPIESIPSYAFNRVPSLWRLDGE 180  
QY 181 LKKLEYISSEGAPEGLFNKYLNLGMCNIKMPNLTPLVGLBELEMSGNHFFPIRPGSPHG 240  
DB 181 LKKLEYISSEGAPEGLFNKYLNLGMCNIKMPNLTPLVGLBELEMSGNHFFPIRPGSPHG 240  
QY 241 LSSLKXLWVMSQVSLIERNAPDGLASLVLELNAHNESSLPELFTPLRYLVLELHNN 300  
DB 241 LSSLKXLWVMSQVSLIERNAPDGLASLVLELNAHNESSLPELFTPLRYLVLELHNN 300  
QY 301 PNKDCDILWLAWLREYIPTNSTCCGRCHAPMMRGYLVVEVDOASQCSAPFIMDAPR 360  
DB 301 PNKDCDILWLAWLREYIPTNSTCCGRCHAPMMRGYLVVEVDOASQCSAPFIMDAPR 360  
QY 361 DLNISGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRI SVINDGTNFSHVLLSDTG 420  
DB 361 DLNISGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRI SVINDGTNFSHVLLSDTG 420  
QY 421 VYTCWTVNAGNSASAYLNVSABLNTSNYSFFTVTVETTEISPEDTTRKYKVPVPTS 480  
DB 421 VYTCWTVNAGNSASAYLNVSABLNTSNYSFFTVTVETTEISPEDTTRKYKVPVPTS 480  
QY 481 TGYQPAYTSTTVLIQTRVPKQVAVPATDTDKMQTSLDDEVMTTKIIIGCFVAVTLLA 540  
DB 481 TGYQPAYTSTTVLIQTRVPKQVAVPATDTDKMQTSLDDEVMTTKIIIGCFVAVTLLA 540  
QY 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDIPAAATSAATAPSGVSGEGAVVLPT 600  
DB 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDIPAAATSAATAPSGVSGEGAVVLPT 600  
QY 601 IHHDHINYTKPAHGAHWTENSLGNLSHPTVTITISEPVIIQHTKDKVQETQI 653  
DB 601 IHHDHINYTKPAHGAHWTENSLGNLSHPTVTITISEPVIIQHTKDKVQETQI 653  
RESULT 5  
AAB65217  
ID AAB65217 standard; Protein; 653 AA.  
XX AC AAB65217;  
XX AC AAB65217;  
XX DT 02-APR-2001 (first entry)  
XX DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.  
XX KW Human; secreted and transmembrane protein; PRO; cytostatic;  
XX KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX KW diagnostic assay.  
XX OS Homo sapiens.  
XX FN WO2000073454-A1.  
XX PD 07-DEC-2000.  
XX EF 30-MAR-2000; 2000MO-US08439.  
XX PR 02-JUN-1999; 99MO-US12252.  
XX PR 23-JUN-1999; 99US-0141037.  
XX PR 07-JUL-1999; 99US-0143048.  
XX PR 20-JUL-1999; 99US-0144758.  
XX PR 26-JUL-1999; 99US-0145698.  
XX PR 28-JUL-1999; 99US-0146222.  
XX PR 17-AUG-1999; 99US-0149396.  
XX PR 15-SEP-1999; 99MO-US21090.  
XX PR 15-SEP-1999; 99MO-US21547.

08-OCT-1999; 99US-0158663.  
 30-NOV-1999; 99WO-US28313.  
 01-DEC-1999; 99WO-US28301.  
 16-DEC-1999; 99WO-US30095.  
 20-DEC-1999; 99WO-US30911.  
 05-JAN-2000; 2000WO-US00219.  
 06-JAN-2000; 2000WO-US00376.  
 11-FEB-2000; 2000WO-US03565.  
 18-FEB-2000; 2000WO-US04341.  
 22-FEB-2000; 2000WO-US04414.  
 24-FEB-2000; 2000WO-US04914.  
 24-FEB-2000; 2000WO-US05004.  
 15-MAR-2000; 2000WO-US05841.  
 15-MAR-2000; 2000WO-US06884.  
 20-MAR-2000; 2000WO-US07377.  
 (GETH ) GENENTECH INC.  
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 Grimaldi CJ, Gurney AU, Kljavin IO, Napier MA, Pan J, Paoni NF;  
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 Zhang Z;  
 WPI; 2001-032160/04.  
 N-PSDB; AAF44179.  
 PRO polynucleotides used to produce polypeptides used to target  
 bioactive molecules such as toxins, radiolabels or antibodies, to  
 specific cells, to cause targeted cell death -  
 Claim 12; Fig 157; 935pp; English.  
 The present invention describes human secreted and transmembrane PRO  
 proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 can be used for targeted delivery of bioactive molecules, such as  
 toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 sequences, and their fragments, can be used as hybridisation probes, in  
 chromosomal and gene mapping, and in the generation of anti-sense RNA  
 and DNA. They may also be used to produce transgenic animals which are  
 used to develop and screen therapeutically useful reagents. The PRO  
 nucleotide and protein sequence can be used for tissue typing and in  
 treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 AAF65154 to AAF65300 represent human PRO polynucleotide and protein  
 sequences given in the exemplification of the present invention.  
 Sequence 653 AA;  
 Query Match 100.0%; Score 3440; DB 22; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
 Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MKLLWQVTHHTWNAILLFVYLTQVWILCAIAAASAGPQNCPSVCSNPFKIV 50  
 1 MKLLWQVTHHTWNAILLFVYLTQVWILCAIAAASAGPQNCPSVCSNPFKIV 60  
 61 CTRGLSEVPQGPSNRYLNLMNENIQADTFRLHLHLVQLGRNSIRQIEVGFN 120  
 61 CTRGLSEVPQGPSNRYLNLMNENIQADTFRLHLHLVQLGRNSIRQIEVGFN 120  
 121 GLASINTLEIFDNWLTVPISGAPEYLSKRLWLNRPNIESPSYAFNRPVSLMLDICE 180  
 121 GLASINTLEIFDNWLTVPISGAPEYLSKRLWLNRPNIESPSYAFNRPVSLMLDICE 180  
 181 LKLEYISEGAFGLFNLYNLGMCNIKDMPNLTPLVGLLELMSCGNHFFPIRPGSFH 240  
 181 LKLEYISEGAFGLFNLYNLGMCNIKDMPNLTPLVGLLELMSCGNHFFPIRPGSFH 240  
 241 LSSLKLLWVANSQVSLIERNAFGLASLVELNLAAHNLGSLPDLFTPLRYLVELHLHN 300  
 241 LSSLKLLWVANSQVSLIERNAFGLASLVELNLAAHNLGSLPDLFTPLRYLVELHLHN 300

QY 301 PWNCDILMAWLREYIPTNSTCCGRCHAPMHMGRYLVEVDQASFOCSAPFINDAPR 360  
 DB 301 PWNCDILMAWLREYIPTNSTCCGRCHAPMHMGRYLVEVDQASFOCSAPFINDAPR 360  
 QY 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHSHRPRISVLNDGTLNFSHVLSDTG 420  
 DB 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHSHRPRISVLNDGTLNFSHVLSDTG 420  
 QY 421 VYTCMVNTVAGNSAGAYLVNSTAEINTSNYSPTTPTVTTTETTESPEDTRKYPVPTTS 480  
 DB 421 VYTCMVNTVAGNSAGAYLVNSTAEINTSNYSPTTPTVTTTETTESPEDTRKYPVPTTS 480  
 QY 481 TGYOPAYTSTTVLIQTRVPKQVAVPATDTTDMQOTSLDEVMKTKIIGCPVAVTLLA 540  
 DB 481 TGYOPAYTSTTVLIQTRVPKQVAVPATDTTDMQOTSLDEVMKTKIIGCPVAVTLLA 540  
 QY 541 AAMLVIFYKLKRKHQRQSTVTAARTVEIIQVDESDI PAATSAATAAPSGVSGEAVVLP 600  
 DB 541 AAMLVIFYKLKRKHQRQSTVTAARTVEIIQVDESDI PAATSAATAAPSGVSGEAVVLP 600  
 QY 601 IHDHINTYKPAHGAHWNTENSLGSLHPTVTITSEFYIIQHTKDKVQETQI 653  
 DB 601 IHDHINTYKPAHGAHWNTENSLGSLHPTVTITSEFYIIQHTKDKVQETQI 653  
 RESULT 6  
 ABU66788  
 ID ABU66788 standard; Protein; 653 AA.  
 XX AC ABU66788;  
 XX XX 23-MAY-2003 (first entry)  
 DT Human PRO polypeptide #219.  
 DE Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder;  
 KW cytostatic.  
 XX OS Homo sapiens.  
 XX FN US2003036180-A1.  
 XX PD 20-FEB-2003.  
 XX PF 09-MAY-2002; 2002US-0143114.  
 XX PR 31-MAR-1997; 97WO-US05230.  
 PR 12-JUN-1998; 98WO-US12456.  
 PR 14-JUL-1998; 98WO-US14552.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 20-APR-1999; 99WO-US05190.  
 PR 14-MAY-1999; 99WO-US08615.  
 PR 02-JUN-1999; 99WO-US10733.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04343.  
PR 22-FEB-2000; 2000WO-US04144.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06315.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13709.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 23-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06665.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796492.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887875.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924415.  
PR 09-AUG-2001; 2001US-0927796.  
  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
PR XX (GETH ) GENENTECH INC.  
PR PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PR PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PR PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
PR DR WPI; 2003-332040/31.  
PR DR N-PSDB; ACA03821.  
PR XX  
PR PT New secreted and transmembrane PRO nucleic acids, useful for gene  
PR PT therapy, in chromosome and gene mapping, as chromosome markers, in  
PR PT tissue typing, and in chromosome identification  
PR XX  
PR PS Claim 12; Fig 438; 660pp; English.  
PR CC The present invention relates to the isolation of novel human PRO  
PR CC polypeptides, and the polynucleotide sequences encoding them. The  
PR CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
PR CC polypeptides are useful for detecting other PRO polypeptides, for  
PR CC linking bioactive molecules to cells expressing PRO polypeptides,  
PR CC for modulating biological activities of cells expressing PRO  
PR CC polypeptides, and for identifying agonists or antagonists.  
PR CC The PRO polypeptides are useful for stimulating the release of  
PR CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
PR CC the proliferation or differentiation of chondrocytes, and detecting the  
PR CC presence of tumours. The polynucleotide sequences encoding PRO  
PR CC polypeptides are useful as hybridisation probes, in chromosome and  
PR CC gene mapping, in the generation of antisense RNA and DNA, in the  
PR CC preparation of PRO polypeptides, for generating transgenic animals or  
PR CC knockout animals, for the genetic analysis of individuals with genetic  
PR CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human  
PR CC PRO polypeptides of the invention.  
PR CC Note: The sequence data for this patent was obtained in electronic  
PR CC format directly from the USPTO web site at  
PR CC seqdata.uspto.gov/psipsdEntry.html.  
PR XX  
PR SQ Sequence 653 AA;  
  
Query Match 100.0%; Score 3440; DB 24; Length 653;  
Best Local Similarity 100.0%; Pred. NO. 6.4e-278; Mismatches 0; Indels 0; Gaps 0;  
Matches 653; Conservative 0;  
  
QY 1 MKLLWQVTVHHHTWNAILLPFVLTQVWILCAIAAASAGQNCPSVCSCNQSKVV 60  
DB 1 MKLLWQVTVHHHTWNAILLPFVLTQVWILCAIAAASAGQNCPSVCSCNQSKVV 60  
  
QY 61 CTRGLSEVPQGISNTRYLNLMENNIQMTQDTFRLHLEVLQGRNSIRQIEVGAFN 120  
DB 61 CTRGLSEVPQGISNTRYLNLMENNIQMTQDTFRLHLEVLQGRNSIRQIEVGAFN 120  
  
QY 121 GLASINTLELFDNWLTVPGAPYLSKRLRLNMPISIESYAFNRVPSLMRLDLGE 180  
DB 121 GLASINTLELFDNWLTVPGAPYLSKRLRLNMPISIESYAFNRVPSLMRLDLGE 180  
  
QY 181 LKLEYISEGAPEGLFNKLYNLGMCKNDMPNLTPLVGLLEEMSGNHPPETRPSFHG 240  
DB 181 LKLEYISEGAPEGLFNKLYNLGMCKNDMPNLTPLVGLLEEMSGNHPPETRPSFHG 240  
  
QY 241 LSSLLKLVNMSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLVELLHNN 300  
DB 241 LSSLLKLVNMSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLVELLHNN 300  
  
QY 301 PWNCDIILANWLREYIPTNSTCCGRCHAPMHRGRYLVVDQASFOCSAPFINDAPR 360  
DB 301 PWNCDIILANWLREYIPTNSTCCGRCHAPMHRGRYLVVDQASFOCSAPFINDAPR 360  
  
QY 361 DLNTSEGMRELKCRTPMSSVKWLLPENGTVLASHHPRISVLNDGTLANFSHVLLSDTG 420  
DB 361 DLNTSEGMRELKCRTPMSSVKWLLPENGTVLASHHPRISVLNDGTLANFSHVLLSDTG 420

Y 421 VYTCMTNAGNSASAYLVNSTAEALNTSNYSFFTVTVVETTEISPEDTTRKYKVPPTTS 480  
b 421 VYTCMTNAGNSASAYLVNSTAEALNTSNYSFFTVTVVETTEISPEDTTRKYKVPPTTS 480  
Y 481 TGYQPAYTSTTVLIQTTTRVPKQVAVPATDQKQTSLSDEVNKTIIIGCFVAVTLLA 540  
b 481 TGYQPAYTSTTVLIQTTTRVPKQVAVPATDQKQTSLSDEVNKTIIIGCFVAVTLLA 540  
Y 541 AAMLIYPYKLRKHQRSTVTAARTVEIIQVDEDPAAATSAATAAPSGVSGEGAVLPT 600  
b 541 AAMLIYPYKLRKHQRSTVTAARTVEIIQVDEDPAAATSAATAAPSGVSGEGAVLPT 600  
Y 601 IHDHINNTYKPAHGAHNTENSLSLHPTVTITSEPIIQTHTKDKVQETQI 653  
b 601 IHDHINNTYKPAHGAHNTENSLSLHPTVTITSEPIIQTHTKDKVQETQI 653

RESULT 7  
BU67064  
D ABU67064 standard; Protein; 653 AA.  
C ABU67064;  
X T 27-MAY-2003 (first entry)  
X Human secreted/transmembrane, PRO, protein SEQ ID 438.  
X Human; secreted protein; transmembrane protein; PRO;  
X inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
X infertility; birth defects; premature aging; AIDS; biosensor;  
X acquired immunodeficiency syndrome; cancer; diabetic complication;  
X bioreactor; tumour.  
X Homo sapiens.  
X US2003032155-A1.  
X 13-FEB-2003.  
X 03-MAY-2002; 2002US-0137865.  
R 31-MAR-1997; 97WO-US050230.  
R 12-JUN-1998; 98WO-US12456.  
R 14-JUL-1998; 98WO-US14552.  
R 28-AUG-1998; 98WO-US17888.  
R 10-SEP-1998; 98WO-US18824.  
R 14-SEP-1998; 98WO-US19093.  
R 14-SEP-1998; 98WO-US19094.  
R 14-SEP-1998; 98WO-US19177.  
R 16-SEP-1998; 98WO-US19330.  
R 17-SEP-1998; 98WO-US19437.  
R 07-OCT-1998; 98WO-US21141.  
R 29-OCT-1998; 98WO-US22991.  
R 29-OCT-1998; 98WO-US22992.  
R 20-NOV-1998; 98WO-US24955.  
R 01-DEC-1998; 98WO-US25108.  
R 05-JAN-1999; 98WO-US00106.  
R 08-MAR-1999; 98WO-US05028.  
R 10-MAR-1999; 98WO-US05190.  
R 20-APR-1999; 98WO-US08615.  
R 14-MAY-1999; 98WO-US10733.  
R 02-JUN-1999; 98WO-US12252.  
R 01-SEP-1999; 98WO-US20111.  
R 08-SEP-1999; 98WO-US20594.  
R 13-SEP-1999; 98WO-US20944.  
R 13-SEP-1999; 98WO-US21090.  
R 15-SEP-1999; 98WO-US211547.  
R 05-OCT-1999; 98WO-US23089.  
R 29-NOV-1999; 98WO-US28214.  
R 30-NOV-1999; 98WO-US28313.  
R 30-NOV-1999; 98WO-US28409.  
R 01-DEC-1999; 98WO-US28301.  
R 01-DEC-1999; 98WO-US28634.

PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04344.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 01-MAR-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000WO-US07177.  
PR 30-MAR-2000; 2000WO-US07532.  
PR 17-MAY-2000; 2000WO-US08439.  
PR 22-MAY-2000; 2000WO-US13705.  
PR 30-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-074259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882536.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

QY 1 MKLLQVTVHHTWVAILLPEVYLTAOVWILCAIAAASAGPQPCVCSNCFSKV 60  
 Db 1 MKLLQVTVHHTWVAILLPEVYLTAOVWILCAIAAASAGPQPCVCSNCFSKV 60  
 QY 61 CTRGLSEVPOGIPSNTRYLNLMMNNIQTQADTFRLHLEHLVQLGRNSIRQIEVGAFN 120  
 Db 61 CTRGLSEVPOGIPSNTRYLNLMMNNIQTQADTFRLHLEHLVQLGRNSIRQIEVGAFN 120  
 QY 121 GLASLNTLELFDNMLTVIPSGAFYLSKRLRNXPETSPSYAFNRPVSLMRLDGE 180  
 Db 121 GLASLNTLELFDNMLTVIPSGAFYLSKRLRNXPETSPSYAFNRPVSLMRLDGE 180  
 QY 181 LKLEYISEGAFEGLEMLKYNLNCWIKDMPNLTPLVGLLEEMSGNHFPIRPGSFHG 240  
 Db 181 LKLEYISEGAFEGLEMLKYNLNCWIKDMPNLTPLVGLLEEMSGNHFPIRPGSFHG 240  
 QY 241 LSSLKKLVNMSQVSLTERNAFOGLASVLELNAHNNLSLPHDLTPPLRYLVELHLHN 300  
 Db 241 LSSLKKLVNMSQVSLTERNAFOGLASVLELNAHNNLSLPHDLTPPLRYLVELHLHN 300  
 QY 301 PNCDCDILMLAWLRYIPTNSTCCGRCHAPMHEGRYLVEVDQASFOCSAPFINDAPR 360  
 Db 301 PNCDCDILMLAWLRYIPTNSTCCGRCHAPMHEGRYLVEVDQASFOCSAPFINDAPR 360  
 QY 361 DLNISEGRVAKLCRTPMSSVKVLLNGTVLASHRHPRISVYNDGTINFSHLLSDTG 420

Db 361 DLNISEGRVAKLCRTPMSSVKVLLNGTVLASHRHPRISVYNDGTINFSHLLSDTG 420  
 QY 421 VYTCWTVNAGNSASAYLNVSTAEALNTSNYSFPTTVTETTESPEDTRKYPVPTTS 480  
 Db 421 VYTCWTVNAGNSASAYLNVSTAEALNTSNYSFPTTVTETTESPEDTRKYPVPTTS 480  
 QY 481 TGYQPAYTSTVLIQTRVPKQVAVPATDTDKMOTSLDEVMKTKLIIGCFVAVTLLA 540  
 Db 481 TGYQPAYTSTVLIQTRVPKQVAVPATDTDKMOTSLDEVMKTKLIIGCFVAVTLLA 540  
 QY 541 AAMLIVPYKLKRKHQORSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVVLEPT 600  
 Db 541 AAMLIVPYKLKRKHQORSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVVLEPT 600  
 QY 601 IHDHINVTYKPAHGHNTENSLSLHPTVTIISBPYIIQTHTKKQVQETOI 653  
 Db 601 IHDHINVTYKPAHGHNTENSLSLHPTVTIISBPYIIQTHTKKQVQETOI 653

RESULT 8  
 ABUS9869  
 ID ABUS9869 standard, Protein, 653 AA.  
 AC ABUS9869;  
 XX  
 DT 13-MAY-2003 (first entry)  
 XX  
 DE Novel secreted and transmembrane protein PRO111.  
 XX  
 KM Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KM cardiac insufficiency disorder; cancer; tumour; immune response;  
 KM adrenal cortical capillary endothelial growth; c-fos induction;  
 KM vascular endothelial growth factor inhibition; VEGF inhibition;  
 KM endothelial cell growth inhibitor; T-lymphocyte stimulation;  
 KM retinal neurons cell survival; rod photoreceptor cell survival;  
 KM retinal disorder; retinitis pigmentosa; kidney disorder;  
 KM mammalian kidney mesangial cell proliferation; Berger disease;  
 KM dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KM chondrocyte redifferentiation; sports injury; arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003017563-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 07-MAY-2002; 2002US-0140808.  
 XX  
 PR 31-MAR-1997; 97WO-US05230.  
 PR 12-JUN-1996; 96WO-US12456.  
 PR 14-JUL-1998; 98WO-US14552.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 15-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99WO-US05190.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear utricular supporting cells, the proliferation of r-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing.

The present sequence represents a PRO protein of the invention.

Sequence 653 AA;

Query Match 100.0%; Score 3440; DB 24; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
 Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



15-SEP-1999; 99WO-US21090.  
 15-SEP-1999; 99WO-US21547.  
 05-OCT-1999; 99WO-US23089.  
 29-NOV-1999; 99WO-US28214.  
 30-NOV-1999; 99WO-US28313.  
 30-NOV-1999; 99WO-US28409.  
 01-DEC-1999; 99WO-US28301.  
 01-DEC-1999; 99WO-US28634.  
 02-DEC-1999; 99WO-US28551.  
 02-DEC-1999; 99WO-US28564.  
 02-DEC-1999; 99WO-US28565.  
 16-DEC-1999; 99WO-US30095.  
 20-DEC-1999; 99WO-US30311.  
 20-DEC-1999; 99WO-US30999.  
 22-DEC-1999; 99WO-US30720.  
 30-DEC-1999; 99WO-US31243.  
 30-DEC-1999; 99WO-US31274.  
 05-JAN-2000; 2000WO-US00219.  
 06-JAN-2000; 2000WO-US00277.  
 06-JAN-2000; 2000WO-US00376.  
 11-FEB-2000; 2000WO-US03565.  
 18-FEB-2000; 2000WO-US04341.  
 22-FEB-2000; 2000WO-US04342.  
 24-FEB-2000; 2000WO-US04414.  
 24-FEB-2000; 2000WO-US04914.  
 01-MAR-2000; 2000WO-US05004.  
 01-MAR-2000; 2000WO-US05601.  
 02-MAR-2000; 2000WO-US05746.  
 02-MAR-2000; 2000WO-US05841.  
 10-MAR-2000; 2000WO-US06319.  
 15-MAR-2000; 2000WO-US06884.  
 20-MAR-2000; 2000WO-US07377.  
 21-MAR-2000; 2000WO-US07532.  
 30-MAR-2000; 2000WO-US08439.  
 17-MAY-2000; 2000WO-US13705.  
 22-MAY-2000; 2000WO-US14042.  
 30-MAY-2000; 2000WO-US14941.  
 02-JUN-2000; 2000WO-US15264.  
 28-JUL-2000; 2000WO-US20710.  
 11-AUG-2000; 2000WO-US22031.  
 23-AUG-2000; 2000WO-US21522.  
 24-AUG-2000; 2000WO-US21328.  
 08-NOV-2000; 2000WO-US30952.  
 10-NOV-2000; 2000WO-US30873.  
 01-DEC-2000; 2000WO-US32678.  
 20-DEC-2000; 2000WO-US34956.  
 28-FEB-2001; 2001WO-US06520.  
 01-MAR-2001; 2001WO-US06656.  
 25-MAY-2001; 2001WO-US17092.  
 01-JUN-2001; 2001WO-US17800.  
 20-JUN-2001; 2001WO-US19692.  
 22-JUN-2001; 2001WO-US20116.  
 29-JUN-2001; 2001WO-US21066.  
 09-JUL-2001; 2001WO-US21735.  
 20-DEC-2000; 2000US-0747259.  
 28-FEB-2001; 2001US-0796498.  
 09-MAR-2001; 2001US-0802706.  
 14-MAR-2001; 2001US-0806599.  
 22-MAR-2001; 2001US-0816744.  
 05-APR-2001; 2001US-0828366.  
 10-MAY-2001; 2001US-0854208.  
 10-MAY-2001; 2001US-0854280.  
 18-MAY-2001; 2001US-0860216.  
 25-MAY-2001; 2001US-0865028.  
 25-MAY-2001; 2001US-0865034.  
 01-JUN-2001; 2001US-0872035.  
 05-JUN-2001; 2001US-0874503.  
 14-JUN-2001; 2001US-0882636.  
 19-JUN-2001; 2001US-0886342.  
 21-JUN-2001; 2001US-0887879.  
 18-JUL-2001; 2001US-0908827.  
 06-AUG-2001; 2001US-0924419.  
 09-AUG-2001; 2001US-0927796.

PR 16-DEC-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff Z, Gao W;  
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2003-148238/14.  
 DR N-PSDB; ABX89359.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments  
 XX  
 PS Claim 12; Fig 438; 659pp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or differentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC is the amino acid sequence of a novel human PRO protein.  
 XX  
 SQ Sequence 653 AA;

Query Match 100.0%; Score 3440; DB 24; Length 653;  
 Best local similarity 100.0%; Pred. No. 6.4e-278;  
 Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLLQVTVHHHTNAILLPFVLTQAQWILCAIAAASAGPQCPSVCSNQSFKVV 60  
 DB 1 MKLLQVTVHHHTNAILLPFVLTQAQWILCAIAAASAGPQCPSVCSNQSFKVV 60  
 QY 61 CTRRGLSEVPQIPSNTRYLNMENNIIQIADTFRHLHLEVLQLGNSIRQIEVGFN 120  
 DB 61 CTRRGLSEVPQIPSNTRYLNMENNIIQIADTFRHLHLEVLQLGNSIRQIEVGFN 120  
 QY 121 GLASLNTLELFDNNLTIPSGAFYLSKRLRLNPNPIESIPSYAFNRVPSLRLDLGE 180  
 DB 121 GLASLNTLELFDNNLTIPSGAFYLSKRLRLNPNPIESIPSYAFNRVPSLRLDLGE 180  
 QY 181 LKKLEYISSEGAPEGFLPNLYLNLCNKNKMPNLTPLVGLSELEMSGNHPEIRPGSFHG 240  
 DB 181 LKKLEYISSEGAPEGFLPNLYLNLCNKNKMPNLTPLVGLSELEMSGNHPEIRPGSFHG 240  
 QY 241 LSSLKXKLWVNSQVSLIERNAPDGLASLVLELNALNNLSLPHDLFTPLRYLVELHLHFN 300

Db 241 LSSLLKLVWMSQVSLIERNAFDGLASIVELNLAHNNLSLDPHDLFTPLRYLVHLLHN 300  
Qy 301 PNVCCDILNLAWLREVIPNSTRCCGCHAPMGRGYLYVEVDOASFCAPFIMDAPR 360  
Db 301 PNVCCDILNLAWLREVIPNSTRCCGCHAPMGRGYLYVEVDOASFCAPFIMDAPR 360  
Qy 361 DLNISEGRMAELKCRTPPMSSSVKWLPPNGTIVLSHARPRISVLNDGTLNFSHVLLSDTG 420  
Db 361 DLNISEGRMAELKCRTPPMSSSVKWLPPNGTIVLSHARPRISVLNDGTLNFSHVLLSDTG 420  
Qy 421 VYTCMTNVAGNSASAVLNSTAEINTSNYSFFFTVTVTETTESPEDTKKYKPEVPTS 480  
Db 421 VYTCMTNVAGNSASAVLNSTAEINTSNYSFFFTVTVTETTESPEDTKKYKPEVPTS 480  
Qy 481 TGYQPAYTSTTVLQTTVPKQVAVPATDITDKMOTSLDEVMTKTKIIIGCFVAVTLLA 540  
Db 481 TGYQPAYTSTTVLQTTVPKQVAVPATDITDKMOTSLDEVMTKTKIIIGCFVAVTLLA 540  
Qy 541 AAMLIVFYKLRKHOOORSTVTAARTVEIIQVDEDIPAAATSAATAPSGVSGEGAVVLPT 600  
Db 541 AAMLIVFYKLRKHOOORSTVTAARTVEIIQVDEDIPAAATSAATAPSGVSGEGAVVLPT 600  
Qy 601 IHDHINYNTPKPAHGAHTWENSLGNSLHPTVTIIEPVYIIQTHTKDKVQETQI 653  
Db 601 IHDHINYNTPKPAHGAHTWENSLGNSLHPTVTIIEPVYIIQTHTKDKVQETQI 653

RESULT 9  
ID ABUS9110 standard; Protein; 653 AA.  
XX ABUS9110;  
XX XX  
DT 28-APR-2003 (first entry)  
DE Novel human secreted or transmembrane protein PRO1111.  
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX XX  
PN US2002132252-A1.  
XX 19-SEP-2002.  
XX 14-NOV-2001; 2001US-0990442.  
XX 05-NOV-1997; 97WO-US200069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US08520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 03-JUN-1998; 98US-087759P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.

PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Raton DL;  
PI Perrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-247083/24.

XX N-PSDB; ABX80269.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX are therapeutically useful for enhancing immune response and in cancer  
XX treatments

XX Claim 12; Fig 157; 548pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
XX in modulating at least one biological activity of a cell expressing a PRO  
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,  
XX PRO943, PRO828, PRO826, PRO1068 or PRO335, PRO826, PRO819, PRO1126,  
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
XX useful for treating conditions or disorders where angiogenesis would be  
XX beneficial, e.g. wound healing and antagonist of this polypeptide are  
XX useful for treating cancerous tumours. PRO812 inhibits vascular  
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial  
XX cells and is thus useful for inhibiting endothelial cell growth in  
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,  
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
XX stimulated T-lymphocytes and are therapeutically useful for enhancing  
XX immune response. PRO826, PRO826, PRO1068 or PRO1132 enhance survival of  
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
XX rod photoreceptor cells) and therefore are useful for treating retinal  
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
XX and therefore are useful for treating kidney disorders associated with  
XX decreased mesangial cell function such as Berger disease or other  
XX nephropathies associated with dermatitis, herpeticiformis or Crohn's  
XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
XX proliferation and/or redifferentiation of chondrocytes in culture and  
XX are thus useful for treating sports injuries, and arthritis. This  
XX is the amino acid sequence of a novel human PRO protein.

XX Sequence 653 AA;

Query Match 100.0%; Score 3440; DB 24; Length 653;  
Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MLLWQVTHHTWNAILLPFVYLTQVWILCAATAAASAGFQNCPCVCSNCFQSKV 60  
b 1 MLLWQVTHHTWNAILLPFVYLTQVWILCAATAAASAGFQNCPCVCSNCFQSKV 60  
Y 61 CTRGLSEVPQGPSNTRYLNLMENNMIQADTFRLHLHLVQLGRNSIRQIEVGAFN 120  
b 61 CTRGLSEVPQGPSNTRYLNLMENNMIQADTFRLHLHLVQLGRNSIRQIEVGAFN 120  
Y 121 GLASLNTLSELPDNLTVIPSGAFYLSKRLRLWLNPNPIESPSYAFNRVPSLRLDLGE 180  
b 121 GLASLNTLSELPDNLTVIPSGAFYLSKRLRLWLNPNPIESPSYAFNRVPSLRLDLGE 180  
Y 181 LKKLEYISGAFEGFLNLYLNGLMCNIDMPNLTPVLGLELEMSGNHFFPIRPGSFHG 240  
C 181 LKKLEYISGAFEGFLNLYLNGLMCNIDMPNLTPVLGLELEMSGNHFFPIRPGSFHG 240

QY 241 LSSSEKKLWVMSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLPTPLRYLYVELHLHN 300  
DB 241 LSSSEKKLWVMSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLPTPLRYLYVELHLHN 300  
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DB 301 PWNCDIDLAWMLREYIPNNSCCGRCCHAPMGRGYLVEVDQASFQCSAPPIMDAPR 360  
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DB 361 DLNISEGRMAELKCRTPPMSSVKWLLPNTGVLSHSHPRISVLNDGTLPFSHVLLSDTG 420  
QY 421 VYTCVNTVAGNSASAYLVNSTAELNTSNYSPTTIVTTELSPEDTTRKKVPEPTTS 480  
DB 421 VYTCVNTVAGNSASAYLVNSTAELNTSNYSPTTIVTTELSPEDTTRKKVPEPTTS 480  
QY 481 TGYOPAYTISTTVLIQTTRVPKQVAVPATDTDKMOTSLDEVMKTKIIIGCFVAVTLLA 540  
DB 481 TGYOPAYTISTTVLIQTTRVPKQVAVPATDTDKMOTSLDEVMKTKIIIGCFVAVTLLA 540  
QY 541 AAMLIVFYKLRKHQRSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVLPT 600  
DB 541 AAMLIVFYKLRKHQRSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVLPT 600  
QY 601 IHDHINYNTYKPAHGAHWNTENSLNSLHPTVTIISBPYIIQTHTKDKVQETQI 653  
DB 601 IHDHINYNTYKPAHGAHWNTENSLNSLHPTVTIISBPYIIQTHTKDKVQETQI 653

RESULT 10

ABUS5257  
ID ABUS5257 standard; Protein; 653 AA.

XX AC ABUS5257;

XX DT 22-APR-2003 (first entry)

XX DE Human secreted/transmembrane protein, #93.

XX KW Human; PRO; secreted; transmembrane; pharmaceutical;  
XX KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
XX KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
XX KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.

XX OS Homo sapiens.

XX PN US2003027162-A1.

XX PD 06-FEB-2003.

XX PF 15-NOV-2001; 2001US-0997428.

XX PR 05-NOV-1997; 97WO-US200069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.





PR	02-JUN-1998;	98US-087609P.	PR	07-JUL-1998;	98US-091978P.
PR	02-JUN-1998;	98US-087759P.	PR	07-JUL-1998;	98US-091982P.
PR	03-JUN-1998;	98US-087827P.	PR	09-JUL-1998;	98US-092182P.
PR	04-JUN-1998;	98US-088021P.	PR	10-JUL-1998;	98US-092472P.
PR	04-JUN-1998;	98US-088025P.	PR	20-JUL-1998;	98US-093339P.
PR	04-JUN-1998;	98US-088026P.	PR	30-JUL-1998;	98US-094651P.
PR	04-JUN-1998;	98US-088028P.	PR	04-AUG-1998;	98US-095282P.
PR	04-JUN-1998;	98US-088029P.	PR	04-AUG-1998;	98US-095285P.
PR	04-JUN-1998;	98US-088030P.	PR	04-AUG-1998;	98US-095301P.
PR	04-JUN-1998;	98US-088033P.	PR	04-AUG-1998;	98US-095302P.
PR	04-JUN-1998;	98US-088326P.	PR	04-AUG-1998;	98US-095318P.
PR	05-JUN-1998;	98US-088167P.	PR	04-AUG-1998;	98US-095321P.
PR	05-JUN-1998;	98US-088202P.	PR	04-AUG-1998;	98US-095325P.
PR	05-JUN-1998;	98US-088212P.	PR	10-AUG-1998;	98US-095916P.
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PR	10-JUN-1998;	98US-088734P.	PR	11-AUG-1998;	98US-096143P.
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PR	10-JUN-1998;	98US-088742P.	PR	12-AUG-1998;	98US-096329P.
PR	10-JUN-1998;	98US-088810P.	PR	17-AUG-1998;	98US-096757P.
PR	10-JUN-1998;	98US-088826P.	PR	17-AUG-1998;	98US-096766P.
PR	11-JUN-1998;	98US-088858P.	PR	17-AUG-1998;	98US-096768P.
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PR	12-JUN-1998;	98US-089105P.	PR	17-AUG-1998;	98US-096891P.
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PR	16-JUN-1998;	98US-089512P.	PR	17-AUG-1998;	98US-096895P.
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PR	17-JUN-1998;	98US-089598P.	PR	18-AUG-1998;	98US-096959P.
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PR	17-JUN-1998;	98US-089653P.	PR	19-AUG-1998;	98US-097141P.
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PR	18-JUN-1998;	98US-089807P.	PR	24-AUG-1998;	98US-097661P.
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PR	19-JUN-1998;	98US-089952P.	PR	26-AUG-1998;	98US-097971P.
PR	22-JUN-1998;	98US-090246P.	PR	26-AUG-1998;	98US-097974P.
PR	22-JUN-1998;	98US-090252P.	PR	26-AUG-1998;	98US-097978P.
PR	22-JUN-1998;	98US-090254P.	PR	26-AUG-1998;	98US-097979P.
PR	23-JUN-1998;	98US-090349P.	PR	26-AUG-1998;	98US-097986P.
PR	23-JUN-1998;	98US-090355P.	PR	26-AUG-1998;	98US-098014P.
PR	24-JUN-1998;	98US-090429P.			
PR	24-JUN-1998;	98US-090431P.			
PR	24-JUN-1998;	98US-090435P.			
PR	24-JUN-1998;	98US-090444P.			
PR	24-JUN-1998;	98US-090445P.			
PR	24-JUN-1998;	98US-090472P.			
PR	24-JUN-1998;	98US-090535P.			
PR	24-JUN-1998;	98US-090540P.			
PR	24-JUN-1998;	98US-090542P.			
PR	24-JUN-1998;	98US-090557P.			
PR	25-JUN-1998;	98US-090576P.			
PR	25-JUN-1998;	98US-090578P.			
PR	25-JUN-1998;	98US-090600P.			
PR	25-JUN-1998;	98US-090694P.			
PR	25-JUN-1998;	98US-090695P.			
PR	25-JUN-1998;	98US-090696P.			
PR	25-JUN-1998;	98US-090862P.			
PR	26-JUN-1998;	98US-090863P.			
PR	01-JUL-1998;	98US-091360P.			
PR	01-JUL-1998;	98US-091344P.			
PR	02-JUL-1998;	98US-091478P.			
PR	02-JUL-1998;	98US-091519P.			
PR	02-JUL-1998;	98US-091626P.			
PR	02-JUL-1998;	98US-091628P.			
PR	02-JUL-1998;	98US-091633P.			
PR	02-JUL-1998;	98US-091646P.			
PR	02-JUL-1998;	98US-091673P.			
			Query Match 100.0%; Score 3440; DB 24; length 653; Best Local Similarity 100.0%; Pred. No. 6.4e-278; Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MKLLWQVTHHTWNAILLPFVYLTQVWILCAIAIAAASAGPNCPSVCSCSNQPSKV 60	Qy	1	MKLLWQVTHHTWNAILLPFVYLTQVWILCAIAIAAASAGPNCPSVCSCSNQPSKV 60
Db	1	MKLLWQVTHHTWNAILLPFVYLTQVWILCAIAIAAASAGPNCPSVCSCSNQPSKV 60	Db	1	MKLLWQVTHHTWNAILLPFVYLTQVWILCAIAIAAASAGPNCPSVCSCSNQPSKV 60
Qy	61	CTRGISEVPQGISNTRYLMNENNIQIADTFRLHLEHLVQLGRNSIROIEVGAFN 120	Qy	61	CTRGISEVPQGISNTRYLMNENNIQIADTFRLHLEHLVQLGRNSIROIEVGAFN 120
Db	61	CTRGISEVPQGISNTRYLMNENNIQIADTFRLHLEHLVQLGRNSIROIEVGAFN 120	Db	61	CTRGISEVPQGISNTRYLMNENNIQIADTFRLHLEHLVQLGRNSIROIEVGAFN 120
Qy	121	GLASINTLELFDNNLTVIPSGAFYLSKLRELMRNPNPIESISYAFNRVPSLMRLDGE 180	Qy	121	GLASINTLELFDNNLTVIPSGAFYLSKLRELMRNPNPIESISYAFNRVPSLMRLDGE 180
Db	121	GLASINTLELFDNNLTVIPSGAFYLSKLRELMRNPNPIESISYAFNRVPSLMRLDGE 180	Db	121	GLASINTLELFDNNLTVIPSGAFYLSKLRELMRNPNPIESISYAFNRVPSLMRLDGE 180
Qy	181	LKKLEYISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLLELEMSGNHPEIRPGSFHG 240	Qy	181	LKKLEYISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLLELEMSGNHPEIRPGSFHG 240
Db	181	LKKLEYISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLLELEMSGNHPEIRPGSFHG 240	Db	181	LKKLEYISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLLELEMSGNHPEIRPGSFHG 240
Qy	241	LSSLKLWVMSQVSLIERNAPDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHN 300	Qy	241	LSSLKLWVMSQVSLIERNAPDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHN 300
Db	241	LSSLKLWVMSQVSLIERNAPDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHN 300	Db	241	LSSLKLWVMSQVSLIERNAPDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHN 300
Qy	301	PWNCDDILMLAWLREYIPTNSTCCORCHAPWHRGCRYLVEVDQASFOCSAPPIMDAPR 360	Qy	301	PWNCDDILMLAWLREYIPTNSTCCORCHAPWHRGCRYLVEVDQASFOCSAPPIMDAPR 360
Db	301	PWNCDDILMLAWLREYIPTNSTCCORCHAPWHRGCRYLVEVDQASFOCSAPPIMDAPR 360	Db	301	PWNCDDILMLAWLREYIPTNSTCCORCHAPWHRGCRYLVEVDQASFOCSAPPIMDAPR 360

301	PWNCDCLILAWLREVLPYPTNSTCCGRCHAPMEMRGRIYLVETDQASFCQSPAPFINDAPR	360
361	DLINISEGMAELKCRTPPMSSVKLLPMGTVLSHASHPRPISVLNDGTILNFSHVLLSDTG	420
361	DLINISEGMAELKCRTPPMSSVKLLPMGTVLSHASHPRPISVLNDGTILNFSHVLLSDTG	420
421	VYTCMVTVNAGSNASAYLVNSTAELNTSNYSFPTTVTVETTSISEDTTRKYKVPVPTS	480
421	VYTCMVTVNAGSNASAYLVNSTAELNTSNYSFPTTVTVETTSISEDTTRKYKVPVPTS	480
481	TGYQPAYTTSITVLIQTRVPKQVAVPATDTRKQOTSLDEVNKTTKLIIGCFVAVTLLA	540
481	TGYQPAYTTSITVLIQTRVPKQVAVPATDTRKQOTSLDEVNKTTKLIIGCFVAVTLLA	540
541	AAMLIVFYKLEKRRHQORSTVTAARTVBEIIQVDEDIPAATSAATAAPSGVSEGAVALPT	600
541	AAMLIVFYKLEKRRHQORSTVTAARTVBEIIQVDEDIPAATSAATAAPSGVSEGAVALPT	600
601	IHDHINYNTYKPAFGAWTENSLSNLSLEPTVTTTISEPYIIQTHTKDKVOETQI	653
601	IHDHINYNTYKPAFGAWTENSLSNLSLEPTVTTTISEPYIIQTHTKDKVOETQI	653

RSIT, T 12

RESULT I  
BUT60547

D ABI160541 standard: protein: 653 AA.

ABU60541:

01-MAY-2003 (first entry)

Human secreted/transmembrane protein, #93:

Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.

Homosapiens.

US2002160384-A1.

31-OCT-2002.

14-NOV-2001: 2001US-0992598.

05-NOV-1997: 97WO-US20069.

'K 16-SEP-1998; 98WO-US19330;  
'R 17-SEP-1998; 98WO-US19437.

'R 07-OCT-1998; 98WO-US21141.  
'R 01-DEC-1998; 98WO-US25108.

'R 05-JAN-1999; 99W0-US00106.  
'R 08-MAR-1999; 99W0-US05028.

'R 02-JUN-1999; 99WC-US12252.  
'R 15-SEP-1999; 99WC-US21090.

99WO-US21547.  
15-SEP-1999;  
30-NOV-1999;  
99WO-US28313

99WC-US28301.  
01-DEC-1999;  
01-DEC-1999.

R 16-DEC-1999; 99WO-US30095.  
R 20 DEC 1999. 99WO-US30811

05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00379

>R 11-FEB-2000; 2000WO-US03565.  
10 FEB 2000 2000WO H504341  
10 FEB 2000 2000WO H504341

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US05004.

2R 10-MAR-2000; 2000WO-US06319.

20-MAR-2000; 2000WO-US07377.

PR 15-MAY-2000; 2000WO-US13358.

PR	22-MAY-2000;	2000WO-US1140432;
PR	30-MAY-2000;	2000WO-US1145941;
PR	30-JUN-2000;	2000WO-US1152641;
PR	28-JUL-2000;	2000WO-US207110;
PR	11-AUG-2000;	2000WO-US220311;
PR	23-AUG-2000;	2000WO-US235222;
PR	24-AUG-2000;	2000WO-US233328;
PR	08-NOV-2000;	2000WO-US309552;
PR	21-DEC-2000;	2000WO-US334678;
PR	28-FEB-2001;	2001WO-US065520;
PR	01-JUN-2001;	2001WO-US117800;
PR	20-JUN-2001;	2001WO-US119692;
PR	29-JUN-2001;	2001WO-US210666;
PR	09-JUL-2001;	2001WO-US211735;
PR	16-JUN-1997;	97US-04978735;
PR	17-OCT-1997;	97US-06225050;
PR	12-NOV-1997;	97US-06531110;
PR	13-NOV-1997;	97US-06531110;
PR	24-NOV-1997;	97US-06677010;
PR	25-FEB-1998;	98US-07594545;
PR	20-MAR-1998;	98US-07783101;
PR	28-APR-1998;	98US-08332220;
PR	07-MAY-1998;	98US-08446000;
PR	28-MAY-1998;	98US-08710660;
PR	02-JUN-1998;	98US-08760770;
PR	02-JUN-1998;	98US-08760909;
PR	02-JUN-1998;	98US-08775590;
PR	03-JUN-1998;	98US-08782770;
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PR	04-JUN-1998;	98US-08803320;
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PR	05-JUN-1998;	98US-08821200;
PR	05-JUN-1998;	98US-08821200;
PR	09-JUN-1998;	98US-08855550;
PR	10-JUN-1998;	98US-08873740;
PR	10-JUN-1998;	98US-08873780;
PR	10-JUN-1998;	98US-08874420;
PR	10-JUN-1998;	98US-08881000;
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PR	11-JUN-1998;	98US-08883580;
PR	11-JUN-1998;	98US-08886610;
PR	11-JUN-1998;	98US-08887660;
PR	12-JUN-1998;	98US-08910500;
PR	16-JUN-1998;	98US-08944000;
PR	16-JUN-1998;	98US-08951200;
PR	16-JUN-1998;	98US-08951420;
PR	17-JUN-1998;	98US-08953320;
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PR	17-JUN-1998;	98US-08959900;
PR	17-JUN-1998;	98US-08960000;
PR	17-JUN-1998;	98US-08960530;
PR	18-JUN-1998;	98US-08980100;
PR	18-JUN-1998;	98US-08990770;
PR	18-JUN-1998;	98US-08990800;
PR	28-AUG-2001;	2001WO-US341992;

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P,  
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP,  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
Zhang Z;

IX



DR WPI: 2003-288106/28.  
DR N-PSDB; AEX90247.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -  
XX  
XX Claim 12; Fig 157; 650pp; English.  
XX  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
XX comprising a sequence without signal peptide and the nucleic acid  
XX encoding them. The polypeptides can be used to raise antibodies that  
XX specifically bind to the PRO polypeptide, for linking a bioactive  
XX molecule to a cell expressing a PRO protein and for modulating at least  
XX one biological activity of a cell. The PRO polypeptides or  
XX polynucleotides are also useful in gene therapy, in chromosome  
XX identification, as chromosome markers, or in generating probes. The PRO  
XX polypeptides are useful as molecular markers for protein  
XX electrophoresis, and the isolated nucleic acids may be used for  
XX recombinantly expressing those markers. The PRO polypeptides and nucleic  
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful  
XX in diagnostic assays for PRO, and in affinity purification of PRO from  
XX recombinant cell culture or natural sources. The sequences presented in  
XX ABU60478-ABU60624 are the PRO polynucleotides of the invention.  
XX Note: The sequence data for this patent is also available in electronic  
XX format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 653 AA;  
Query Match 100.0%; Score 3440; DB 24; Length 653;  
Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLLMQVTYHHHTNAILLPVYLLTAQWILCAIAAASAGPQCPSVCSCSNQPSKV 60  
DB 1 MKLLMQVTYHHHTNAILLPVYLLTAQWILCAIAAASAGPQCPSVCSCSNQPSKV 60  
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DB 61 CTRGLSEVPOGIPENTRYLNLNENNIOMIQADTFHLLHLEVLQLGNSRQIEVGA 120  
QY 121 GLASINTLELFPNLTVPISGAFYLSKLRELNLNENNIOMIQADTFHLLHLEVLQ 180  
DB 121 GLASINTLELFPNLTVPISGAFYLSKLRELNLNENNIOMIQADTFHLLHLEVLQ 180  
QY 181 LKXLEVISGAFEGFLNLYLNLGNLNDKMPNLTPLVGLSELENSGNHPEIRPGSP 240  
DB 181 LKXLEVISGAFEGFLNLYLNLGNLNDKMPNLTPLVGLSELENSGNHPEIRPGSP 240  
QY 241 LSSLLKXLYWNSQVSLIERNADGLASLVELNLNENNIOMIQADTFHLLHLEVL 300  
DB 241 LSSLLKXLYWNSQVSLIERNADGLASLVELNLNENNIOMIQADTFHLLHLEVL 300  
QY 301 PNWCDCDILAWLWREYIPTNSTCCGRCHAPMHMRGYLVEVDQASQCSPAFIM 360  
DB 301 PNWCDCDILAWLWREYIPTNSTCCGRCHAPMHMRGYLVEVDQASQCSPAFIM 360  
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DB 361 DLNISSEGRAELKCRTPPMSVYKLLPNTGTVLSHARHPRISVLNDGTLNFSH 420  
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DB 421 VYTCMTNVAGNSNAYLNVSATLNTSNYGFVTVTVEITEISPEDTRKYKVPPTS 480  
QY 481 TGYPAYTSTTVLIOTTVPKQVAPATDTDDKMCSTLDEYKTKLILGCFVAVTLL 540  
DB 481 TGYPAYTSTTVLIOTTVPKQVAPATDTDDKMCSTLDEYKTKLILGCFVAVTLL 540  
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ABU58032  
ID ABU58032 standard; Protein; 653 AA.  
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XX AC ABU58032;  
XX  
XX DT 14-APR-2003 (first entry)  
XX  
XX DE Human PRO polypeptide #64.  
XX  
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
XX KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
XX KW antibody-dependent enzyme mediated prodrug therapy.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2003027163-A1.  
XX  
XX PD 06-FEB-2003.  
XX  
XX PF 15-NOV-2001; 2001US-0997666.  
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XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 98WO-US00106.  
XX 08-MAR-1999; 98WO-US05028.  
XX 02-JUN-1999; 98WO-US12252.  
XX 15-SEP-1999; 98WO-US21090.  
XX 15-SEP-1999; 98WO-US21547.  
XX 30-NOV-1999; 98WO-US28313.  
XX 01-DEC-1999; 98WO-US28301.  
XX 01-DEC-1999; 98WO-US28634.  
XX 16-DEC-1999; 98WO-US30095.  
XX 20-DEC-1999; 98WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 15-MAY-2000; 2000WO-US13358.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 11-AUG-2000; 2000WO-US22031.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23528.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.  
XX 16-JUN-1997; 97US-049787P.  
XX 17-OCT-1997; 97US-062250P.  
XX 12-NOV-1997; 97US-065186P.

R	13-NOV-1997;	97US-065311P.	PR	01-JUL-1998;	98US-091544P.				
R	24-NOV-1997;	97US-066770P.	PR	02-JUL-1998;	98US-091478P.				
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R	17-JUN-1998;	98US-089532P.	PR	17-AUG-1998;	98US-096897P.				
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R	17-JUN-1998;	98US-089653P.	PR	19-AUG-1998;	98US-097141P.				
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R	18-JUN-1998;	98US-089908P.	PR	26-AUG-1998;	98US-097952P.				
R	19-JUN-1998;	98US-089947P.	PR	26-AUG-1998;	98US-097954P.				
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R	22-JUN-1998;	98US-090246P.	PR	26-AUG-1998;	98US-097971P.				
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R	22-JUN-1998;	98US-090254P.	PR	26-AUG-1998;	98US-097978P.				
R	23-JUN-1998;	98US-090349P.	PR	26-AUG-1998;	98US-097979P.				
R	24-JUN-1998;	98US-090429P.	PR	26-AUG-1998;	98US-097986P.				
R	24-JUN-1998;	98US-090431P.	PR	31-AUG-1998;	98US-098014P.				
R	24-JUN-1998;	98US-090435P.	PR	31-AUG-1998;	98US-098525P.				
R	24-JUN-1998;	98US-090444P.	PR	16-SEP-1998;	98US-100634P.				
R	24-JUN-1998;	98US-090445P.	PR	17-SEP-1998;	98US-100858P.				
R	24-JUN-1998;	98US-090472P.	PR	22-DEC-1998;	98US-113298P.				
R	24-JUN-1998;	98US-090535P.	PR	12-MAR-1999;	99US-123957P.				
R	24-JUN-1998;	98US-090540P.	PR	23-JUN-1999;	99US-141037P.				
R	24-JUN-1998;	98US-090542P.	PR	07-JUL-1999;	99US-143048P.				
R	24-JUN-1998;	98US-090557P.	PR						
R	25-JUN-1998;	98US-090676P.	PR						
R	25-JUN-1998;	98US-090678P.	PR						
R	25-JUN-1998;	98US-090690P.	PR						
R	25-JUN-1998;	98US-090694P.	PR						
R	25-JUN-1998;	98US-090695P.	PR						
R	25-JUN-1998;	98US-090696P.	PR						
R	26-JUN-1998;	98US-090862P.	PR						
R	26-JUN-1998;	98US-090863P.	PR						
R	01-JUL-1998;	98US-091360P.	PR						

Query Match 100.0%; Score 3440; DB 24; Length 653;

Best Local Similarity 100.0%; Pred. No. 6.4e-278; Mismatches 0; Indels 0; Caps 0;

Matches 653; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MKLLMQVTVHHTWNAILLPPVYLTQVWILCAIAIAAASAGPQNCPSVCSNQSUV 60

DB 1 MKLLMQVTVHHTWNAILLPPVYLTQVWILCAIAIAAASAGPQNCPSVCSNQSUV 60

QY 61 CTRGLSEVPQIPSNTRYLNLMENNIOQADTFRHLHLEVLQIGNSIROIEVCAF 120

DB 61 CTRGLSEVPQIPSNTRYLNLMENNIOQADTFRHLHLEVLQIGNSIROIEVCAF 120

QY 121 GLASLNTLFLPNLWLTIVIPSGAFYLSKRLRLWLNPNPIESIPSVAFNRVPSLMLDLGE 180  
 DB 121 GLASLNTLFLPNLWLTIVIPSGAFYLSKRLRLWLNPNPIESIPSVAFNRVPSLMLDLGE 180  
 QY 181 LKLEYISGAFEGFLNLYLGLMGNICNDPNLTPLVGLBELENSGNHFFPIRPGSFHG 240  
 DB 181 LKLEYISGAFEGFLNLYLGLMGNICNDPNLTPLVGLBELENSGNHFFPIRPGSFHG 240  
 QY 241 LSSLKKLWNSQVSLIERNAFDGLASLVEELNAHNNLSLPHDLPTPLRYLVELHLHN 300  
 DB 241 LSSLKKLWNSQVSLIERNAFDGLASLVEELNAHNNLSLPHDLPTPLRYLVELHLHN 300  
 QY 301 PNCDCDILWLAWLREYIPTNSTCCGRCHAPMGRGYLVEVDQASQCSAPFIMDAPR 360  
 DB 301 PNCDCDILWLAWLREYIPTNSTCCGRCHAPMGRGYLVEVDQASQCSAPFIMDAPR 360  
 QY 361 DLNISGRVABLKCRTPPMSSVKNLLPNGTVLSHARHPRISVLDGTVLNSHVLSDTG 420  
 DB 361 DLNISGRVABLKCRTPPMSSVKNLLPNGTVLSHARHPRISVLDGTVLNSHVLSDTG 420  
 QY 421 VTCMVTVNAGNSNASAYLNVSIAELNTSNYGFFTTVTVEITEISPEDTTRKYKVPPTS 480  
 DB 421 VTCMVTVNAGNSNASAYLNVSIAELNTSNYGFFTTVTVEITEISPEDTTRKYKVPPTS 480  
 QY 481 TGYQPAYTSTTVLIQTTTRVPQVAPADTDDKQTSLSDEVMTTKIIIGCFVAVILLA 540  
 DB 481 TGYQPAYTSTTVLIQTTTRVPQVAPADTDDKQTSLSDEVMTTKIIIGCFVAVILLA 540  
 QY 541 AAMLIYFYKLRKHQRSTVTAARTVEIIQVDEDIPAATSAATAAPSGVSGEGAVLPT 600  
 DB 541 AAMLIYFYKLRKHQRSTVTAARTVEIIQVDEDIPAATSAATAAPSGVSGEGAVLPT 600  
 QY 601 IHDHINNTYKPAHGAHWNTENSLGSHLPTVTITSEPIYIQTHTKDKVQETQI 653  
 DB 601 IHDHINNTYKPAHGAHWNTENSLGSHLPTVTITSEPIYIQTHTKDKVQETQI 653

RESULT 14

ABU58963 standard; Protein; 653 AA.

XX AC ABU58963;  
 XX DT 16-APR-2003 (first entry)  
 XX DE Human secreted/transmembrane protein, #93.

XX Human; PRO; secreted; transmembrane; signal peptide;  
 XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 XX colon cancer; lung cancer; breast cancer;cancer; gene therapy.

XX OS Homo sapiens.

XX PN US2002142961-AL.

XX PD 03-OCT-2002.

XX PF 19-NOV-2001; 2001US-0989721.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 05-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US04520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 13-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 05-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.



PR 28-JUL-2000; 2000MO-US20710.  
PR 11-AUG-2000; 2000MO-US22031.  
PR 23-AUG-2000; 2000MO-US23522.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30352.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 20-JUN-2001; 2001MO-US19692.  
PR 29-JUN-2001; 2001MO-US21066.  
PR 09-JUL-2001; 2001MO-US21735.  
PR 16-JUN-1997; 97US-849787P.  
PR 17-OCT-1997; 97US-862350P.  
PR 12-NOV-1997; 97US-865186P.  
PR 13-NOV-1997; 97US-865311P.  
PR 24-NOV-1997; 97US-866770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 26-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 02-JUN-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 03-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088728P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088976P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 18-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
  
PR (GETH ) GENENTECH LTD.  
PR Ashkenazi AJ, Baker KP, Rotstein D, Desnoyers L, Eaton DL;  
PR Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski RV;  
PR Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PR Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PR Zhang Z;  
PR WPI; 2003-102117/09.  
PR N-PSDB; ABX64093.  
PR XX

PT Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers -  
XX Claim 12; Fig 157; 649pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC PRO polypeptides are useful for detecting other PRO polypeptides, for  
CC linking bioactive molecules to cells expressing PRO polypeptides,  
CC for modulating biological activities of cells expressing PRO  
CC polypeptides, and for identifying agonists or antagonists.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
CC generating transgenic animals or knockout animals, to construct  
CC hybridisation probes for mapping the gene which encodes the PRO  
CC polypeptide, and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as  
CC chromosome markers, and for generating probes for PCR, Northern  
CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006  
CC represent the human PRO polypeptides of the invention.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsdentry.html.  
XX Sequence 653 AA;  
SQ  
  
Query Match 100.0%; Score 3440; DB 24; Length 653;  
Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKLLKQVTVHHHTWNAILLPVYLTAAWVILCAALAAASAGPONCPSVCSNQFSKVV 60  
DB 1 MKLLKQVTVHHHTWNAILLPVYLTAAWVILCAALAAASAGPONCPSVCSNQFSKVV 60  
  
QY 61 CTRRGSLSEVPGQIPSNTRYLNLMENNIQMIQADTFRLHLHLVQLQGRNSIRQIEVGAFN 120  
DB 61 CTRRGSLSEVPGQIPSNTRYLNLMENNIQMIQADTFRLHLHLVQLQGRNSIRQIEVGAFN 120  
  
QY 121 GLASLNTLELFDNWLTVTPSGAFYLSKRLRLNRPDIESIPSYAFNRVPSLWELDGE 180  
DB 121 GLASLNTLELFDNWLTVTPSGAFYLSKRLRLNRPDIESIPSYAFNRVPSLWELDGE 180  
  
QY 181 LKKLEYISBGAPEGLFNKLYNLGNKDKMPNLTPLVGLSELEMSGNHFFPIRPGSFHG 240  
DB 181 LKKLEYISBGAPEGLFNKLYNLGNKDKMPNLTPLVGLSELEMSGNHFFPIRPGSFHG 240  
  
QY 241 LSSLKKLWVNSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLVBLHLHHN 300  
DB 241 LSSLKKLWVNSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLVBLHLHHN 300  
  
QY 301 PWNCCDILWLAWLREYIPTNSTCCGCHAPMHRGRLVEVDQASQCSAPFIMDAPR 360  
DB 301 PWNCCDILWLAWLREYIPTNSTCCGCHAPMHRGRLVEVDQASQCSAPFIMDAPR 360  
  
QY 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHRISVLNDGTINFSHVLLSDTG 420  
DB 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHRISVLNDGTINFSHVLLSDTG 420  
  
QY 421 VYTCMVTVNAGNSASAVLNYSTAE LNSTSYFFTTVTVEITETSPEDTKRYKVPVPTS 480  
DB 421 VYTCMVTVNAGNSASAVLNYSTAE LNSTSYFFTTVTVEITETSPEDTKRYKVPVPTS 480  
  
QY 481 TGYQPAYTSTTVLIQTTRVPKQVAVPATDITDDXNQTSLSDEVMTTKIIIGCFVAVTLLA 540  
DB 481 TGYQPAYTSTTVLIQTTRVPKQVAVPATDITDDXNQTSLSDEVMTTKIIIGCFVAVTLLA 540  
  
QY 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDIIPATSAATAAPSGVSGEGAVLPT 600  
DB 541 AAMLIVFYKLRKHQORSTVTAARTVEIIQVDEDIIPATSAATAAPSGVSGEGAVLPT 600

2Y 601 IHDHINVTYKPAKGAHWTEHNSLHPTVTITISBPYIIOTHTKDKVQETQI 653  
 |||||  
 2D 601 IHDHINVTYKPAKGAHWTEHNSLHPTVTITISBPYIIOTHTKDKVQETQI 653

## RESULT 16

ABU10878  
 ID ABU10878 standard; Protein, 653 AA.

CC AC

ABU10878;

XX 04-FEB-2003 (first entry)

DE Human PRO polypeptide #64.

W Human; PRO; secreted polypeptide; transmembrane polypeptide;  
 W toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
 W protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
 W antibacterial.

NS Homo sapiens.

W US2002123463-A1.

XX 05-SEP-2002.

XX 19-NOV-2001; 2001US-0989732.

XX 05-NOV-1997; 97WO-US20069.

XX 16-SEP-1998; 98WO-US19330.

XX 07-OCT-1998; 98WO-US19437.

XX 01-DEC-1998; 98WO-US21141.

XX 05-JAN-1999; 99WO-US25108.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 15-SEP-1999; 99WO-US21090.

XX 30-NOV-1999; 99WO-US21547.

XX 01-DEC-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US28634.

XX 20-DEC-1999; 99WO-US30095.

XX 06-JAN-2000; 2000WO-US00219.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 24-FEB-2000; 2000WO-US04914.

XX 02-MAR-2000; 2000WO-US05004.

XX 15-MAR-2000; 2000WO-US05841.

XX 30-MAR-2000; 2000WO-US06319.

XX 15-MAY-2000; 2000WO-US07377.

XX 17-MAY-2000; 2000WO-US13358.

XX 22-MAY-2000; 2000WO-US13705.

XX 30-MAY-2000; 2000WO-US14042.

XX 02-JUN-2000; 2000WO-US15264.

XX 28-JUL-2000; 2000WO-US20710.

XX 11-AUG-2000; 2000WO-US22031.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000WO-US23328.

XX 08-NOV-2000; 2000WO-US10952.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-JUN-2001; 2001WO-US17800.

XX 20-JUN-2001; 2001WO-US19692.

XX 29-JUN-2001; 2001WO-US21066.

XX 09-JUL-2001; 2001WO-US21735.

XX 15-JUN-1997; 97US-04978P.

XX 17-OCT-1997; 97US-062250P.

PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-065770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087603P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088023P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089400P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 Ferrara N, Fong S, Gerber H, Gerritsen MG, Goddard A, Godowski PJ,  
 Grimaldi JC, Gurney AL, Kijavini J, Napier MA, Pan J, Paoni NF,  
 Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,  
 Zhang Z;

WPI; 2003-065810/06.

N-PSDB; AEX17057.

Novel secreted and transmembrane polypeptide for modulating biological  
 activity of cell expressing the polypeptide, identifying agonists or  
 antagonists of polypeptide, and as molecular weight markers -

Claim 12; Fig 157; 655pp; English.

The invention relates to a secreted and transmembrane polypeptide, termed  
 PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 useful for detecting PRO polypeptides and for linking a bioactive  
 molecule to a cell expressing the above polypeptides, where the bioactive  
 molecule is a toxin, radiolabel or an antibody. The bioactive material  
 causes the death of the cell. The polypeptide is useful for identifying  
 agonists or antagonists of the PRO polypeptide, for preparing variants of

CC PRO, as a molecular weight marker for protein electrophoresis purposes  
CC and the PRO polynucleotide is useful for recombinantly expressing those  
CC markers. The polynucleotide is also useful as a hybridisation probe, in  
CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
CC the preparation of PRO polypeptide, for generating transgenic animals or  
CC knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, to construct hybridisation  
CC probes for mapping the gene which encodes PRO and for the genetic  
CC analysis of individuals with genetic disorders, in gene therapy, for  
CC chromosome identification, as a chromosome marker and for generating  
CC probes for PCR, Northern analysis, Southern analysis and Western  
CC analysis. This sequence represents a human PRO polypeptide of the  
CC invention.

XX Sequence 653 AA;  
SQ Query Match 100.0%; Score 3440; DB 24; Length 653;  
Best Local Similarity 100.0%; Pred. No. 6.4e-278;  
Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLLAQVTVHHTWNAILLPPVYLTAQWILCAIAAASAGPQNCPSVCSNQSRYV 60  
DB 1 MKLLAQVTVHHTWNAILLPPVYLTAQWILCAIAAASAGPQNCPSVCSNQSRYV 60  
QY 61 CTRRGLSEVPGIPENTRYLNMENNIOIADTFRHLHLEVLQGRNSTRIQLEVAFN 120  
DB 61 CTRRGLSEVPGIPENTRYLNMENNIOIADTFRHLHLEVLQGRNSTRIQLEVAFN 120  
QY 121 GLASLNTLEFDNNLTVIPSGAFEYLSKRLRLWLNPNIESIPSYAFNRVPSLRDLGE 180  
DB 121 GLASLNTLEFDNNLTVIPSGAFEYLSKRLRLWLNPNIESIPSYAFNRVPSLRDLGE 180  
QY 181 LKLEYISEGAFEGFLNKLNLGNKCNIKDNPNTPLVGLSELEMSGNHPTPQSFHG 240  
DB 181 LKLEYISEGAFEGFLNKLNLGNKCNIKDNPNTPLVGLSELEMSGNHPTPQSFHG 240  
QY 241 LSSLLKLVWMSQVSLIERNAFDGLASIVELNLAHNNLSLPHDLFTPLRYLVVELHLHN 300  
DB 241 LSSLLKLVWMSQVSLIERNAFDGLASIVELNLAHNNLSLPHDLFTPLRYLVVELHLHN 300  
QY 301 PWCDCDILNLAWLRVYIPNISTCCGRCHAPMNRGRYLVVEVDQASFOCSAPFINDAPR 360  
DB 301 PWCDCDILNLAWLRVYIPNISTCCGRCHAPMNRGRYLVVEVDQASFOCSAPFINDAPR 360  
QY 361 DLNISEGRMAELKCTPMSVSKMLLPNGTVLSHARPRISVNDGTLNFSHVLLSDTG 420  
DB 361 DLNISEGRMAELKCTPMSVSKMLLPNGTVLSHARPRISVNDGTLNFSHVLLSDTG 420  
QY 421 VYTCMVTNAGNSASAYLVNSTAELNNTSNYSFFTVTVETTEISPDTRKYPVPTTS 480  
DB 421 VYTCMVTNAGNSASAYLVNSTAELNNTSNYSFFTVTVETTEISPDTRKYPVPTTS 480  
QY 481 TCYQPAYTSTTVLIQTRVPKOVAVPATDTDKQVTSLDEVMKTKIITGCFVAVTLLA 540  
DB 481 TCYQPAYTSTTVLIQTRVPKOVAVPATDTDKQVTSLDEVMKTKIITGCFVAVTLLA 540  
QY 541 AAMLVFFVYKLAKRQQRSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVVLP 600  
DB 541 AAMLVFFVYKLAKRQQRSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEAVVLP 600  
QY 601 IHDHINNTYKPAHGAHWTENSLNSLHPTVTIISSEYIIQTHTKDKVQETOI 653  
DB 601 IHDHINNTYKPAHGAHWTENSLNSLHPTVTIISSEYIIQTHTKDKVQETOI 653

RESULT 17  
AAV28806  
ID AAV28806 standard; Protein; 653 AA.  
XX  
AC AAV28806;  
CX  
JT 17-JAN-2000 (first entry)  
CX

DE cc359\_4 secreted protein.  
XX clone cc359\_4; cc359\_4 protein; human adult brain cDNA library;  
XX secreted protein; signal peptide; transmembrane domain; leucine zipper;  
XX hydrophobic nature; TopPredII computer program; cytokine; tissue growth;  
XX nutritional activity; cell proliferation; immune stimulation;  
XX chaoptin domain; immune suppression; hematopoiesis regulation;  
XX tumour inhibition.  
OS Homo sapiens.  
XX  
XX Location/Qualifiers  
FH Peptide 29..41  
FT /note= "Predicted signal peptide"  
FT Protein 42..653  
FT /note= "Mature cc359\_4 protein"  
FT Domain 94..115  
FT /label= Chaoptin domain-1  
FT /note= "Composed of 41 potentially amphipathic repeats"  
FT Domain 118..139  
FT /label= Chaoptin domain-2  
FT /note= "Composed of 41 potentially amphipathic repeats"  
FT Domain 142..163  
FT /label= Chaoptin domain-3  
FT /note= "Composed of 41 potentially amphipathic repeats"  
FT Domain 261..282  
FT /label= Chaoptin domain-4  
FT /note= "Composed of 41 potentially amphipathic repeats"  
XX W09950405-A1.  
PN 07-OCT-1999.  
XX 30-MAR-1999; 99WO-US06946.  
XX 31-MAR-1999; 98US-0080110.  
PR 29-MAR-1999; 99US-0280591.  
XX (GENY ) GENETICS INST INC.  
XX Jacobs K, Mccoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;  
XX WPI; 1999-610849/52.  
DR N-PSDB; AAX90848.  
XX Polynucleotides encoding secreted human proteins, derived from human  
PT adult brain, human fetal brain, human fetal kidney, and human adult  
PT blood cDNA libraries  
PS Claim 1; Page 97-99; 122pp; English.  
XX The present sequence is the cc359\_4 secreted protein encoded by the cDNA  
CC clone cc359\_4. cc359\_4 was isolated from a human adult brain cDNA library  
CC using methods specific for secreted protein cDNAs. The leader sequence or  
CC signal peptide acts as a transmembrane domain due to its hydrophobic  
CC nature. The TopPredII computer program predicts five potential  
CC transmembrane domains centered around amino acids 20, 410, 490, 530 and  
CC 590. This protein has a leucine zipper motif. The polynucleotide and  
CC protein may effect nutritional activity, cytokine and cell proliferation,  
CC immune stimulation or suppression, hematopoiesis regulation, tissue  
CC growth, tumour inhibition etc.  
XX Sequence 653 AA;  
SQ Query Match 99.7%; Score 3431; DB 20; Length 653;  
Best Local Similarity 99.7%; Pred. No. 3.6e-277;  
Matches 651; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLLAQVTVHHTWNAILLPPVYLTAQWILCAIAAASAGPQNCPSVCSNQSRYV 60  
DB 1 MKLLAQVTVHHTWNAILLPPVYLTAQWILCAIAAASAGPQNCPSVCSNQSRYV 60



2Y 61 CTRRGLSEVPOGIPSNTRYLNLMENNIOIADTFRLHLEHLEVLQGRNSIRQIEVGAFN 120  
 Db 61 CTRRGLSEVPOGIPSNTRYLNLMENNIOIADTFRLHLEHLEVLQGRNSIRQIEVGAFN 120  
 Y 121 GLASLNTLELFDNWLTVIPSGAFYLSKRLWLNRPPIESIPSYAFNRPVPSLMRLDLGE 180  
 Db 121 GLASLNTLELFDNWLTVIPSGAFYLSKRLWLNRPPIESIPSYAFNRPVPSLMRLDLGE 180  
 Y 181 LKLEYISGAFGLFNLKYLNGMCKMKNLTPVGLLEELMSGNHPPIRPGSFHG 240  
 Db 181 LKLEYISGAFGLFNLKYLNGMCKMKNLTPVGLLEELMSGNHPPIRPGSFHG 240  
 Y 241 LSSLUKLWVNSQVSLIERNAFDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHEN 300  
 Db 241 LSSLUKLWVNSQVSLIERNAFDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHEN 300  
 Y 301 PWCDCDILWLAWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFOCSAPFIMDAFR 360  
 Db 301 PWCDCDILWLAWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFOCSAPFIMDAFR 360  
 Y 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLASHRHPRIISVINDGTINFSHVLSDTG 420  
 Db 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLASHRHPRIISVINDGTINFSHVLSDTG 420  
 Y 421 VYTCMTNVNAGNSAYLNVAELNTSNYSPTFTVTETTESPEDTRKYPVPTTS 480  
 Db 421 VYTCMTNVNAGNSAYLNVAELNTSNYSPTFTVTETTESPEDTRKYPVPTTS 480  
 Y 481 TGYOPAVTTSFTVLIQTRVPKQVAVPATDITDKMOTSLDENVKTKIIGCFVAVTLLA 540  
 Db 481 TGYOPAVTTSFTVLIQTRVPKQVAVPATDITDKMOTSLDENVKTKIIGCFVAVTLLA 540  
 Y 541 AAMLIYFKLRKHQRSTVTAARTVEIIQVDDIPAAATSAATAAPSGVSGGAVLPT 600  
 Db 541 AAMLIYFKLRKHQRSTVTAARTVEIIQVDDIPAAATSAATAAPSGVSGGAVLPT 600  
 Y 601 IHDHINTYKPAHGAHWNTENSLNSLHPTVTTSISEPYIIQTHTKDKVOETQI 653  
 Db 601 IHDHINTYKPAHGAHWNTENSLNSLHPTVTTSISEPYIIQTHTKDKVOETQI 653

RESULT 18

EG98014  
 D ABG98014 standard; Protein; 649 AA.

X C ABG98014;

X T 07-JAN-2003 (first entry)

X Human leucine rich repeat domain protein associated protein #1.

X Leucine rich repeat; nervous system; human; neural disorder; apoptosis;  
 X renal disorder; immune disorder; arthritis; asthma; AIDS;  
 X acquired immunodeficiency syndrome; rheumatoid arthritis;  
 X haematopoietic disorder; metabolic disease; reproductive disorder;  
 X pulmonary disease; cardiovascular disease; hyperproliferative disorder;  
 X neurodegenerative disease; Alzheimer's disease; Parkinson's disease;  
 X Huntington's disease; developmental disorder; autoimmune disease;  
 X Addison's disease; haemolytic anaemia; antiphospholipid syndrome;  
 X allergic encephalomyelitis; gene therapy.

X Homo sapiens.

X W0200274959-A2.

X 26-SEP-2002.

X 20-DEC-2001; 2001WO-US50457.

X 03-JAN-2001; 2001US-259479P.

X 09-JAN-2001; 2001US-260616P.

X (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Ramanathan C, Feder J, Mintier G;  
 XX WPI; 2002-750554/81.  
 XX New HLRRNS1 nucleic acids and polypeptides, useful for preventing,  
 XX treating, or ameliorating e.g. renal disorder, immune, hematopoietic,  
 XX metabolic, reproductive, pulmonary, cardiovascular or autoimmune  
 XX diseases -  
 XX Example 5; Page 412-415; 415pp; English.  
 XX The invention describes nucleic acids encoding human leucine-rich repeat  
 XX containing proteins expressed in nervous system tissues, HLRRNS1. The  
 XX HLRRNS1 polypeptide or the polynucleotide is useful for preventing,  
 XX treating, or ameliorating a neural disorder or a disorder related to  
 XX aberrant apoptosis modulation (either directly or indirectly), renal  
 XX disorder, immune disorder (e.g. arthritis, asthma, acquired  
 XX haematopoietic syndrome (AIDS) or rheumatoid arthritis),  
 XX haematopoietic, metabolic, reproductive, pulmonary or cardiovascular  
 XX diseases, hyperproliferative disorders, neurodegenerative diseases  
 XX (e.g. Alzheimer's disease, Parkinson's disease or Huntington's  
 XX disease), developmental disorders, non-infectious disorders, nervous  
 XX system diseases and/or disorders, and autoimmune diseases (e.g.  
 XX Addison's disease, haemolytic anaemia, antiphospholipid syndrome, or  
 XX allergic encephalomyelitis). The polynucleotides are also useful as  
 XX chromosome markers for chromosome identification, gene therapy, and in  
 XX identifying organisms from minute biological samples. This is the amino  
 XX acid sequence of a peptide associated with the leucine-rich repeat  
 XX containing nervous system protein of the invention.

SQ Sequence 649 AA;

Query Match 99.0%; Score 3407; DB 23; Length 649;  
 Best Local Similarity 99.2%; Pred No. 3.6e-275;  
 Matches 648; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MKLLQVTVVHHHTWNAILLPFVYLTAQVWLCAIAAASAGSPQSCSNQSKV 60  
 Db 1 MKLLQVTVVHHHTWNAILLPFVYLTAQVWLCAIAAASAGSPQSCSNQSKV 60  
 QY 61 CTRRGLSEVPOGIPSNTRYLNLMENNIOIADTFRLHLEHLEVLQGRNSIRQIEVGAFN 120  
 Db 61 CTRRGLSEVPOGIPSNTRYLNLMENNIOIADTFRLHLEHLEVLQGRNSIRQIEVGAFN 120  
 QY 121 GLASLNTLELFDNWLTVIPSGAFYLSKRLWLNRPPIESIPSYAFNRPVPSLMRLDLGE 180  
 Db 121 GLASLNTLELFDNWLTVIPSGAFYLSKRLWLNRPPIESIPSYAFNRPVPSLMRLDLGE 180  
 QY 181 LKLEYISGAFGLFNLKYLNGMCKMKNLTPVGLLEELMSGNHPPIRPGSFHG 240  
 Db 181 LKLEYISGAFGLFNLKYLNGMCKMKNLTPVGLLEELMSGNHPPIRPGSFHG 240  
 QY 241 LSSLUKLWVNSQVSLIERNAFDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHEN 300  
 Db 241 LSSLUKLWVNSH---ERNAFDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLHEN 296  
 QY 301 PWCDCDILWLAWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFOCSAPFIMDAFR 360  
 Db 297 PWCDCDILWLAWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFOCSAPFIMDAFR 356  
 QY 361 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLASHRHPRIISVINDGTINFSHVLSDTG 420  
 Db 357 DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLASHRHPRIISVINDGTINFSHVLSDTG 416  
 QY 421 VYTCMTNVNAGNSAYLNVAELNTSNYSPTFTVTETTESPEDTRKYPVPTTS 480  
 Db 417 VYTCMTNVNAGNSAYLNVAELNTSNYSPTFTVTETTESPEDTRKYPVPTTS 476  
 QY 481 TGYOPAVTTSFTVLIQTRVPKQVAVPATDITDKMOTSLDENVKTKIIGCFVAVTLLA 540  
 Db 477 TGYOPAVTTSFTVLIQTRVPKQVAVPATDITDKMOTSLDENVKTKIIGCFVAVTLLA 536

QY 541 AAMLVFYKLRKHQRSTVTAARTVEIIQVDEIDIPATSAATAAPSGVSGEAVLPT 600  
 DB 537 AAMLVFYKLRKHQRSTVTAARTVEIIQVDEIDIPATSAATAAPSGVSGEAVLPT 596  
 QY 601 IHDHINNTYKPAHGAHWTEENSLGSLHPTVTITSEPIIOTHTKQVQETQI 653  
 DB 597 IHDHINNTYKPAHGAHWTEENSLGSLHPTVTITSEPIIOTHTKQVQETQI 649

RESULT 19

AAU18035  
 ID AAB23033 standard; Protein; 694 AA.

AC AAB23033;

XX 16-JAN-2001 (first entry)

XX Human SLIT protein-like splice variant, SECX 352358-1.

XX SECX protein; human; secreted; membrane-associated; cancer;  
 KW proliferation regulator; differentiation regulator; non-malignant tumour;  
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;  
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;  
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
 KW neurological disease; Alzheimer's disease; trauma; wound;  
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;  
 KW anti-HIV; antiinflammatory; antiarthritis; antiarteriosclerotic;  
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiac;  
 KW dermatological; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 654

XX /label= unknown

XX /note= "Encoded by TGA"

XX WO200053742-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06280.

XX 09-MAR-1999; 99US-0123667.

XX 08-MAR-2000; 2000US-0123667.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA;

XX WPI; 2000-594318/56.

XX N-PSDB; AAA93620.

XX Novel human membrane associated or secreted polypeptides and  
 PT polynucleotides useful for diagnosis, prevention and treatment of  
 PT pathological states such as cancer, immune, cardiovascular and  
 PT neurological disorders

XX Claim 1; Fig 5; 151pp; English.

XX Sequences AAB23029-B23048 represent human SECX proteins. The SECX  
 CC proteins of the invention are either secreted or membrane-associated  
 CC proteins and act as regulator of cellular proliferation and  
 CC differentiation. SECX proteins or nucleotides are useful for diagnosing  
 CC the presence of, or predisposition to, a disease associated with altered  
 CC levels of SECX proteins and nucleotides. The SECX proteins are also  
 CC useful to screen compounds that modulate SECX activity or expression. The  
 CC interaction of a SECX protein with other cellular proteins may be useful  
 CC to modulate the activity of a partner protein, cellular proliferation,  
 CC cellular differentiation and cell survival. SECX nucleotides are useful  
 CC for the recombinant expression of SECX protein, and may be used to detect  
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to  
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX

CC nucleic acid sequences are also useful for identifying a cell or tissue  
 CC type in a biological sample, and in forensic biology. SECX primers or  
 CC probes are useful for detecting the presence of SECX nucleotides and for  
 CC screening tissue cultures for contamination. Diseases that may be treated  
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,  
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),  
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,  
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
 CC surgical or traumatic wounds, spinal cord injury), and skeletal  
 CC disorders.

XX SQ Sequence 694 AA;

Query Watch 99.0%; Score 3407; DB 21; Length 694;

Best Local Similarity 99.2%; Pred. No. 4e-275;

Matches 648; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLLMQVTVHHTWNAILLPFVYLTAAQVWILCAIAAASAGPQNCPSVCSNQFSKV 60

DB 1 MKLLMQVTVHHTWNAILLPFVYLTAAQVWILCAIAAASAGPQNCPSVCSNQFSKV 60

QY 61 CTRGSLSEVPQGISNTRYLMENNIOIADTFRLHLEVLQGRNSIROEVGAFN 120

DB 61 CTRGSLSEVPQGISNTRYLMENNIOIADTFRLHLEVLQGRNSIROEVGAFN 120

QY 121 GLASLSTLELFDNMLTVIPSGAFVLSKRLRLNPNFISIPSYAFNRVPSLRLDLGE 180

DB 121 GLASLSTLELFDNMLTVIPSGAFVLSKRLRLNPNFISIPSYAFNRVPSLRLDLGE 180

QY 181 LKLEYISSEGAPEGLFNLKYNLGNMKNKMPNLTPLVGLLEEMSGNHFPETRPFSHG 240

DB 181 LKLEYISSEGAPEGLFNLKYNLGNMKNKMPNLTPLVGLLEEMSGNHFPETRPFSHG 240

QY 241 LSSLLKLVWMSQVSLIERNAPDGLASLVELNLNHNLSLPHDLFTPLRYLVELHLHN 300

DB 241 LSSLLKLVWMSQVSLIERNAPDGLASLVELNLNHNLSLPHDLFTPLRYLVELHLHN 300

QY 301 PNWCDCDILWLAWMLREYIPTNSTCCGRCHAPMGRVLYVEVDQASFOCSAPFINDAPR 360

DB 301 PNWCDCDILWLAWMLREYIPTNSTCCGRCHAPMGRVLYVEVDQASFOCSAPFINDAPR 360

QY 361 DLNTISEGRWELKCRTPPMSSVKLLNGTVLSHSRPHRISVLNDGTAFESHVLLSDTG 420

DB 361 DLNTISEGRWELKCRTPPMSSVKLLNGTVLSHSRPHRISVLNDGTAFESHVLLSDTG 420

QY 421 VYTCMVNTVAGNSASAYLVNSTAELNLSNYSPFTTVTTEISPDITTKYKVPFTTS 480

DB 421 VYTCMVNTVAGNSASAYLVNSTAELNLSNYSPFTTVTTEISPDITTKYKVPFTTS 480

QY 481 TGYQPAYTSTTVLIOTTRVPKQVAVPATDTTDXQNTSLDEWVKTKLIIGCFVAVTLLA 540

DB 481 TGYQPAYTSTTVLIOTTRVPKQVAVPATDTTDXQNTSLDEWVKTKLIIGCFVAVTLLA 540

QY 541 AAMLIVFYKLRKHQRSTVTAARTVEIIQVDEIDIPATSAATAAPSGVSGEAVLPT 600

DB 541 AAMLIVFYKLRKHQRSTVTAARTVEIIQVDEIDIPATSAATAAPSGVSGEAVLPT 600

QY 601 IHDHINNTYKPAHGAHWTEENSLGSLHPTVTITSEPIIOTHTKQVQETQI 653

DB 601 IHDHINNTYKPAHGAHWTEENSLGSLHPTVTITSEPIIOTHTKQVQETQI 653

RESULT 20

AAU18035

ID AAU18035 standard; Protein; 606 AA.

XX AC AAU18035;

XX DT 07-NOV-2001 (first entry)

XX DE Human immunoglobulin polypeptide SEQ ID No 180.

X Immunoglobulin; signal transduction pathway protein; cancer;  
W antineoplastic therapy; gene therapy; neurological disorder; renal disorder;  
W cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;  
W reproductive disorder; immune system disorder; proliferative disorder;  
W muscular disorder.  
S Homo sapiens.  
X WO200155315-A2.  
X 02-AUG-2001.  
X 17-JAN-2001; 2001WO-US01326.  
X 31-JAN-2000; 2000US-0179065.  
R 04-FEB-2000; 2000US-0180628.  
R 24-FEB-2000; 2000US-0184664.  
R 02-MAR-2000; 2000US-0186350.  
R 16-MAR-2000; 2000US-0189874.  
R 17-MAR-2000; 2000US-0190076.  
R 18-APR-2000; 2000US-0198123.  
R 19-MAY-2000; 2000US-0205515.  
R 07-JUN-2000; 2000US-0209467.  
R 28-JUN-2000; 2000US-0214886.  
R 30-JUN-2000; 2000US-0215135.  
R 07-JUL-2000; 2000US-0216647.  
R 07-JUL-2000; 2000US-0216880.  
R 11-JUL-2000; 2000US-0217487.  
R 11-JUL-2000; 2000US-0217496.  
R 14-JUL-2000; 2000US-0218290.  
R 26-JUL-2000; 2000US-0220963.  
R 26-JUL-2000; 2000US-0220964.  
R 14-AUG-2000; 2000US-0224518.  
R 14-AUG-2000; 2000US-0224519.  
R 14-AUG-2000; 2000US-0225213.  
R 14-AUG-2000; 2000US-0225214.  
R 14-AUG-2000; 2000US-0225266.  
R 14-AUG-2000; 2000US-0225267.  
R 14-AUG-2000; 2000US-0225268.  
R 14-AUG-2000; 2000US-0225270.  
R 14-AUG-2000; 2000US-0225447.  
R 14-AUG-2000; 2000US-0225757.  
R 14-AUG-2000; 2000US-0225758.  
R 14-AUG-2000; 2000US-0225759.  
R 18-AUG-2000; 2000US-0226279.  
R 22-AUG-2000; 2000US-0226681.  
R 22-AUG-2000; 2000US-0226682.  
R 22-AUG-2000; 2000US-0227182.  
R 23-AUG-2000; 2000US-0227009.  
R 30-AUG-2000; 2000US-0228924.  
R 01-SEP-2000; 2000US-0229287.  
R 01-SEP-2000; 2000US-0229343.  
R 01-SEP-2000; 2000US-0229344.  
R 01-SEP-2000; 2000US-0229345.  
R 05-SEP-2000; 2000US-0229509.  
R 06-SEP-2000; 2000US-0229513.  
R 06-SEP-2000; 2000US-0230437.  
R 06-SEP-2000; 2000US-0230438.  
R 08-SEP-2000; 2000US-0231242.  
R 08-SEP-2000; 2000US-0231243.  
R 08-SEP-2000; 2000US-0231244.  
R 08-SEP-2000; 2000US-0231413.  
R 08-SEP-2000; 2000US-0231414.  
R 08-SEP-2000; 2000US-0232080.  
R 08-SEP-2000; 2000US-0232081.  
R 12-SEP-2000; 2000US-0231968.  
R 14-SEP-2000; 2000US-0232397.  
R 14-SEP-2000; 2000US-0232398.  
R 14-SEP-2000; 2000US-0232399.  
R 14-SEP-2000; 2000US-0232400.  
R 14-SEP-2000; 2000US-0232401.  
R 14-SEP-2000; 2000US-0233063.  
R 14-SEP-2000; 2000US-0233064.  
R 14-SEP-2000; 2000US-0233065.  
R 21-SEP-2000; 2000US-0234223.  
R 21-SEP-2000; 2000US-0234274.  
R 25-SEP-2000; 2000US-0234997.  
R 25-SEP-2000; 2000US-0234998.  
R 26-SEP-2000; 2000US-0235484.  
R 27-SEP-2000; 2000US-0235834.  
R 27-SEP-2000; 2000US-0235836.  
R 29-SEP-2000; 2000US-0236327.  
R 29-SEP-2000; 2000US-0236367.  
R 29-SEP-2000; 2000US-0236368.  
R 29-SEP-2000; 2000US-0236369.  
R 29-SEP-2000; 2000US-0236370.  
R 02-OCT-2000; 2000US-0236802.  
R 02-OCT-2000; 2000US-0237037.  
R 02-OCT-2000; 2000US-0237038.  
R 02-OCT-2000; 2000US-0237039.  
R 13-OCT-2000; 2000US-0237040.  
R 13-OCT-2000; 2000US-0239335.  
R 13-OCT-2000; 2000US-0239337.  
R 20-OCT-2000; 2000US-0240960.  
R 20-OCT-2000; 2000US-0241221.  
R 20-OCT-2000; 2000US-0241785.  
R 20-OCT-2000; 2000US-0241786.  
R 20-OCT-2000; 2000US-0241787.  
R 20-OCT-2000; 2000US-0241808.  
R 20-OCT-2000; 2000US-0241809.  
R 20-OCT-2000; 2000US-0241826.  
R 01-NOV-2000; 2000US-0244617.  
R 08-NOV-2000; 2000US-0246474.  
R 08-NOV-2000; 2000US-0246475.  
R 08-NOV-2000; 2000US-0246476.  
R 08-NOV-2000; 2000US-0246477.  
R 08-NOV-2000; 2000US-0246478.  
R 08-NOV-2000; 2000US-0246523.  
R 08-NOV-2000; 2000US-0246524.  
R 08-NOV-2000; 2000US-0246525.  
R 08-NOV-2000; 2000US-0246526.  
R 08-NOV-2000; 2000US-0246527.  
R 08-NOV-2000; 2000US-0246528.  
R 08-NOV-2000; 2000US-0246532.  
R 08-NOV-2000; 2000US-0246609.  
R 08-NOV-2000; 2000US-0246810.  
R 08-NOV-2000; 2000US-0246811.  
R 08-NOV-2000; 2000US-0246813.  
R 17-NOV-2000; 2000US-0249207.  
R 17-NOV-2000; 2000US-0249208.  
R 17-NOV-2000; 2000US-0249209.  
R 17-NOV-2000; 2000US-0249210.  
R 17-NOV-2000; 2000US-0249211.  
R 17-NOV-2000; 2000US-0249212.  
R 17-NOV-2000; 2000US-0249213.  
R 17-NOV-2000; 2000US-0249214.  
R 17-NOV-2000; 2000US-0249215.  
R 17-NOV-2000; 2000US-0249216.  
R 17-NOV-2000; 2000US-0249217.  
R 17-NOV-2000; 2000US-0249218.  
R 17-NOV-2000; 2000US-0249244.  
R 17-NOV-2000; 2000US-0249245.  
R 17-NOV-2000; 2000US-0249264.  
R 17-NOV-2000; 2000US-0249265.  
R 17-NOV-2000; 2000US-0249297.  
R 17-NOV-2000; 2000US-0249299.  
R 17-NOV-2000; 2000US-0249300.  
R 01-DEC-2000; 2000US-0250160.  
R 01-DEC-2000; 2000US-0250391.  
R 05-DEC-2000; 2000US-0251030.  
R 05-DEC-2000; 2000US-0251988.  
R 06-DEC-2000; 2000US-0256719.  
R 06-DEC-2000; 2000US-0256719.  
R 08-DEC-2000; 2000US-0251479.  
R 08-DEC-2000; 2000US-0251856.  
R 08-DEC-2000; 2000US-0251858.

PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMAN) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-457725/49.  
XX N-PSDB; AAS28823.  
XX

Isolated novel immunoglobulin polypeptide for monitoring the presence and progression of diseases and for diagnosis -

Claim 1; SEQ ID No 180; 551pp; English.

Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the invention. The polypeptides and their associated polynucleotides can be used to diagnose a pathological condition or a susceptibility to a pathological condition in a subject by determining the presence or absence of a mutation in a DNA sequence or determining the presence or amount of expression of the protein. Alternatively the identification of a binding partner to a sequence allows determination of changes in protein activity. The sequences can be used as research tools for receptors or other signal transduction pathway proteins that interact with the polypeptides of the invention and can be used to treat, prevent or diagnose various types of disorders such as neurological disorders, cardiovascular disorders, gastrointestinal disorders, reproductive disorders, immune system disorders, renal disorders, muscular disorders, pulmonary disorders, proliferative disorders and cancer.  
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 606 AA;

Query Match 92.5%; Score 3181; DB 22; Length 606;  
Best Local Similarity 100.0%; Pred. No. 2.3e-256;  
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
48 SVCSNQSFKVCTRGSEVSEVQGPISNTRVNLNMENNIQIADTRHHLHLEVLQ 107  
1 SVCSNQSFKVCTRGSEVSEVQGPISNTRVNLNMENNIQIADTRHHLHLEVLQ 60  
  
108 RNSIRQIEVGAENGASLNTLEFDNLTVIPSGAFYLSKRLRELWLNPNPIPSYAF 167  
61 RNSIRQIEVGAENGASLNTLEFDNLTVIPSGAFYLSKRLRELWLNPNPIPSYAF 120  
  
168 NRVPISLRDLGELKKLEVISGAFEGFLNLYKINLGNKNDPNLTPVGLLEEMSG 227  
121 NRVPISLRDLGELKKLEVISGAFEGFLNLYKINLGNKNDPNLTPVGLLEEMSG 180  
  
228 NHFPEIRPDSFGLSLKLLWNSQVSLIERNAPDGLASVLNLAHNLSLPHOLF 287  
181 NHFPEIRPDSFGLSLKLLWNSQVSLIERNAPDGLASVLNLAHNLSLPHOLF 240  
  
288 PLRYVVELHHPNPNCCDILWLAWLREYIPTNSTCCGCHAPMHRGRLYVEVDQAS 347  
241 PLRYVVELHHPNPNCCDILWLAWLREYIPTNSTCCGCHAPMHRGRLYVEVDQAS 300  
  
348 FQCSAPFINDAPDLNISGRVAELKCRTPMSSVKLLPNTGLSHASRPRI SVLNDG 407  
301 FQCSAPFINDAPDLNISGRVAELKCRTPMSSVKLLPNTGLSHASRPRI SVLNDG 360  
  
408 TLNFSHLLSDTGVTWNTVAGNSASAYLNSTAEINTSNYSFFTVVTEISPE 467  
361 TLNFSHLLSDTGVTWNTVAGNSASAYLNSTAEINTSNYSFFTVVTEISPE 420  
  
468 DTRKYKVPPTSTGQPAYTSTTVLQTTTRPVQAVPATDTRDKMGTSLDEVMKTK 527  
421 DTRKYKVPPTSTGQPAYTSTTVLQTTTRPVQAVPATDTRDKMGTSLDEVMKTK 480

QY 528 IIIGCFVAVTLLAAMLIVFYKLRKHQORSTVTAARTVLIIOVDEDI PAATSAAATAAP 587  
DB 481 IIIGCFVAVTLLAAMLIVFYKLRKHQORSTVTAARTVLIIOVDEDI PAATSAAATAAP 540  
QY 588 SCVSGEGAVLPTIHDHINYNNTYKPAHGAHWNTENSLGNSLHPTVTIISBPYIIOTHTKOK 647  
DB 541 SCVSGEGAVLPTIHDHINYNNTYKPAHGAHWNTENSLGNSLHPTVTIISBPYIIOTHTKOK 600  
QY 648 VQETQI 553  
DB 601 VQETQI 606  
  
RESULT 21  
AAB23034  
ID AAB23034 standard; Protein; 590 AA.  
XX  
AC AAB23034;  
XX  
DT 16-JAN-2001 (first entry)  
XX  
DE Human SLIT protein-like splice variant, SECC 3352358-2.  
XX  
KW SECC protein; human; secreted; membrane-associated; cancer;  
KW proliferation regulator; differentiation regulator; non-malignant tumour;  
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;  
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;  
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
KW neurological disease; Alzheimer's disease; trauma; wounding;  
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;  
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;  
KW neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;  
KW dermatological; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200053742-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-US06280.  
XX  
PR 09-MAR-1999; 99US-0123667.  
PR 08-MAR-2000; 2000US-0123667.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA;  
XX  
DR WPI; 2000-594318/56.  
DR N-PSDB; AAA93621.  
XX  
PT Novel human membrane associated or secreted polypeptides and  
PT polynucleotides useful for diagnosis, prevention and treatment of  
PT pathological states such as cancer, immune, cardiovascular and  
PT neurological disorders -  
XX  
XX Claim 1; Fig 6; 151pp; English.  
XX  
CC Sequences AAB23029-B23048 represent human SECC proteins. The SECC  
CC proteins of the invention are either secreted or membrane-associated  
CC and act as regulator of cellular proliferation and  
CC differentiation. SECC proteins or nucleotides are useful for diagnosing  
CC the presence of, or predisposition to, a disease associated with altered  
CC levels of SECC proteins and nucleotides. The SECC proteins are also  
CC useful to screen compounds that modulate SECC activity or expression. The  
CC interaction of a SECC protein with other cellular proteins may be useful  
CC to modulate the activity of a partner protein, cellular proliferation,  
CC cellular differentiation and cell survival. SECC nucleotides are useful  
CC for the recombinant expression of SECC protein, and may be used detect  
CC SECC mRNA or genetic lesions in the SECC gene. They may also be used to  
CC modulate SECC expression (e.g., using antisense oligonucleotides). SECC

C nucleic acid sequences are also useful for identifying a cell or tissue  
C type in a biological sample, and in forensic biology. SEX primers or  
C probes are useful for detecting the presence of SEX nucleotides and for  
C screening tissue cultures for contamination. Diseases that may be treated  
C or prevented using SEX proteins or nucleotides include cancer (e.g.,  
C colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
C (including autoimmune diseases, transplant rejection, allergies, AIDS),  
C infections, inflammatory disorders, arthritis, haematopoietic disorders,  
C skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
C neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
C surgical or traumatic wounds, spinal cord injury), and skeletal  
C disorders.

X	Q	Sequence	590 AA;
		Query Match	85.8%; Score 2951; DB 21; Length 590;
		Best Local Similarity	97.8%; Pred. No. 3.5e-237;
		Matches 562; Conservative	4; Mismatches 10; Indels 0; Gaps 0;
Y	1	MKLLQVTVHHHTWNAILLPFVYLTAAQVILCAIAAASAGPQCPSCVCSNQFSKV 60	
b	1	MKLLQVTVHHHTWNAILLPFVYLTAAQVILCAIAAASAGPQCPSCVCSNQFSKV 60	
Y	61	CTRGISEVPGIPSNTRYINLMENNIQIOADTRHLHLEVLQIGRNSIRQIEVGAFN 120	
b	61	CTRGISEVPGIPSNTRYINLMENNIQIOADTRHLHLEVLQIGRNSIRQIEVGAFN 120	
Y	121	GLASLTLELFDNLVTPISGAFYLSKRLWLNPNPIESIPSAFNRVPSLMRLDGE 180	
b	121	GLASLTLELFDNLVTPISGAFYLSKRLWLNPNPIESIPSAFNRVPSLMRLDGE 180	
Y	181	LKKLEVISGAFGLFNLYLNGMKNKMPNLPVGLBLEMSGNHFPIRPGSFHG 240	
b	181	LKKLEVISGAFGLFNLYLNGMKNKMPNLPVGLBLEMSGNHFPIRPGSFHG 240	
Y	241	LSSLKKLWVNSQVSLIERNADGLASLVELNLAHNNLSLPHDFTPLRYLVELLHHN 300	
b	241	LSSLKKLWVNSQVSLIERNADGLASLVELNLAHNNLSLPHDFTPLRYLVELLHHN 300	
Y	301	PWCDCDILWALWREYIPTNSTCCGRCHAPMHMERGYLVEVDQASFCQCSAPPINDAPR 360	
b	301	PWCDCDILWALWREYIPTNSTCCGRCHAPMHMERGYLVEVDQASFCQCSAPPINDAPR 360	
Y	361	DLNISGRMAELKCRTPPMSVXWLPNGTVLSHSHRPRISVLNDGTINSHVLLSDTG 420	
b	361	DLNISGRMAELKCRTPPMSVXWLPNGTVLSHSHRPRISVLNDGTINSHVLLSDTG 420	
Y	421	VYTCMTNVAGNSNAYLNSTAEALNTSNISFTTIVTVEITTEISPEDTRKYKVPVPTS 480	
b	421	VYTCMTNVAGNSNAYLNSTAEALNTSNISFTTIVTVEITTEISPEDTRKYKVPVPTS 480	
Y	481	TGQPAYTTSVTLIQTTRVPKQVAVPADTDDKQTSLSDEVNKTIIIGCFVAVTLLA 540	
b	481	TGQPAYTTSVTLIQTTRVPKQVAVPADTDDKQTSLSDEVNKTIIIGCFVAVTLLA 540	
Y	541	AAMLIVPKLRKHQRSTVTAARTVEIIQVSDIP 576	
b	541	AAMLIVPKLRKHQRSTVTAARTVEIIQVSDIP 576	

RESULT 22  
BB10349  
D ABB10349 standard; Protein; 553 AA.  
X ABB10349;  
X 10-JAN-2002 (first entry)  
X Human cDNA SEQ ID NO: 657.  
X Human; gene therapy; neural disorder; immune system disorder;  
X muscular disorder; reproductive disorder; gastrointestinal disorder;  
X pulmonary disorder; cardiovascular disorder; renal disorder;

KW proliferative disorder; inflammation.  
XX Homo sapiens.  
XX WO200154474-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01349.  
XX 31-JAN-2000; 2000US-179055P.  
XX 04-FEB-2000; 2000US-180628P.  
XX 24-FEB-2000; 2000US-184664P.  
XX 02-MAR-2000; 2000US-186350P.  
XX 16-MAR-2000; 2000US-189874P.  
XX 17-MAR-2000; 2000US-190076P.  
XX 18-APR-2000; 2000US-198123P.  
XX 19-MAY-2000; 2000US-205515P.  
XX 28-JUN-2000; 2000US-209467P.  
XX 30-JUN-2000; 2000US-214886P.  
XX 07-JUL-2000; 2000US-215135P.  
XX 07-JUL-2000; 2000US-216647P.  
XX 11-JUL-2000; 2000US-216880P.  
XX 11-JUL-2000; 2000US-217487P.  
XX 11-JUL-2000; 2000US-217496P.  
XX 14-JUL-2000; 2000US-218290P.  
XX 26-JUL-2000; 2000US-220963P.  
XX 26-JUL-2000; 2000US-220964P.  
XX 14-AUG-2000; 2000US-224518P.  
XX 14-AUG-2000; 2000US-224519P.  
XX 14-AUG-2000; 2000US-225213P.  
XX 14-AUG-2000; 2000US-225214P.  
XX 14-AUG-2000; 2000US-225266P.  
XX 14-AUG-2000; 2000US-225267P.  
XX 14-AUG-2000; 2000US-225268P.  
XX 14-AUG-2000; 2000US-225270P.  
XX 14-AUG-2000; 2000US-225447P.  
XX 14-AUG-2000; 2000US-225757P.  
XX 14-AUG-2000; 2000US-225758P.  
XX 14-AUG-2000; 2000US-225759P.  
XX 18-AUG-2000; 2000US-226279P.  
XX 22-AUG-2000; 2000US-226681P.  
XX 22-AUG-2000; 2000US-226688P.  
XX 23-AUG-2000; 2000US-227182P.  
XX 23-AUG-2000; 2000US-227099P.  
XX 30-AUG-2000; 2000US-228924P.  
XX 01-SEP-2000; 2000US-229287P.  
XX 01-SEP-2000; 2000US-229343P.  
XX 01-SEP-2000; 2000US-229344P.  
XX 05-SEP-2000; 2000US-229509P.  
XX 05-SEP-2000; 2000US-229513P.  
XX 06-SEP-2000; 2000US-230437P.  
XX 06-SEP-2000; 2000US-230438P.  
XX 08-SEP-2000; 2000US-231242P.  
XX 08-SEP-2000; 2000US-231243P.  
XX 08-SEP-2000; 2000US-231244P.  
XX 08-SEP-2000; 2000US-231413P.  
XX 08-SEP-2000; 2000US-231414P.  
XX 08-SEP-2000; 2000US-232080P.  
XX 12-SEP-2000; 2000US-231968P.  
XX 14-SEP-2000; 2000US-232397P.  
XX 14-SEP-2000; 2000US-232398P.  
XX 14-SEP-2000; 2000US-232399P.  
XX 14-SEP-2000; 2000US-232400P.  
XX 14-SEP-2000; 2000US-232401P.  
XX 14-SEP-2000; 2000US-233063P.  
XX 14-SEP-2000; 2000US-233064P.  
XX 14-SEP-2000; 2000US-233065P.  
XX 21-SEP-2000; 2000US-234233P.  
XX 21-SEP-2000; 2000US-234274P.  
XX 25-SEP-2000; 2000US-234937P.

PR	25-SEP-2000;	2000US-234998P.	XX	(HUMA-) HUMAN GENOME SCI INC.
PR	26-SEP-2000;	2000US-235484P.	PA	
PR	27-SEP-2000;	2000US-235834P.	XX	Rosen CA, Barash SC, Ruben SM;
PR	27-SEP-2000;	2000US-235836P.	PI	
PR	29-SEP-2000;	2000US-236327P.	XX	WPI; 2001-476161/51.
PR	29-SEP-2000;	2000US-236367P.	DR	N-PSDB; ABA06571.
PR	29-SEP-2000;	2000US-236368P.	XX	
PR	29-SEP-2000;	2000US-236369P.	XX	
PR	29-SEP-2000;	2000US-236370P.	PT	Isolated nucleic acid molecule encoding an inflammation-associated
PR	29-SEP-2000;	2000US-236370P.	PT	polypeptide is used in preventing, treating or ameliorating a medical
PR	02-OCT-2000;	2000US-236802P.	PT	condition
PR	02-OCT-2000;	2000US-237037P.	XX	
PR	02-OCT-2000;	2000US-237038P.	XX	Claim 11; SEQ ID NO: 657; 859pp + Sequence Listing; English.
PR	02-OCT-2000;	2000US-237039P.	PS	
PR	02-OCT-2000;	2000US-237040P.	XX	
PR	13-OCT-2000;	2000US-239935P.	CC	The present invention provides human cDNAs, proteins and related genomic
PR	13-OCT-2000;	2000US-239937P.	CC	DNA. These can be used in the treatment of neural, immune system,
PR	20-OCT-2000;	2000US-240960P.	CC	muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
PR	20-OCT-2000;	2000US-241221P.	CC	renal and proliferative disorders and inflammation. The present sequence
PR	20-OCT-2000;	2000US-241785P.	CC	is a protein of the invention.
PR	20-OCT-2000;	2000US-241786P.	XX	
PR	20-OCT-2000;	2000US-241787P.	XX	
PR	20-OCT-2000;	2000US-241808P.	XX	
PR	20-OCT-2000;	2000US-241809P.	XX	
PR	20-OCT-2000;	2000US-241826P.	XX	
PR	01-NOV-2000;	2000US-244617P.	XX	
PR	08-NOV-2000;	2000US-246474P.	QY	101 LEVLQGRNSIRQIEVGAFNGLASLNTLELFDNWLTVIPSGAFEYLSKLRELWLNPIE 160
PR	08-NOV-2000;	2000US-246475P.	DB	1 LEVLQGRNSIRQIEVGAFNGLASLNTLELFDNWLTVIPSGAFEYLSKLRELWLNPIE 60
PR	08-NOV-2000;	2000US-246476P.	QY	161 SIPSYAFNRVPSLMELDLGELKLEYSISGAFEGFLNKLKYNLGMKNIKMPNLTPLVGL 220
PR	08-NOV-2000;	2000US-246477P.	DB	61 SIPSYAFNRVPSLMELDLGELKLEYSISGAFEGFLNKLKYNLGMKNIKMPNLTPLVGL 120
PR	08-NOV-2000;	2000US-246478P.	QY	221 EELEMSGNHFPFPIRPGSPHGLSSLKLLWVNSQVSLIERNAFQGLASIVELNLAHNLSS 280
PR	08-NOV-2000;	2000US-246523P.	DB	121 EELEMSGNHFPFPIRPGSPHGLSSLKLLWVNSQVSLIERNAFQGLASIVELNLAHNLSS 180
PR	08-NOV-2000;	2000US-246526P.	QY	281 LEHDLFTPLRYLVELHLHHPNWCDCILWLAWMLREYIPTNSTCCGRCHAPMGRYL 340
PR	08-NOV-2000;	2000US-246611P.	DB	181 LEHDLFTPLRYLVELHLHHPNWCDCILWLAWMLREYIPTNSTCCGRCHAPMGRYL 240
PR	08-NOV-2000;	2000US-246613P.	QY	341 VEVDQASQCSAPFIMDAPRDNISSEGMALCKRTPEMSSVKVLLPNGTVLSHSHRPR 400
PR	17-NOV-2000;	2000US-249207P.	DB	241 VEVDQASQCSAPFIMDAPRDNISSEGMALCKRTPEMSSVKVLLPNGTVLSHSHRPR 300
PR	17-NOV-2000;	2000US-249208P.	QY	401 ISVLNDGTLIFSHVLLSDTGYTCMTNNAAGNSASAYLVNSTAELNLSYSPFTTVE 460
PR	17-NOV-2000;	2000US-249210P.	DB	301 ISVLNDGTLIFSHVLLSDTGYTCMTNNAAGNSASAYLVNSTAELNLSYSPFTTVE 360
PR	17-NOV-2000;	2000US-249211P.	QY	461 TTEISPEDTTRKYKVPVPTTSTGYQPAYTTSTTVLIQTRVPKQAVPATDTRKQTSLD 520
PR	17-NOV-2000;	2000US-249212P.	DB	361 TTEISPEDTTRKYKVPVPTTSTGYQPAYTTSTTVLIQTRVPKQAVPATDTRKQTSLD 420
PR	17-NOV-2000;	2000US-249218P.	QY	521 EVMKTKIIIGCFVAVTLAAAMLIFFYKLRKHQORSTVTAARTVELIQVDEIDIPAATS 580
PR	17-NOV-2000;	2000US-249244P.	DB	421 EVMKTKIIIGCFVAVTLAAAMLIFFYKLRKHQORSTVTAARTVELIQVDEIDIPAATS 480
PR	17-NOV-2000;	2000US-249245P.	QY	581 AATAAPSGVSGEAVLPTTHDHINNYNTPAHGAHWNTENSLGNSLHPTVTTTISEPVII 640
PR	17-NOV-2000;	2000US-249257P.	DB	481 AATAAPSGVSGEAVLPTTHDHINNYNTPAHGAHWNTENSLGNSLHPTVTTTISEPVII 540
PR	17-NOV-2000;	2000US-249297P.	QY	641 QTHTKDKVQETQI 653
PR	17-NOV-2000;	2000US-249299P.	DB	541 QTHTKDKVQETQI 553
PR	01-DEC-2000;	2000US-249300P.	XX	RESULT 23
PR	01-DEC-2000;	2000US-250160P.	ABP66936	
PR	01-DEC-2000;	2000US-250391P.	ID	ABP66936 standard; Protein; 553 AA.
PR	05-DEC-2000;	2000US-250391P.	XX	
PR	05-DEC-2000;	2000US-251988P.	AC	ABP66936;
PR	05-DEC-2000;	2000US-256719P.	XX	
PR	06-DEC-2000;	2000US-251479P.	XX	
PR	08-DEC-2000;	2000US-251856P.	XX	
PR	08-DEC-2000;	2000US-251868P.	XX	
PR	08-DEC-2000;	2000US-251869P.	XX	
PR	08-DEC-2000;	2000US-251989P.	XX	
PR	08-DEC-2000;	2000US-251990P.	XX	
PR	11-DEC-2000;	2000US-254057P.	XX	
PR	05-JAN-2001;	2001US-259678P.	XX	

T 09-DEC-2002 (first entry)  
X Human polypeptide SEQ ID NO 657.  
E  
X Human, neotropic; neuroprotective; cytostatic; dermatological; virucide;  
W immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
W antiparkinsonian; antiskilling; antianaemic; antiarthritis; cancer;  
W antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
W antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
W antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
W neurological disease; infection; nephrotropic; gene therapy; vaccine.  
K  
S Homo sapiens.  
V US2002090672-A1.  
D 11-JUL-2002.  
C  
P 17-JAN-2001; 2001US-0764853.  
K 31-JAN-2000; 2000US-179065P.  
R 04-FEB-2000; 2000US-180628P.  
R 28-JUN-2000; 2000US-214986P.  
R 07-JUL-2000; 2000US-216647P.  
R 07-JUL-2000; 2000US-216980P.  
R 11-JUL-2000; 2000US-217487P.  
R 11-JUL-2000; 2000US-217496P.  
R 14-JUL-2000; 2000US-218290P.  
R 26-JUL-2000; 2000US-220963P.  
R 26-JUL-2000; 2000US-220964P.  
R 14-AUG-2000; 2000US-224518P.  
R 14-AUG-2000; 2000US-224519P.  
R 14-AUG-2000; 2000US-225267P.  
R 14-AUG-2000; 2000US-225268P.  
R 14-AUG-2000; 2000US-225270P.  
R 14-AUG-2000; 2000US-225447P.  
R 14-AUG-2000; 2000US-225757P.  
R 14-AUG-2000; 2000US-225758P.  
R 22-AUG-2000; 2000US-226868P.  
R 30-AUG-2000; 2000US-228924P.  
R 01-SEP-2000; 2000US-229287P.  
R 01-SEP-2000; 2000US-229343P.  
R 01-SEP-2000; 2000US-229344P.  
R 01-SEP-2000; 2000US-229345P.  
R 05-SEP-2000; 2000US-229509P.  
R 05-SEP-2000; 2000US-229513P.  
R 08-SEP-2000; 2000US-231413P.  
R 21-SEP-2000; 2000US-234223P.  
R 21-SEP-2000; 2000US-234274P.  
R 25-SEP-2000; 2000US-234997P.  
R 27-SEP-2000; 2000US-235834P.  
R 29-SEP-2000; 2000US-236327P.  
R 29-SEP-2000; 2000US-236368P.  
R 29-SEP-2000; 2000US-236369P.  
R 29-SEP-2000; 2000US-236370P.  
R 02-OCT-2000; 2000US-236802P.  
R 02-OCT-2000; 2000US-237037P.  
R 02-OCT-2000; 2000US-237038P.  
R 02-OCT-2000; 2000US-237039P.  
R 13-OCT-2000; 2000US-237040P.  
R 13-OCT-2000; 2000US-239335P.  
R 20-OCT-2000; 2000US-240960P.  
R 20-OCT-2000; 2000US-241785P.  
R 01-NOV-2000; 2000US-241809P.  
R 17-NOV-2000; 2000US-244517P.  
R 08-DEC-2000; 2000US-249299P.  
R 08-DEC-2000; 2000US-251856P.  
R 08-DEC-2000; 2000US-251868P.  
R 08-DEC-2000; 2000US-251869P.  
A (ROSE/) ROSEN C A.  
A (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.  
XX Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2002-681727/73.  
DR N-PSDB; ABV83908.  
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and  
PT treatment of immune, hyperproliferative, renal, respiratory, and  
PT cardiovascular, reproductive, endocrine, gastrointestinal and  
PT neurological disorders -  
XX  
PS Claim 11; SEQ ID NO 657; 369pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (ABV83682-ABV84101) and proteins  
CC (ABP6710-ABP67129) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 553 AA;  
  
Query Match 84.0%; Score 2888; DB 23; Length 553;  
Best Local Similarity 99.8%; Pred. No. 5.7e-232;  
Matches 552; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 101 LEVLQGRNSIRQIEVGAFNGLASLNTLEFDNWLTVPSCAFYLSKRLRLNRP 160  
DB 1 LEVLQGRNSIRQIEVGAFNGLASLNTLEFDNWLTVPSCAFYLSKRLRLNRP 60  
QY 161 SIPSVAFNRPVPSLMELDLGELKKLEYISEGAFEGFLNKLNLGMCNKDMPNLTPLVGL 220  
DB 61 SIPSVAFNRPVPSLMELDLGELKKLEYISEGAFEGFLNKLNLGMCNKDMPNLTPLVGL 120  
QY 221 BELEMSGNHFFPIRPGSPHGLSSLLKLVWMSQVSLIERNAPDGLASIVELNLAHNLS 280  
DB 121 BELEMSGNHFFPIRPGSPHGLSSLLKLVWMSQVSLIERNAPDGLASIVELNLAHNLS 180  
QY 281 LPHDLFTPLRYLVLELHHPNWCDCDILWLAWLREYIPTNSTCCGCHAPMEMRGYRL 340  
DB 181 LPHDLFTPLRYLVLELHHPNWCDCDILWLAWLREYIPTNSTCCGCHAPMEMRGYRL 240  
QY 341 VEVDQASQCAPPITMDAPDLNISSEGRMAELKCRTPPMSSVKLLPNGTVLSHSHRPR 400  
DB 241 VEVDQASQCAPPITMDAPDLNISSEGRMAELKCRTPPMSSVKLLPNGTVLSHSHRPR 300  
QY 401 ISVLNDGTLNPSHVLSDTGVTCTMTNVAGNSASAYLNSTAEINTSNYSFETTTVE 460  
DB 301 ISVLNDGTLNPSHVLSDTGVTCTMTNVAGNSASAYLNSTAEINTSNYSFETTTVE 360  
QY 461 TTEISPEDTTRKYKFPVPTTSTGYQPAYTTTTLVLIQTRVPEKQVAVPATDTDRMQSLD 520  
DB 361 TTEISPEDTTRKYKFPVPTTSTGYQPAYTTTTLVLIQTRVPEKQVAVPATDTDRMQSLD 420  
QY 521 EVNKTTKIIIGCFVAVTLLAAAMLIVFYKLRKHQQRSTVTAARTVHIIQVDEIPAA 580  
DB 421 EVNKTTKIIIGCFVAVTLLAAAMLIVFYKLRKHQQRSTVTAARTVHIIQVDEIPAA 480  
QY 581 AAATAAPSGVSGEAVLPTTHDHNNTYKPAAGAHNTENSIGNSLHPTVTTSISEVII 640  
DB 581 AAATAAPSGVSGEAVLPTTHDHNNTYKPAAGAHNTENSIGNSLHPTVTTSISEVII 640



Db 481 AAATAAPSGVGEAGVLPVTHDHNINVTYKPAHGAHWHTNSLNSLHPVTWTTISBPYII 540  
QY 641 QTHTKQKVOETQI 553  
Db 541 QTHTKQKVOETQI 553

RESULT 24  
AAB23044  
ID AAB23044 standard; Protein; 448 AA.  
CX AAB23044;  
CX 16-JAN-2001 (first entry)  
CX Human SLIT protein-like splice variant, SECX 3352358-S153A.  
CX SECX protein; human; secreted; membrane-associated; cancer;  
KW proliferation regulator; differentiation regulator; non-malignant tumour;  
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;  
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;  
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
KW neurological disease; Alzheimer's disease; trauma; wound;  
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;  
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;  
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;  
KW dermatological; gene therapy.  
CX Homo sapiens.  
CX OS  
CX WO200053742-A2.  
CX 14-SEP-2000.  
CX 09-MAR-2000; 2000HO-US06280.  
CX 09-MAR-1999; 99US-0123667.  
CX 08-MAR-2000; 2000US-0123667.  
CX (CURA-) CURAGEN CORP.  
CX Shimketa RA;  
CX WPI; 2000-594318/56.  
CX N-PSDB; AAA93631.  
CX Novel human membrane associated or secreted polypeptides and  
CX polynucleotides useful for diagnosis, prevention and treatment of  
CX pathological states such as cancer, immune, cardiovascular and  
CX neurological disorders  
CX Claim 1; Fig 17B; 151pp; English.  
CX  
CX Sequences AAB23029-B3048 represent human SECX proteins. The SECX  
CX proteins of the invention are either secreted or membrane-associated  
CX proteins and act as regulator of cellular proliferation and  
CX differentiation. SECX proteins or nucleotides are useful for diagnosing  
CX the presence of, or predisposition to, a disease associated with altered  
CX levels of SECX proteins and nucleotides. The SECX proteins are also  
CX useful to screen compounds that modulate SECX activity or expression. The  
CX interaction of a SECX protein with other cellular proteins may be useful  
CX to modulate the activity of a partner protein, cellular proliferation,  
CX cellular differentiation and cell survival. SECX nucleotides are useful  
CX for the recombinant expression of SECX protein, and may be used to detect  
CX SECX mRNA or genetic lesions in the SECX gene. They may also be used to  
CX modulate SECX expression (e.g., using antisense oligonucleotides). SECX  
CX nucleic acid sequences are also useful for identifying a cell or tissue  
CX type in a biological sample, and in forensic biology. SECX primers or  
CX probes are useful for detecting the presence of SECX nucleotides and for  
CX screening tissue cultures for contamination. Diseases that may be treated  
CX or prevented using SECX proteins or nucleotides include cancer (e.g.,  
CX colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
CX (including autoimmune diseases, transplant rejection, allergies, AIDS),

CC infections, inflammatory disorders, arthritis, haematopoietic disorders,  
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
CC surgical or traumatic wounds, spinal cord injury), and skeletal  
CC disorders.  
CX Sequence 448 AA;  
QY Query Match 69.4%; Score 2389, DB 21; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.8e-190;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 45 NCPVSCSCSNQFQSVCTRRGLSEVPQGIQADTFRLHLHLEVL 104  
Db 1 NCPVSCSCSNQFQSVCTRRGLSEVPQGIQADTFRLHLHLEVL 60  
QY 105 QUGRNSIRQIEVGAFNGLASLNTLELFDNMLTVTPSGAFYLSKRLRLWLNPIEIPS 164  
Db 61 QUGRNSIRQIEVGAFNGLASLNTLELFDNMLTVTPSGAFYLSKRLRLWLNPIEIPS 120  
QY 165 YAPNRVPSLMRLDGLKLEYISGAFEGFLNLYLNLGMCNKIDPNLTPVLGLEELE 224  
Db 121 YAPNRVPSLMRLDGLKLEYISGAFEGFLNLYLNLGMCNKIDPNLTPVLGLEELE 180  
QY 225 MSGNHFFPIRPGSFHGLSSKLLKLVWMSQVSLIERNAPDGLASLVELNLHNNLSLPHD 284  
Db 181 MSGNHFFPIRPGSFHGLSSKLLKLVWMSQVSLIERNAPDGLASLVELNLHNNLSLPHD 240  
QY 285 LFTPLRYLVELHLHNPWNCDDILNLAWLREYIPNNSCTCCGCHAPMGRGYLVEVD 344  
Db 241 LFTPLRYLVELHLHNPWNCDDILNLAWLREYIPNNSCTCCGCHAPMGRGYLVEVD 300  
QY 345 QASFOCSAPFTMDAPRDNLNISEGRMAELKCRTPMSSVKWLLPNGTVLSHSHRPRISVL 404  
Db 301 QASFOCSAPFTMDAPRDNLNISEGRMAELKCRTPMSSVKWLLPNGTVLSHSHRPRISVL 360  
QY 405 NDGTLNFSHLLSDGTGVTTCMTVNVAGNSASAYLVNSTAEINTSNYSFPTVTVEI 464  
Db 361 NDGTLNFSHLLSDGTGVTTCMTVNVAGNSASAYLVNSTAEINTSNYSFPTVTVEI 420  
QY 465 SPEDTTRKYKVPVPTTSTGQPAYTTSTT 492  
Db 421 SPEDTTRKYKVPVPTTSTGQPAYTTSTT 448

RESULT 25  
AAB43091  
ID AAB43091 standard; Protein; 441 AA.  
CX AAB43091;  
CX 08-FEB-2001 (first entry)  
CX Human ORFX ORP2855 polypeptide sequence SEQ ID NO:5710.  
CX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
CX Homo sapiens.  
CX WO200058473-A2.  
CX PN

X 05-OCT-2000.  
D 31-MAR-2000; 2000WO-US08621.  
E 31-MAR-1999; 99US-0127607.  
F 02-APR-1999; 99US-0127636.  
G 05-APR-1999; 99US-0127728.  
H 30-MAR-2000; 2000US-0540763.  
I (CURA-) CURAGEN CORP.  
J Shinkets RA, Leach M;  
K WPI; 2000-602362/57.  
L N-PSDB; AAC77300.  
M Novel nucleic acids and peptides derived from open reading frame X,  
N useful for treating e.g. cancers, proliferative open disorders,  
O neurodegenerative disorders and cardiovascular disease -  
P Claim 11; Page 4877-4878; 5507pp; English.  
Q AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
R which represent the human ORFX open reading frames 1 to 3161. The ORFX  
S sequences have activities such as: cytostatic; hepatotropic; vulnary;  
T antiproliferative; antiparkinsonian; neurotropic; neuroprotective;  
U osteoprotective; anticonvulsant; antiarthritic; immunosuppressant;  
V immunostimulant; cardiac; thrombolytic; coagulant; vasotrophic;  
W antidiabetic; hypotensive; dermatological; immunosuppressive;  
X antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
Y antithyroid; and antianemic. The sequences can be used for determining  
Z the presence of or predisposition to, or preventing or treating  
AA pathological conditions associated with an ORFX-associated disorder. The  
AB nucleic acids can be used to express ORFX proteins in gene therapy  
AC vectors. The proteins and nucleic acids may be used to treat cancers,  
AD proliferative disorders, neurodegenerative disorders, osteoarthritis,  
AE graft vs host disease, cardiovascular disease, diabetes mellitus,  
AF hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
AG erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
AH bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
AI allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
AJ nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
AK coagulation; to inhibit thrombosis; and as a contraceptive.  
AL Sequence 441 AA;  
AM  
AN Query Match 67.2%; Score 2312; DB 21; Length 441;  
AO Best Local Similarity 99.5%; Pred. No. 4.6e-184;  
AP Matches 439; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
AQ  
AR 213 NLTPLVGLEELMSGNHPPPEIRPGSFHGLSLKLLVWVNSQVSLIERNAPDGLASLVELN 272  
AS 1 NLTPLVMEELMSGNHPPPEIRPGSFHGLSLKLLVWVNSQVSLIERNAPDGLASLVELN 60  
AT 273 LAPNLSLPHDLPTPLRYLVHLLHNPWNCDDILWLAWLREYIPTNSTCCGRCHAP 332  
AU 61 LAPNLSLPHDLPTPLRYLVHLLHNPWNCDDILWLAWLREYIPTNSTCCGRCHAP 120  
AV 333 MEMRGYLVNDVQASFOQCAPIMDAPDLNISSEGRMAELKCRTPPMSSVKKWLLPNTGVL 392  
AW 121 MEMRGYLVNDVQASFOQCAPIMDAPDLNISSEGRMAELKCRTPPMSSVKKWLLPNTGVL 180  
AX 393 SHASRHPRI SVLNDGTLNFSHVLLSDTGVYTCMTVNVAGNSNAYLNVSFAELNTSNYS 452  
AY 181 SHASRHPRI SVLNDGTLNFSHVLLSDTGVYTCMTVNVAGNSNAYLNVSFAELNTSNYS 240  
AZ 453 FFTVTVTETHEISPEPTTKKYPVTTSTGTQPAYTSTTVLQITTRVPKQVAPATDTT 512  
BA 241 FFTVTVTETHEISPEPTTKKYPVTTSTGTQPAYTSTTVLQITTRVPKQVAPATDTT 300  
BB 513 DRKQTSLEDEVMKTKIIIGCFVAVTLLAAAMLVIFYKLRKHQRSTVTAARTVEIIQVD 572

Db 301 DRKQTSLEDEVMKTKIIIGCFVAVTLLAAAMLVIFYKLRKHQRSTVTAARTVEIIQVD 360  
Qy 573 EDIPAAATSAATAAPSGVSGGAVVLPITHDHINVTYKPAHGAHWTSNLSLHPTVT 632  
Db 361 EDIPAAATSAATAAPSGVSGGAVVLPITHDHINVTYKPAHGAHWTSNLSLHPTVT 420  
Qy 633 TISEPYIIQTHTKDKVQSTQI 653  
Db 421 TISEPYIIQTHTKDKVQSTQI 441  
RESULT 26  
AAEL3006  
ID AAEL3006 standard; Protein; 713 AA.  
XX  
XX AAEL3006;  
XX  
DT 28-JAN-2002 (first entry)  
XX Human leucine-rich repeat (LRR) family member protein.  
DE  
XX Human; leucine-rich repeat; LRR; 31939 protein; therapy;  
KW cell proliferation; differentiation disorder; cancer; neuronal disorder;  
KW neurological disorder; demyelinating disease; multiple sclerosis;  
KW degenerative disease; Alzheimer's disease; Huntington's disease;  
KW spinocerebellar degeneration; nervous system; bone disorder; diabetes mellitus;  
KW osteoporosis; immune disorder; rheumatoid arthritis; diabetes mellitus;  
KW cardiovascular disorder; liver disorder; viral disease; pain;  
KW metabolic disorder; chromosomal mapping; tissue typing; forensic biology;  
KW cytostatic; neurotropic; neuroprotective; anticonvulsant; osteopathic;  
KW antirheumatic; antiarthritic; virucide; analgesic.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..38 /label= Signal\_peptide  
FT Protein 39..713 /note= "Mature human 31939 protein"  
FT Domain 56..85 /label= N-terminal\_LRR\_domain  
FT Domain 87..110 /label= LRR\_domain  
FT Domain 111..134 /label= LRR\_domain  
FT Domain 135..158 /label= LRR\_domain  
FT Domain 159..182 /label= LRR\_domain  
FT Domain 183..207 /label= LRR\_domain  
FT Domain 208..229 /label= LRR\_domain  
FT Domain 230..253 /label= LRR\_domain  
FT Domain 254..277 /label= LRR\_domain  
FT Domain 278..301 /label= LRR\_domain  
FT Domain 311..362 /label= C-terminal\_LRR\_domain  
FT Domain 378..438 /label= Immunoglobulin\_domain  
XX WO200175105-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US10380.  
XX 31-MAR-2000; 2000US-193919P.  
XX (MILL-) MILLENNIUM PHARM INC.  
PA



Q Sequence 713 AA;  
Query Match 56.1%; Score 1931; DB 23; Length 713;  
Best Local Similarity 56.3%; Pred. No. 5.8e-152;  
Matches 379; Conservative 94; Mismatches 151; Indels 49; Gaps 9;  
Y 30 ILCAAIATAAASAGPQNCPSVCSNQFSKVCTRGSLSEVPQIGIPSNTRYLNLMENNIQM 89  
b 41 VAVTSAAGGSPSPATSCPVACSCSNQASRVICTREDLAEPASIPVNTRYLNQENGIVQ 100  
Y 90 IQADTFPHLHLEVLQGLGRNSIRQIEVGAFNGLASINTLELFDNMLTVIPSGAFYLSKL 149  
b 101 IRTDTPKHLRHLLEILQSKNLVRKIEVGAFNGLPSTNLELFDNMLTVIPSGAFYLSKL 160  
Y 150 RELMLRNPIESIPYAFNRVPSLRMLDLGELKLEIYISGAPEGLFNLYNLMGNMNIK 209  
b 161 RELMLRNPIESIPYAFNRVPSLRMLDLGELKLEIYISGAPEGLFNLYNLMGNMNIK 220  
Y 210 DMNLTPLVLEELSGNHPPIRPGSFHGLSSLKGLWVNSQVSLIERNAPDGLASLV 269  
b 221 DIPNLTALVRLFEELSGNLDLIRPGSFQGLTSRKLWLMHAQVATIERNAFDLKSLE 280  
Y 270 ELMLAHNNLSLPHDLFTFLRYLVELHLHHPNWCDCDILMLAWMLREYIPTNSTCCGRC 329  
b 281 ELMLSHNNLSLPHDLFTFLHRLERVHLNHPNHCNCDVLSWMLKETVPSNTTCCARC 340  
Y 330 HAPMHEGRYLYEVDOASQCSAPPTMDAPRLINSEGMALCKRT-PPMSSVYKLLPN 388  
b 341 HAPAGUKGRIYELDQSHPTCYAPVIVEPTDLNVTGMAALCKRTCTSTSVNMLTPN 400  
Y 389 GTVLSHASHPRIIVLNDGTLNFSVLLSDTGVYTCWVTVNAGNSAGYLVNSTAEI-- 446  
b 401 GTLWTHGSYRVRISVLHDGTLNFTAVTVQDTGYTCWVTVNAGNTTASATLNVSAVDPA 460  
Y 447 -----NTSNYSFTTIVTVEIISPEDT-----TRKPKVPPT-- 479  
b 461 AGGTGSGGGGPGSGGSGGGGYFTTIVTVEITLTPQGEALQPRGTEKEPGETD 520  
Y 480 -----SRGYOPAVTSTTVLIQTR-VKQVAVPATDITDKMTSLDVMKTKIKIIG 531  
b 521 VNGGEPGDAAGPASSITTAPASRPRTKEAFTVPTDVTENALKDLDDYWKTKIKIIG 580  
Y 532 CFVAVTLAAALIVPYKURKHQRQSTVTAARTVEIIVQVEDIPAAAT-----SAAATAA 586  
b 581 CFVAITPFAAVMLVAFYKLRKHQHLKHGPTRTVEIINVEDLPAASAVSVAATAAVAS 640  
Y 587 PSVSGEGAVLPTI-HDHINTY-KPAHGAFTENSIGNSL-----HPTVTTISEPVII 640  
b 641 GGVGSDSHCALPALERDLNHHYVAAAFKARYSNPSGGCGGKGPGLNSIHEPLF 700  
Y 641 QTHTKDKVQETQI 653  
b 701 KSGSKENVQETQI 713  
RESULT 28  
AAU91335  
AAU91335 standard; Protein; 713 AA.  
AAU91335;  
18-JUN-2002 (first entry)  
Human novel secreted protein LP223(a).  
Human; secreted protein; cancer; autoimmune disease;  
arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease;  
meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction;  
mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia;  
rheumatoid arthritis; hypothyroidism; allergic response; liver failure;  
multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;  
autism; panic disorder; learning disability; feeding disorder;  
sleep pattern disorder; balance; perception; Th1-dependent insulinitis;

XX adult respiratory distress syndrome; ARDS.  
XX Homo sapiens.  
XX WO200214358-A2.  
XX 21-FEB-2002.  
XX 30-JUL-2001; 2001WO-US21124.  
XX 11-AUG-2000; 2000US-224642P.  
XX 19-OCT-2000; 2000US-241779P.  
XX (ELIL ) LILLY & CO ELI.  
XX Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;  
XX WPI; 2002-304057/34.  
XX N-PSDB; ABK62087.  
XX Novel polypeptides and polynucleotides of secreted proteins useful for  
XX treating various diseases such as multiple sclerosis, cancer,  
XX autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's  
XX disease .  
XX Claim 9; Page 200-203; 235pp; English.  
XX The invention relates to a novel human secreted polypeptide having  
XX sequence 90% identical to the polypeptide sequences of LP105, LP061,  
XX LP224, LP240, LP239(a), LP243(a), LP253(b), LP258, LP251(a),  
XX LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b),  
XX or LP223(b). Also included are the nucleic acids encoding the LP  
XX proteins (including complement, fragments encoding mature forms of the  
XX polypeptide or variant), a vector comprising the nucleic acid, a  
XX host cell comprising the vector, the preparation of the protein,  
XX an anti-LP antibody, ant/agonists of LP and anti-LP-encoding mRNA  
XX ribozymes. The secreted protein or its agonist is useful in the  
XX manufacture of a medicament for treating a mammal suffering from a  
XX disease (and in diagnosis), condition or disorder associated with  
XX aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,  
XX arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,  
XX meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,  
XX mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid  
XX arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple  
XX sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive  
XX disorder, autism, panic disorder, learning disabilities, ALS  
XX (amyotrophic lateral sclerosis) psychoses, disorders in feeding,  
XX sleep patterns, balance, and perception, Th1-dependent insulinitis, adult  
XX respiratory distress syndrome (ARDS). The secreted protein is further  
XX useful for identifying compounds that bind to the secreted protein. The  
XX present sequence represents a novel secreted protein of the invention.

Sequence 713 AA;

Query Match 56.1%; Score 1931; DB 23; Length 713;  
Best Local Similarity 56.3%; Pred. No. 5.8e-152;  
Matches 379; Conservative 94; Mismatches 151; Indels 49; Gaps 9;  
QY 30 ILCAAIATAAASAGPQNCPSVCSNQFSKVCTRGSLSEVPQIGIPSNTRYLNLMENNIQM 89  
DB 41 VAVTSAAGGSPSPATSCPVACSCSNQASRVICTREDLAEPASIPVNTRYLNQENGIVQ 100  
QY 90 IQADTFPHLHLEVLQGLGRNSIRQIEVGAFNGLASINTLELFDNMLTVIPSGAFYLSKL 149  
DB 101 IRTDTPKHLRHLLEILQSKNLVRKIEVGAFNGLPSTNLELFDNMLTVIPSGAFYLSKL 160  
QY 150 RELMLRNPIESIPYAFNRVPSLRMLDLGELKLEIYISGAPEGLFNLYNLMGNMNIK 209  
DB 161 RELMLRNPIESIPYAFNRVPSLRMLDLGELKLEIYISGAPEGLFNLYNLMGNMNIK 220  
QY 210 DMNLTPLVLEELSGNHPPIRPGSFHGLSSLKGLWVNSQVSLIERNAPDGLASLV 269  
DB 221 DIPNLTALVRLFEELSGNLDLIRPGSFQGLTSRKLWLMHAQVATIERNAFDLKSLE 280

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270  EQNLAHNNLSSLPDHLPTPLRYLVELHLHHPNPNCDLILWLANKLREYIPTMSTCCGR 329
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
281  ELLSHNNLNSLPDHLPTPLRHLBRVHLHHPNPNCDVLWLSNWLKETVPSMTCCAC 340
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
330  HAPEMRGKRYLYEVDQASFOCSAPPEINDAPRDLNISEGRMAELKCRIT-PPMSSVKWLLFN 388
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
341  HAPAGLKGRYIGELDQSHFTCVAPVIPPPTDLNVTGMAAELKCRITGTSMTSVNVLTFN 400
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
389  GTVLSHASRHPRI SVLNDGTLNFSHVLLSDTGVTTCWTVNVAGNSNASAVLNVYSTAEL-- 446
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
401  GLIMTHGSTRVETSVLHDGTLNFNTVTVQDTGQVTCWTVNSAGNTASATLNVA SVDVPA 460
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
447  -----NTSNYSFFTVTVTETE:SPEDT-----TRKXPVPTT-- 479
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
461  AGGTSGGGGPGGGGGGGGGVGYTFVTVTVETETCPGEEALQPRGTEKPPGPTTGG 520
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
480  -----STGYOPATYTTSTFVLIQTR-VPKQVAVPATDITDKWQISLDEWMTKIIIG 531
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
521  VMGGRPGDAAGPASSSTTAPAPSSRTEKAFVTPITDVTEVALKDLDDWMTKIIIG 580
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
532  CFVAVTLIAAAMLIYFYKLRKHQOORSTVTAARTVEIIQVDEDI PAAT-----SAAATAA 586
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
581  CFVAITFMAAVMLVAFYKLRQHQLHKHGGSTRVETIINVEDELPAASAVSVAASAAVAS 640
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
587  PSGVSEGA VLPITI-HDHINYNTY-KPAHCNHTWENSLGNSL----HPTVTITSEPYII 640
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
641  GCGVGDGSHALPALERDHLHHHYVMAAFKCHYSSNTPSGCGGKGKPGPOLNSIHEPLIF 700
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

941  QTHTKDKVQETQI 653
    :::|||:|||:|||
701  KSGSKENVQETQI 713
    :::|||:|||:|||

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RESULT 29	
ABU52381	
ID	ABU52381 standard; Protein; 713 AA.
XX	
AC	ABU52381;
XX	
XX	
DT	03-MAR-2003 (first entry)
XX	
DE	Human GPCR related protein NOV31a.
XX	
XX	
KW	Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytosstatic.

PR	30-MAR-2001;	2001US-280233P.	
PR	02-APR-2001;	2001US-280502P.	
PR	02-MAY-2001;	2001US-288052P.	
PR	02-MAY-2001;	2001US-288066P.	
PR	02-MAY-2001;	2001US-288228P.	
PR	17-MAY-2001;	2001US-291766P.	
PR	07-JUN-2001;	2001US-296693P.	
PR	08-JUN-2001;	2001US-296856P.	
PR	05-JUL-2001;	2001US-303230P.	
PR	05-JUL-2001;	2001US-303317P.	
PR	08-AUG-2001;	2001US-310513P.	
PR	13-AUG-2001;	2001US-311978P.	
PR	14-AUG-2001;	2001US-312191P.	
PR	16-AUG-2001;	2001US-312916P.	
PR	17-AUG-2001;	2001US-313182P.	
PR	20-AUG-2001;	2001US-313626P.	
PR	21-AUG-2001;	2001US-314018P.	
PR	27-AUG-2001;	2001US-315227P.	
PR	10-SEP-2001;	2001US-318403P.	
PR	10-SEP-2001;	2001US-318510P.	
PR	14-SEP-2001;	2001US-322966P.	
PR	14-SEP-2001;	2001US-322360P.	
PR	27-SEP-2001;	2001US-325378P.	
PR	09-NOV-2001;	2001US-332486P.	
PR	09-NOV-2001;	2001US-345399P.	
PR	07-MAR-2002;	2002US-0094886.	
XX			
XX	{CURA-}	CURAGEN CORP.	
PA			
XX			
XX			
PI	Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M, Burgess CE;		
PI	Vernet CM, Li L, Gorman L, Maliyankar UM, Boldog FL, Guo X;		
PI	Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ, Pena CEA;		
PI	Gargolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;		
PI	Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;		
PI	Larochele WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;		
XX			
DR	WPI: 2003-058423/05.		
XX	N-PSDB; ABX70472.		
XX			
PT	NOVX polypeptides and polymynucleotides, useful for treating a syndrome		
PT	related to a human disease associated with the NOVX polypeptide e.g.,		
PT	cancer		
XX			
PS	Claim 1; Page 189; 413pp; English.		
XX			
CC	The present invention relates to the isolation of novel human		
CC	polypeptides referred to as NOVX (NOVI-NOV44), variants of these		
CC	proteins, and the polymynucleotide sequences encoding them. The NOVX		
CC	proteins of the invention are G-protein coupled receptor (GPCR)		
CC	related proteins. The sequences of the invention are useful in the		
CC	manufacture of a medicament for treating a syndrome related to a		
CC	human disease associated with the polypeptides e.g. cancer.		
CC	ABUS2311-ABUS408 represent the human NOVX proteins of the invention.		
XX			
XX	Sequence 713 AA;		
XX			
XX	Query Match	56.1%; Score 1931; DB 24; Length 713;	
XX	Best Local Similarity	56.3%; Pred. No. 5,8e-152;	
XX	Matches 379; Conservative	94; Mismatches 151; Indels 49; Gaps 9;	
QY	30	ILCAAIAAAGAGPNCFSVSCSNQFSKYVCTRRGLSEVPGIISNTRYLNLMENNITQM	89
DB	41	VAVTSAAGGSGPPATSCFVACSCSNQASGRVCTRRDLAEVPASIPVNTRYLNQENGIOV	100
QY	90	IQADTFRHLHLEVLQLGNSIRIQEVGAFNGLASLNTLELFDNWLTVIPSGAFEYLSKL	149
DB	101	IRTDFFKHLHLEIILQSKNLVRKIEVGAPNGLPSLNTLELFDNRLTVPVTPQAFYLSKL	160
QY	150	RELWLRRNPISIPSYANRPVSLWRDLGLBKLEYISEGAPGLFNLKYNILGCMNIK	209
DB	161	RELWLRRNPISIPSYANRPVSLWRDLGLBKLEYISEAFAFGLVNLRYNLGCMNLK	220
QY	210	DMPNLTPILWGLEEMSGNHFPFIRPQSFHGILSSKLCVLWVNSQVSLIERNAFDGLASLV	269

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b 221 DFNLTALVRLSELESGNRDLIRPGSFQGLTSLRKLWLMHAQVATIERNAFDLKSLE 280
Y 270 ELMLAHNNLSLPHDLFTPLRYLVELHLHNNPNCDDILMLAWMLREYIPTNSTCCORC 329
b 281 ELNLSHNNLSLPHDLFTPLRYLVELHLHNNPNCDDILMLAWMLREYIPTNSTCCORC 340
Y 330 HAPMHRGRYLVEVDQASQCSAPFIMDAPRLNISBGRMAELKCRTPPMSSVKWLLPN 388
b 341 HAPAGLKGRIYIGELDQSHFTCYAVIVEPPTDLNVTGMAELKCRKTSMTSVNMLTFN 400
Y 389 GTVLSHASRPRLSVLNDGTINPNSHVLSDGTGYTCMTNVAGNSASAYLNVAEL-- 446
b 401 GLMTHGSRVRLSVLHDGTINPNTVQDTQCYTCMTNSAGNTASATLNVAEDPVA 460
Y 447 -----NTSNYSFFTVTVTVEITEISPEOT-----TRKYKVPPT-- 479
b 461 AGGTGGGGGPGSGGGVGGGGYIFVTVTETLQPGSEALOPRTEKPPGPTDG 520
Y 480 -----STGYOPAYTSTTVLIQTR-VPKQVAVPATDTDKMQTSLDVMKTKIIIG 531
b 521 VMGGGRPGDAAGPAGSSSTAPAPRSRSPTEKAFVPTIDVTENALKDLDDVMKTKIIIG 580
Y 532 CFVAVTLLAAALIVFYKLRKHQORSTVTAARTVEIIVQVEDIPAAH-----SAAATAA 586
b 581 CFVATFMAAVMLVAFYKLRKHQORSTVTAARTVEIIVQVEDIPAAH-----SAAATAA 640
Y 587 PGVSGEGAVLPTI-HDHINNTY-KPAHGAHTWNSLNSL-----HPTVTITSEPII 640
b 641 GGGVGGDSHLALPALERDLNHHVYAAAFKAHYSNPSGGCGGKGGPPGLNSIHEPLF 700
Y 641 QHTTKKYQETOI 653
b 701 KSGSKENVQETOI 713

RESULT 30
AY08100
D AAY08100 standard; Protein; 640 AA.
C AAY08100;
F 11-SEP-2000 (first entry)
E Human PRO331 protein.
V Inflammatory cell infiltration; immune response; T cell proliferation;
anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthritis;
T cell-mediated disease; spondyloarthritis; sclerosis; renal disease;
inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;
diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;
multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;
sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;
skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;
food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;
idiopathic pulmonary fibrosis; graft rejection; PRO245; human;
PRO331.
S Homo sapiens.
W WO9914241-A2.
C 25-MAR-1999.
F 17-SEP-1998; 98WO-US19437.
C 17-SEP-1997; 97US-0059119.
C 18-SEP-1997; 97US-0053263.
C 28-OCT-1997; 97US-0063550.
C 12-NOV-1997; 97US-0065186.
C 21-NOV-1997; 97US-0066364.
C 24-NOV-1997; 97US-0066770.
C 04-JUN-1998; 98US-0088026.

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XX PA (GETH ) GENENTECH INC.
XX Fong S, Goddard A, Gurney AL, Tumas D, Wood WI,
XX WPI; 1999-229499/19.
DR N-PSDB; AAX37738.
XX Composition containing novel polypeptide PRO245, its agonist or
XX antagonist -
XX Example 1; Fig 33; 177pp; English.
XX This invention describes a novel composition containing (apart from a
XX carrier or excipient), a novel PRO245 polypeptide (I), its agonist or
XX antagonist, or their fragments, for modulating: (i) infiltration of
XX inflammatory cells into tissue, (ii) an immune response; or (iii) T cell
XX proliferation. The composition increases or decreases any of the effects
XX (i)-(iii). The products of the invention have anti-inflammatory,
XX anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists
XX and their fragments, are used to treat immune-related diseases,
XX particularly T cell-mediated diseases. The diseases treated include
XX systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
XX arthritis, spondyloarthropathies, systemic sclerosis (scleroderma),
XX idiopathic inflammatory myopathies (dermatomyositis, polymyositis),
XX Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune
XX hemolytic anemia (immune pancytopenia, paroxysmal nocturnal
XX hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic
XX purpura), immune-mediated thrombocytopenia, thyroiditis (Grave's disease,
XX Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic
XX thyroiditis), diabetes mellitus, immune-mediated renal disease
XX (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis,
XX idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic
XX inflammatory demyelinating polyneuropathy, infectious hepatitis
XX (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune
XX chronic active hepatitis, primary biliary cirrhosis, granulomatous
XX hepatitis, and sclerosing cholangitis, inflammatory bowel disease
XX (ulcerative colitis; Crohn's disease), gluten-sensitive enteropathy, and
XX Whipple's disease. Autoimmune or immune-mediated skin diseases including
XX bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,
XX asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
XX urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,
XX hypersensitivity pneumonitis, and transplantation associated diseases
XX (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists
XX or fragment can also be used as an adjuvant in treatment of tumors.
XX Antibodies against (I) can also be used for diagnosing such diseases.
XX This sequence represents the human PRO331 protein which is described in
XX the method of the invention.
XX Sequence 640 AA;
XX Query Match 54.2%; Score 1865; DB 20; Length 640;
XX Best Local Similarity 56.4%; Pred. No. 1.6e-146;
XX Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;
QY 22 VYLTAAQVILCAATAAASAGPQCPSCVCSNCFKVCVTRRGISEVPGQIPSNITLYN 81
Db 29 VLLALQLLVAGLVRA-----QTCPSVCSCSNCFKVCVTRRGISEVPGQIPSNITLYN 82
QY 82 LMENNIQMIQADTFPHLHVLVQLGRNSIRQIEVGAPNGLASLNTLELFDNWLTVIPSG 141
Db 83 LHENGIOIKVNSFKHLRHLILQLSRNHITIGAPNGLANLNTLELFDNRLTTPNG 142
QY 142 APEYLSKLRELWLRNPNPTIESPYAFNRVPSIMDLGLCKLKEYISEGAFEGFLNLYL 201
Db 143 AFVYLSKLKELWLRNPNPTIESPYAFNRVPSIRLRLDLGLCKLKEYISEGAFEGFLNLYL 202
QY 202 NLGMCNFKDMNPLPLVGLLELEMSGNHFPPIRPGSPHGLSSLLKKLWMMMSQVSLIRNA 261
Db 203 NLAMCNREIPNLPLIKLDELDSGNHLSAIRPGSPQGLMHLQKLMWISQIOVIERNA 262
QY 262 PDGLASLVELNLAHNNLSLPHDLFTPLRYLVELHLHNNPNCDDILMLAWMLREYIPT 321

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Db 263 FDLQSLVEINLAHNNLTLLPHDLFTPLHLHLERLHLHNPNCNCDILMLSWIKDAPS 322  
 QY 322 NSTCCGRCHAPMGRYLYVEVDQASFOCSAPFFIMDAPRLNISEGRMAELKCR-TTPMS 380  
 Db 323 NTACCARCNTPEPLKGRYIGELDQNYFTCYAPVIVEPPADLVNTEGMAELKCRASLT 382  
 QY 381 SVKLLPNTGTVLHASRPRISVLNDGTLNFSHLLSDTGVTCTMTNVAAGNSAYLN 440  
 Db 383 SVSWITPNTGTVLHASRPRISVLNDGTLNFSHLLSDTGVTCTMTNVAAGNSAYLN 442  
 QY 441 VSTAEIANTSNYSFFTTVTVEITETSPED---TTRKYPVP-----TTSTGYQPAYTSTT 492  
 Db 443 VTAA--TTTPSYESTVTVTETMESPQDEARTDNNVGPFPVVDWEITNV-----TTSLT 494  
 QY 493 VLIQTR-VPKQAVPATDITDKMGTSLDEVMKTKIIIGCFVAVTLLAAMLIYFKLR 551  
 Db 495 P--QSTRSTEXTFTIPVTDINSGL-PGIDEVMKTKIIIGCFVAVTLLAAMLIYFKLR 551  
 QY 552 KRHOQRSTVTAARTVELIIOVDDEIPAAATSAATAAPSGVSEGAVALPTI-HDHIN-YNT 609  
 Db 552 KQHRQNHAPTRIVEIINVDDEITGTPM-----ESHLPMPALEHEHLNHS 600  
 QY 610 YKPAHGAHWTENSLSNLSHPTVTITISEPYIIQHTKDKVOETQI 653  
 Db 601 YKSPFNHTTWTI-NSIH---SSVHEPLLRMSKDNVOETQI 640

RESULT 31

AAW85722  
 ID AAW85722 standard; Protein; 640 AA.  
 AC AAW85722;  
 DT 27-SEP-1999 (first entry)  
 XX Novel protein (Clone AS209\_1).  
 KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;  
 KW cell differentiation; immunostimulation; immunosuppression;  
 KW haematopoiesis regulation; tissue growth; activin; inhibin;  
 KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;  
 KW ligand; anti-inflammatory; tumour suppression; gene therapy.  
 XS Homo sapiens.  
 PN WO9920644-A1.  
 PD 29-APR-1999.  
 PF 16-OCT-1998; 98WO-US22034.  
 PR 18-OCT-1997; 97US-0955557.  
 XX (GEMY ) GENETICS INST INC.  
 PI Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;  
 PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;  
 XX WPI; 1999-288272/24.  
 DR N-PSDB; AAX08687.  
 PT New polynucleotides encoding secreted human proteins  
 XX Claim 26; Page 109-111; 136pp; English.  
 CC The new human secreted proteins are encoded by polynucleotides  
 CC obtained from human placenta, adult testes, fetal kidney, fetal  
 CC brain, adult brain, adult brain and adult blood cDNA libraries.  
 CC The polynucleotides and proteins are predicted to have biological  
 CC activities which would make them suitable for treating, preventing or  
 CC ameliorating medical conditions in humans and animals. Suggested  
 CC activities include nutritional activity, cytokine and cell  
 CC proliferation/differentiation activity, immune stimulating (e.g. as

CC vaccines) or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombotic  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC cadherin/tumour invasion suppressor activity, and tumour inhibition  
 CC activity. The polynucleotides are also stated to be useful for gene  
 CC therapy. The sequences identified by a secretory leader  
 CC sequence motif in the polynucleotide and it is thought that the  
 CC encoded proteins have biological activity by virtue of their secreted  
 CC nature. This polypeptide was encoded by a clone designated AS209\_1  
 CC (See AAX08687).  
 XX  
 SQ Sequence 640 AA;  
 Query Match 54.2%; Score 1865; DB 20; Length 640;  
 Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
 Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
 QY 22 VYLAQWILCAATAAASAGPQNCPSVCSNOFSCVCTRGSLSEVPQIPSNRYLN 81  
 Db 29 VLLALQLLVAGLVRA-----QTCPSVCSNOFSCVCTRGSLSEVPQIPSNRYLN 82  
 QY 82 LMENNIQIADTFRHLHLLEVLQLGNSIRQISVGAFNGLASLNTLELFDNMLTVPISG 141  
 Db 83 LHENQIQLKVNSEFKLRLHLLEVLQLGNSIRQISVGAFNGLASLNTLELFDNMLTVPISG 142  
 QY 142 AFEYLKSLRELWLNPNIESIPSYAFNRVPSLMLDLGELKCLSVTISEGAPEGLNLYL 201  
 Db 143 APVYLSKULKELWLNPNIESIPSYAFNRVPSLMLDLGELKCLSVTISEGAPEGLNLYL 202  
 QY 202 NLGMCNIKDMENLTPLVGLBELENSGNHPPEIRPGSPHGLSSLLKCLWMSQVSLIERNA 261  
 Db 203 NLGMCNIKDMENLTPLVGLBELENSGNHPPEIRPGSPHGLSSLLKCLWMSQVSLIERNA 262  
 QY 262 FDGLASLVELLAENNLSSLPDLFTPLRYLVELHLHNPNCNCDILMLSWIKDAPS 321  
 Db 263 FDLQSLVEINLAHNNLTLLPHDLFTPLHLHLERLHLHNPNCNCDILMLSWIKDAPS 322  
 QY 322 NSTCCGRCHAPMGRYLYVEVDQASFOCSAPFFIMDAPRLNISEGRMAELKCR-TTPMS 380  
 Db 323 NTACCARCNTPEPLKGRYIGELDQNYFTCYAPVIVEPPADLVNTEGMAELKCRASLT 382  
 QY 381 SVKLLPNTGTVLHASRPRISVLNDGTLNFSHLLSDTGVTCTMTNVAAGNSAYLN 440  
 Db 383 SVSWITPNTGTVLHASRPRISVLNDGTLNFSHLLSDTGVTCTMTNVAAGNSAYLN 442  
 QY 441 VSTAEIANTSNYSFFTTVTVEITETSPED---TTRKYPVP-----TTSTGYQPAYTSTT 492  
 Db 443 VTAA--TTTPSYESTVTVTETMESPQDEARTDNNVGPFPVVDWEITNV-----TTSLT 494  
 QY 493 VLIQTR-VPKQAVPATDITDKMGTSLDEVMKTKIIIGCFVAVTLLAAMLIYFKLR 551  
 Db 495 P--QSTRSTEXTFTIPVTDINSGL-PGIDEVMKTKIIIGCFVAVTLLAAMLIYFKLR 551  
 QY 552 KRHOQRSTVTAARTVELIIOVDDEIPAAATSAATAAPSGVSEGAVALPTI-HDHIN-YNT 609  
 Db 552 KQHRQNHAPTRIVEIINVDDEITGTPM-----ESHLPMPALEHEHLNHS 600  
 QY 610 YKPAHGAHWTENSLSNLSHPTVTITISEPYIIQHTKDKVOETQI 653  
 Db 601 YKSPFNHTTWTI-NSIH---SSVHEPLLRMSKDNVOETQI 640

RESULT 32

AAV13394  
 ID AAV13394 standard; Protein; 640 AA.  
 XX AAV13394;  
 XX 25-JUN-1999 (first entry)  
 DE Amino acid sequence of protein PRO331.  
 XX



W Secreted protein; transmembrane protein; human; enterocolitis;  
W Zollinger-Ellison syndrome; gastrointestinal ulceration;  
W congenital microvillus atrophy; skin disease; cell growth;  
W abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
W Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
W fibromodulin; dermal scarring; Usher Syndrome; Atrophila areata;  
W anti-thrombotic; wound healing; tissue repair.

X Homo sapiens.

S WO9914328-A2.

X 25-MAR-1999.

K 16-SEP-1998; 98WO-US19330.

K 25-NOV-1997; 97US-0066840.

K 17-SEP-1997; 97US-0059113.

K 17-SEP-1997; 97US-0059115.

K 17-SEP-1997; 97US-0059117.

K 17-SEP-1997; 97US-0059119.

K 17-SEP-1997; 97US-0059121.

K 17-SEP-1997; 97US-0059122.

K 17-SEP-1997; 97US-0059184.

K 18-SEP-1997; 97US-0059263.

K 18-SEP-1997; 97US-0059266.

K 15-OCT-1997; 97US-0063125.

K 17-OCT-1997; 97US-0062285.

K 17-OCT-1997; 97US-0062287.

K 21-OCT-1997; 97US-0063486.

K 24-OCT-1997; 97US-0062814.

K 24-OCT-1997; 97US-0062816.

K 24-OCT-1997; 97US-0063045.

K 24-OCT-1997; 97US-0063120.

K 24-OCT-1997; 97US-0063121.

K 24-OCT-1997; 97US-0063127.

K 24-OCT-1997; 97US-0063128.

K 27-OCT-1997; 97US-0063329.

K 27-OCT-1997; 97US-0063327.

K 28-OCT-1997; 97US-0063541.

K 28-OCT-1997; 97US-0063542.

K 28-OCT-1997; 97US-0063544.

K 28-OCT-1997; 97US-0063549.

K 28-OCT-1997; 97US-0063550.

K 28-OCT-1997; 97US-0063564.

K 29-OCT-1997; 97US-0063435.

K 29-OCT-1997; 97US-0063704.

K 29-OCT-1997; 97US-0063732.

K 29-OCT-1997; 97US-0063738.

K 29-OCT-1997; 97US-0063734.

K 29-OCT-1997; 97US-0064215.

K 29-OCT-1997; 97US-0063735.

K 31-OCT-1997; 97US-0063870.

XX

PT New isolated human genes and polypeptides used in, e.g. treatment of  
gastrointestinal ulceration

XX Claim 12; Fig 104; 320pp; English.

CC AAY13344-403 represent secreted and transmembrane human proteins.  
The cDNA sequences are obtained from cDNA libraries, prepared from  
fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CC The encoded polypeptides have specific uses based on their homology to  
known polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
associated with the preservation and maintenance of gastrointestinal  
mucosa and the repair of acute and chronic mucosal lesions

CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal  
ulceration and congenital microvillus atrophy), skin diseases associated  
with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial  
cancers such as lung squamous cell carcinoma of the vulva and gliomas),  
potent effects on cell growth and development, diseases related to  
growth or survival of nerve cells including Parkinson's disease.

CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as  
for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used  
as a target for anti-tumor drugs. PRO533 may be used in the treatment  
of Usher Syndrome or Atrophila areata; PRO269 can be used as an  
anti-thrombotic agent; PRO287 polypeptides and portions may have  
therapeutic applications in wound healing and tissue repair; PRO317 can  
be used for treating problems of the kidney, uterus, endometrium, blood  
vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 640 AA;

Query Match 54.2%; Score 1865; DB 20; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;

Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;

QY 22 VYLTAVWILCAIAAASAGPQNCPSYSCSNQPSKVCYKRNREYVPGDSTNTRLEN 81

DB 29 VLLALQLLVAGLVRA-----QTCPSYSCSNQPSKVCYKRNREYVPGDSTNTRLEN 82

QY 82 LMENNIQMIQADTFERHLHLEVLQIGRNSIRQIEVGAFAENGLASLNTLELFDNWLTVIPSG 141

DB 83 LHENQIQIKVNSFKHLRHLLELQLSRHHRTIEIGAFAGLANLNTLELFDNWLTVIPSG 142

QY 142 APEYLSKLELWLRNPIESIPSYAFNRVPSLMRLDLGELKKLEYISGAFGLPNLYL 201

DB 143 AFVYLSKLELWLRNPIESIPSYAFNRVPSLMRLDLGELKKLEYISGAFGLPNLYL 202

QY 202 NLGCMNICKMPNLTPLVGLLEEMSGNEPPEPRPGSPHGLSLKGLWYNSQVSLIERNA 261

DB 203 NLAMCNLEIPNLTPLIKLELDLSGNHLSAIRPGSPHGLSLKGLWYNSQVSLIERNA 262

QY 262 FDGLASVLELNLAHNNLSLPHDLFTPLRYLVELLHNNPWNCDILNLAWLREYIPT 321

DB 263 FDLQSLVEINLAHNNLTLLPHDLFTPLHLEIRIHLHNNPWNCDILNLAWLREYIPT 322

QY 322 NSTCCGRCHAPHHMGRYLVEVDQASFOCSAPPIMDAPDLNISGRMAELKCR-TPPMS 380

DB 323 NTACCARGCTPENLGRYIGELDQNYFTCYAPVVEPPADLVNTEGMAELKCRASLT 382

QY 381 SVKWLPLNGTVLSHASRPRISVLDGTLNFSVLLSDTVYTCMTVNVAGNSASAYIN 440

DB 383 SVSWITPNGTVWTHGAYKVRVAVLSDGTLNFTVQDTGNYTCWNSVGVNTTASATLN 442

QY 441 VSTAEINTSNYSFFTVTVETTESPED---TTRKYKVP-----TSTGQPAYTSTT 492

DB 443 VTAA---TTTPSYFTVTVETTESPED---TTRKYKVP-----TSTGQPAYTSTT 494

QY 493 VLIQITR-VPKOVAVPATDTTDMQVTSDEYKTKIIGCFVAVTLAAALVFKLR 551

DB 495 P--QSTRSTKTFIPVTDINSGLPGIDEVKKTKIIGCFVAVTLAAALVFKLR 551

QY 552 KKHQRSTVTAARTVEIIQVDEDIIPAATSAATAAPGCVSGEGAVLFTI-HDHIN-YNT 609

DB 552 KQHQRNEHAPTRTVEIINVDDIEITGDTFM-----ESHLPMPAIEHLEHLYNS 600

(GETH ) GENENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.

N-PSDB; AAX52265.

[illegible]

thyroiditis; Grave's disease; demyelinating disease; multiple sclerosis;  
Crohn's disease; hepatobiliary disease; hepatitis; asthma; human;  
graft-versus-host-disease.

Homo sapiens.

Key  
Location/Qualifiers  
Modified-site 40..46  
/note= "N-myristoylation site"  
Modified-site 73..79  
/note= "N-myristoylation site"  
Modified-site 118..124  
/note= "N-myristoylation site"  
Modified-site 183..187  
/note= "cAMP and cGMP-dependent protein kinase phosphorylation site"  
Modified-site 191..197  
/note= "N-myristoylation site"  
Modified-site 228..234  
/note= "N-myristoylation site"  
Modified-site 237..243  
/note= "N-myristoylation site"  
Modified-site 268..272  
/note= "Casein Kinase II phosphorylation site"  
Modified-site 278..282  
/note= "N-glycosylation site"  
Modified-site 364..368  
/note= "N-glycosylation site"  
Modified-site 390..394  
/note= "N-glycosylation site"  
Modified-site 391..397  
/note= "N-myristoylation site"  
Modified-site 412..416  
/note= "N-glycosylation site"  
Modified-site 415..419  
/note= "N-glycosylation site"  
Modified-site 417..421  
/note= "Casein Kinase II phosphorylation site"  
Modified-site 422..428  
/note= "N-myristoylation site"  
Modified-site 433..439  
/note= "N-myristoylation site"  
Modified-site 434..438  
/note= "N-glycosylation site"  
Modified-site 442..446  
/note= "N-glycosylation site"  
Modified-site 465..469  
/note= "Casein Kinase II phosphorylation site"  
Modified-site 488..492  
/note= "N-glycosylation site"  
Modified-site 531..537  
/note= "N-myristoylation site"  
Modified-site 579..583  
/note= "Casein Kinase II phosphorylation site"  
Modified-site 606..610  
/note= "N-glycosylation site"  
Modified-site 620..624  
/note= "Casein Kinase II phosphorylation site"

WO200015797-A2.

23-MAR-2000.

15-SEP-1999; 99WO-US21547.

17-SEP-1998; 98US-0100858.

17-SEP-1998; 98WO-US19437.

(GETH ) GENENTECH INC.

Fong S, Goddard A, Gurney AL, Tumas D, Wood WL;

WPI; 2000-271435/23.

DR N-PSDB; AA252207.  
XX Composition for treatment and diagnosis of immune related diseases e.g.  
PT Grave's disease comprises a PRO245, PRO217, PRO301, PRO286, PRO335,  
PT PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably  
PT antibodies) -  
XX Example 1; Fig 14; 201pp; English.

XX The present sequence is the human protein PRO331, encoded by UNQ292 cDNA,  
CC designated as clone DNA0981. It is isolated from human foetal brain  
CC tissue. Portions of PRO331 has homology to the LIG-1 protein.  
CC It enhances or suppresses the infiltration of inflammatory cells into  
CC tissues, proliferation of T-lymphocytes and modulates the immune  
CC response. This sequence is useful for treatment of immune related  
CC disorders, like SLE, rheumatoid/juvenile arthritis, spondyloarthritis,  
CC systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such  
CC as dermatomyositis, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
CC autoimmune haemolytic anaemia, thrombocytopenia, thyroiditis e.g. Grave's  
CC disease, diabetes mellitus, immune-mediated renal disease e.g.  
CC Glomerulonephritis, demyelinating diseases such as multiple sclerosis and  
CC Guillain-Barre syndrome, hepatobiliary diseases like hepatitis and  
CC primary biliary cirrhosis, inflammatory and fibrotic lung diseases such  
CC as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or  
CC immune-mediated skin diseases such as psoriasis, allergies like asthma,  
CC immunological diseases of the lungs such as eosinophilic pneumonia and  
CC transplantation associated diseases such as graft-versus-host-disease.

XX Sequence 640 AA;

Query Match 54.2%; Score 1865; DB 21; Length 640;

Best Local Similarity 56.4%; Pred. No. 1.6e-146;

Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;

QY 22 VYLTQWILCAAIAAASAGPQNCPSVCSNCFQVCTRRGLSEVPGQIPSNRYLN 81  
DB 29 VLLALQLLVAGLVRA-----QTCPSVCSNCFQVCTRRGLSEVPGQIPSNRYLN 82  
QY 82 LMENNTOMQADTFPHLHLEVLQGRNSIQIYVGAFAFGASLNTLELFWLTVPSG 141  
DB 83 LHENQIQIKVNSFKHRLHLEVLQGRNSIQIYVGAFAFGASLNTLELFWLTVPSG 142  
QY 142 APEYLSKLRLEMLRNPIESIPSYAFNRVPSLMRLDGLKLEKLEYSISGAFEGFLNRYL 201  
DB 143 AFVYLSKLRLEMLRNPIESIPSYAFNRVPSLMRLDGLKLEKLEYSISGAFEGFLNRYL 202  
QY 202 NIGMKNIKDMPNLTPLVGLERLEMSGNHFPPIRPGSHGLSSLLKLVWNSQVSLIENNA 261  
DB 203 NLAMCNLRREIPNLTPLIKLDELDSGNHLSAIRPGSFQGLMHLQKLVWNSQVSLIENNA 262  
QY 262 PDGLASVLEMLAHNNLSLPHDFTPLRYLVLEHLHNPWNCDDILWLAWLREVIPT 321  
DB 263 FNLQSLVEINLAHNNLTLLPHDLFTPLHLERHLEHLHNPWNCDDILWLAWLREVIPT 322  
QY 322 NSTCCGRCHAPMHMRGYLVEVDQASFOCSAPFIMDAPRDLNISSEGRMAELKCR-TTPMS 380  
DB 323 NTACCARCNTPNLKGRIYIGELDQNYFTCYAPVIVPPADLVNTEGMAAELKCRASLT 382  
QY 381 SVKMLLPNGTULSHASRHPRIISVLNDGTLNPSHVLSDYGVYTCMTVNVAGNSASVLYN 440  
DB 383 SVSWITPNTGVTMGAYKVRIVAVLSGDTLNTVNTVQDTGMTCVNSVSGNTTASATLN 442  
QY 441 VSTAEINTSNYSFFTTVTVTETTESPDE---TTRKYKVP-----TTSTGYOPATYTTST 492  
DB 443 VTAA--TITPFSVFTVTETTESPDEARTDNNVGGTTPVVDWETTV-----TTSLT 494  
QY 493 VLIQTR-VPRQVAVPATDTRDKMOTSLDEVMKTKIIGCFVAVTLLAAAMLVFKLR 551  
DB 495 P--QSTRSTKTFITPVDINSIGI--PGIDEVMKTKIIGCFVAVTLLAAAMLVFKLR 551  
QY 552 KRHOQRSTVTAARTVEIIQVEDIPAAATSAATAAPSGVSGEAVLPTI-HDHIN-YNT 609  
DB 552 KQHFQNHAPTRVVEIINVDEITGDTFM-----ESHLPWPAIEHNLHNS 600

QY 610 YPKAGAHKWTENSLNHPHTTISEBPIIQTHTKDKVQTOI 653  
DB 601 YKSPFNHTTWTI-NSIH---SSVHEPLLIRMSKDNVQTOI 640

RESULT 35  
AAU12355  
ID AAU12355 standard; Protein; 640 AA.

AC AAU12355;  
XX 24-OCT-2001 (first entry)  
XX Human PRO331 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
XX adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.

XX WO20010466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX 09-DEC-1999; 99US-0170262.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 30-DEC-1999; 99WO-US31243.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US03176.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 01-MAR-2000; 2000WO-US05601.

XX 20-MAR-2000; 2000WO-US07377.

XX 21-MAR-2000; 2000WO-US07532.

XX 30-MAR-2000; 2000WO-US08439.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

XX 10-NOV-2000; 2000WO-US30873.

XX (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood W, Zhang Z;

XX WPI; 2001-408281/43.  
XX N-PSDB; AAS21427.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
XX other PRO polypeptides, link bioactive molecules to cells expressing  
XX PRO polypeptides, and detect the presence of mammalian tumours e.g.  
XX lung, breast, prostate, cervical -  
XX  
XX  
XX Claim 12; Fig 368; 813pp; English.

CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
CC PRO polypeptides. The PRO polypeptides are useful to detect other  
CC PRO polypeptides, to link bioactive molecules to cells expressing  
CC PRO polypeptides, to modulate biological activities of cells expressing  
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample of  
CC some of the 275 sequences are also useful to stimulate the release of  
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
CC proliferation or differentiation of chondrocytes, the proliferation or  
CC gene expression in pericyte cells, the release of proteoglycans from  
CC cartilage, the proliferation of inner ear utricular supporting cells or  
CC of T-lymphocytes, the release of a cytokine from peripheral blood  
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
CC molecules involved in binding interactions. The polynucleotides encoding  
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy.  
XX  
SQ Sequence 640 AA;

Query Match 54.2%; Score 1865; DB 22; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1,6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;

QY 22 VYLTAQWILCAAIAAASAGQNCPSVCSNCSNPSKVVCTRRGLSEVQDQIPNTRYLN 81  
DB 29 VLLALQLLVAGLVRA-----QTCPSCVCSNCSNPSKVICVRKRLREYDPDGISTRLLN 82  
QY 82 IMENNIQMIQADTFERHLEVLQIGRNSIRQIEVGAFLNGLASLNTLELFPNLTVPISG 141  
DB 83 LHENQIQIIVKNSFXHRLHEILQSRNHIETIEGAFNGLANLTLELFPNLTTPNG 142  
QY 142 AFEYLSKLFELMRNNPIESIPSYAFNRVPSLMRLDLGELKXLEYISEGAFEGFLNLYL 201  
DB 143 AFVYLSKLFELMRNNPIESIPSYAFNRVPSLMRLDLGELKXLEYISEGAFEGFLNLYL 202  
QY 202 NLGCMQIKMNMNLTPLVGLLEELMSGNHPPEIRPGSFGLSLKGLWMSQVSLIERNA 261  
DB 203 NLAMCNLRIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKLMWISQIQIUIERNA 262  
QY 262 FDGLASLVELNLAHNNLSLPHDLFTPLRYLVELHHPNPNWNCDCDILLAWLWREYIPT 321  
DB 263 FNLQSLVELNLAHNNLTLLPHDLFTPLHLEIRHHPNPNWNCDCDILLWSWIKDAPS 322  
QY 322 NSTCCGRCHAPMHMRGRYLVVDQASFOCSAPFIMDAPRDLNISEGRMAELKCR-TPPMS 380  
DB 323 NTACCACNTPENLKRGYIGELDQNYFTCYAPVIVEPPADLNVTEGMAELKCRASLTSLT 382  
QY 381 SVKLLPNGTVLSHARRHERISVANDGTINPSHVLLSDTVVTCMTNVNAGNSASAYLN 440  
DB 383 SVSWITPFGTVMTGAYKVRIDAVLSDGTLNFTNVVQDTGYTCWVNSVNGTITASATLN 442  
QY 441 VSTAELNTSNYSFPTTVTVETTEISPED---TTRKYKVPV-----TTSTGYQPAVTTSTT 492  
DB 443 VTAA--TTTPFSYFSTVTVETMEPSODEARTDDNNVGPVVDVDETINV-----TTSLT 494  
QY 493 VLIQTR-VPKVAVPATDTTDMQTSLEVMKTKIILGCFVAVTLAAAMLIVPYKLR 551  
DB 495 P--QSTRSEKTFPTIPVTDINSGI-PGIDEVMKTKIILGCFVAILLAAVNLVIFYKWR 551  
QY 552 KRHQRSVTVAARTVEIIQVDEDIIPAATAAATAAPSGVSGEGAVVLPIT-HDHN-INT 609  
DB 552 KOHRQNHAPRTVBEIINVDEITGTPM-----ESHLPMPAIEHEHLNHYNS 600  
QY 610 YKPAHAHTEHSLNLSLHPTVTTTISEPIIQTHTKDKVQTOI 653  
DB 601 YKSPFNHTTWTI-NSIH---SSVHEPLLIRMSKDNVQTOI 640

RESULT 36





495 P--QSTRSTSTKTIPTIPVDINSGL-PCIDEVMKTKIIIGCFVAITLMAVWLVIFYKWR 551  
552 KRHOORSTVTAARTVEIIQVDEIPAAATSAATAAPSGVSGEAVVLPPI-HDHIN-YNT 609  
552 KQHRQNHAPHTVTEIIVDDITGDTM-----ESLPMFAIEHEHLNHYNS 600  
610 YKPAHGAHWTEISLNSLHPVTVTIIEBPYIIQHTKVKQVETQI 653  
601 YKSPFNHTTIVNTI-NSIH---SSVEHPLLIRWNSKDNVQETQI 640

RESULT 38  
AB55292  
D AAB65292 standard; Protein; 640 AA.  
X C AAB65292;  
X T 02-APR-2001 (first entry)

X E Human PRO331 protein sequence SEQ ID NO:501.  
X W Human; secreted and transmembrane protein; PRO; cytostatic;  
X W cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
X W diagnostic assay.  
X S Homo sapiens.

WO2000073454-A1.

07-DEC-2000.

30-MAR-2000; 2000WO-US08439.

02-JUN-1999; 99WO-US12252.

23-JUN-1999; 99US-0141037.

07-JUL-1999; 99US-0143048.

20-JUL-1999; 99US-0144758.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

17-AUG-1999; 99US-0149396.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

08-OCT-1999; 99US-0158663.

30-NOV-1999; 99WO-US28313.

01-DEC-1999; 99WO-US28301.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30911.

05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.

02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.

XX Claim 12; Fig 314; 935pp; English.  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridization probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridization probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 640 AA;

Query Match 54.2%; Score 1865; DB 22; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
QY 22 VYITAQWILCAIAAASAGPQNCSPQSCNORPKVCTRGSLSEVPQGIPTNYLN 81  
DB 29 VLLALQLLVVAGLVRA-----QTCPSVCSCSQPFKVCVKRLREVDPGISTNLLN 82  
QY 82 LMENNIQMIQADTFRIHLHLVQLGRNSIRQIEVGAFNGLASLNTLELFDNWLTVIPSG 141  
DB 83 LHENQIQIIVKNSFKHLHLLEILQLSRNHRTTEIGAFNGLANLNTLELFDNLTTPNG 142  
QY 142 AFYLSKLRLHLWLNNDPIESIPYAFNRPVSLRLDGLKLELYISEGAFEGLENLYL 201  
DB 143 AFVYLSKLRLWLNNDPIESIPYAFNRPVSLRLDGLKLELYISEGAFEGLENLYL 202  
QY 202 NLGMCNIKOMPNTPLVGLRELEMSGNHFEIRPGSGFHGLSSLKCLWVWNSQVSLIERNA 261  
DB 203 NLAMCNREIPNLTPLIKDELDSGNHLSAIRPGSQGLMHLQKLMWISQIQVIERNA 262  
QY 262 FDGLASLVELNLAHNNLSLPHDLFTPLRYLVHLHNPWNCDCDILMLAWLREYIPT 321  
DB 263 FDNQLSLVEINLAHNNLTLLPHDLFTPEHLERHLHNPWNCDCDILMLSWWIKOMAPS 322  
QY 322 NSTCGGCHAPMHRGELYVEVDQASQCSAPFIMDAPRLNISSEGMAELKCR-TPPMS 380  
DB 323 NTACCRCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLVTEGMAELKCEASTSLT 382  
QY 381 SVKMILLPNGTVLSHARHPRISVLNDGTLNPSHVLSDTGVTTCMTWTVNAGNSAYLN 440  
DB 383 SVSWITPNTGTWTHGAVKVRIVLSDGTLNFTNVQDTGMYTCWNSVGNNTTASATLN 442  
QY 441 VSTAELATSNYSPTTWTVTETLSPED---TTRKYPVP-----TTSTGYQPAYTSTT 492  
DB 443 VTAA--TTTPESYFTVTVTETMPSQDEARTDNNVGTTPVDWETINV-----TTSLT 494  
QY 493 VLIQTR-VPRQVAVPATDTTDKRMQTSIDELVMKTKIIICGFVAVTLLAAMLVIFVKLR 551  
DB 495 P--QSTRSTSTKTIPTIPVDINSGL-PCIDEVMKTKIIIGCFVAITLMAVWLVIFYKMR 551  
QY 552 KRHOORSTVTAARTVEIIQVDEIPAAATSAATAAPSGVSGEAVVLPPI-HDHIN-YNT 609  
DB 552 KQHRQNHAPHTVTEIIVDDITGDTM-----ESLPMFAIEHEHLNHYNS 600  
QY 610 YKPAHGAHWTEISLNSLHPVTVTIIEBPYIIQHTKVKQVETQI 653  
DB 601 YKSPFNHTTIVNTI-NSIH---SSVEHPLLIRWNSKDNVQETQI 640

RESULT 39  
AAB53089  
ID AAB53089 standard; Protein; 640 AA.  
XX

(GETH ) GENENTECH INC.  
ASKENAZI AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi CU, Gurney AL, Kijavini IG, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;

WPI: 2001-032160/04.  
N-FSDB; AAF44261.

PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -



AA053089;  
28-FEB-2001 (first entry)  
Human angiogenesis-associated protein PRO331, SEQ ID NO:137.  
Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
Alzheimer's disease; Huntington's disease; stroke; drug screening;  
gene therapy; transgenic animal.  
Homo sapiens.  
WO200053753-A2.  
14-SEP-2000.  
05-JAN-2000; 2000WO-US00219.  
08-MAR-1999; 99WO-US05028.  
12-MAR-1999; 99US-0123957.  
14-MAY-1999; 99US-0134287.  
02-JUN-1999; 99WO-US12252.  
23-JUN-1999; 99US-0141037.  
20-JUL-1999; 99US-0144758.  
26-JUL-1999; 99US-0145698.  
01-SEP-1999; 99WO-US20111.  
08-SEP-1999; 99WO-US20594.  
15-SEP-1999; 99WO-US21090.  
15-SEP-1999; 99WO-US21547.  
15-SEP-1999; 99WO-US23089.  
30-NOV-1999; 99WO-US28313.  
02-DEC-1999; 99WO-US28409.  
02-DEC-1999; 99WO-US28564.  
02-DEC-1999; 99WO-US28565.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WJ;  
WPI: 2001-090793/10.  
X-PSDB; AAC97475.  
New isolated nucleic acid for producing a PRO polypeptide, analyzing  
genetic disorders and treating cardiovascular, endothelial or  
angiogenic disorders, such as atherosclerosis, wounds or cancer -  
Claim 69; Fig 52; 293pp; English.  
The invention relates to novel human angiogenesis-associated proteins  
designated PRO proteins (AA053064-B53097), and to nucleic acids encoding  
PRO proteins. The invention also relates to vectors and host cells  
comprising a PRO nucleic acid, the recombinant production of a PRO  
protein, PRO antibodies specific for a PRO protein, fusion proteins  
comprising a PRO protein, agonists or antagonists of a PRO protein, and  
compounds which inhibit the expression of a PRO gene. The invention  
additionally encompasses methods of identifying modulators of PRO  
expression or activity; diagnosing a cardiovascular, endothelial or  
angiogenic disorder, or a susceptibility to such a disorder by detecting  
mutations in a PRO gene, or the expression level of a PRO gene within a  
particular tissue; treating a cardiovascular, endothelial or angiogenic  
disorder via the administration of a PRO protein, PRO nucleic acid, or  
PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
administration of a PRO protein, or an agonist or antagonist thereof.  
PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
agonists and PRO antagonists may be used as therapeutic agents to treat

cardiovascular, endothelial or angiogenic disorders, such as  
atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
disease, or stroke. PRO nucleic acids are additionally useful in the  
recombinant production of PRO proteins, as hybridisation probes to  
screen libraries to isolate cDNAs with sequence identity to PRO proteins.  
to map genes encoding PRO proteins, to analyse genetic disorders, and in  
gene therapy. PRO nucleic acids can also be used to produce transgenic  
animals useful for the development and screening of potential  
therapeutic agents. The present sequence represents a PRO protein of the  
invention.  
XX Sequence 640 AA;  
SQ  
Query Match 54.2%; Score 1865; DB 22; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
QY 22 VYLTAQVWILCAATAAASAGPQPCSVCSNQSFKVCTVTRGLSEVPQIPSENTRYLN 81  
DB 29 VLLALQLLVAGLYRA-----QTCPSVCSNQSFKVICVRKNLREVPDGLSNTLLN 82  
QY 82 LMENNIQIADTFPHLHLEVLQIGRNSIQIIVGAFNGLASLNTLEFNNWLTVPESG 141  
DB 83 LHENQIQIKVNSFKHLRLHLEILQSRNHRTITIGAFNGLANLTLEFNNRUTTPG 142  
QY 142 APEYLSKLRLEWLNPNIESIPSAFNEVPSLMDLDELKELKLYIISGAPGEGFLNLYL 201  
DB 143 AFVYLSKLRLEWLNPNIESIPSAFNEVPSLMDLDELKELKLYIISGAPGEGFLNLYL 202  
QY 202 NLGMCNIXDMPNLTEPLVGLLEMSGNHFPPIRPGSFGLSSKKLWVMSQVSLIERN 261  
DB 203 NLAMCNLREIPNLTEPLIKLDELISGNHLSAIRPGSFGLMHLQKLWVMSQVSLIERN 262  
QY 262 FGLASLVELMLAHNLSLSDHLEPLRLYLVEHLHNPNCDCDILMLAWLREIYPT 321  
DB 263 FDMQLSVEINLAHNLTLLPHDLFTPLHLELRLHNPNCDCDILMLSWIKDMAPS 322  
QY 322 NSTCCGRCHAPMHRGRLVVEVDQASFOCSAPFINDAPDLNISEGRMAELKCR-TPPMS 380  
DB 323 NYACCARCNTPENLAGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAELKCRASLT 382  
QY 381 SVKLLPNGTVLHASRHPRIISVLDGTLNFSVLLSDTGYTCMTVNTVAGNSASAYLN 440  
DB 383 SVSWITPNTGVTWTHGAYKVRIVAVLSDGTLNFTNVTVQDTGMTCNVSNGVITASATLN 442  
QY 441 VSTAEINTSNVSFFTTVTVEITTEISPED---TTRKYKEVP-----TTSYGQPAYTSTT 492  
DB 443 VTAA--TTTPFSYFTVTVEITTEISPED---TTRKYKEVP-----TTSYGQPAYTSTT 494  
QY 493 VLIQTR-VFKOVAVPATDTTDXMGTSLDEVMKTKIILGCFVATLLAAALIVFYKLR 551  
DB 495 P--QSTRSEKTFTEFTVDINSGL-PGIDENVKTKIILGCFVATLLAAALIVFYKLR 551  
QY 552 KBHQQRSTVTAARTVEIIQVDEDIIPAATAAATAAPSGVSGEGAVVLPIT-HDHN-YNT 609  
DB 552 KBHQQRSTVTAARTVEIIQVDEDIIPAATAAATAAPSGVSGEGAVVLPIT-HDHN-YNT 609  
QY 610 YKPAHGAHWTEISLNSLHPTVTITSEPIYIOTHTYKQVQETQI 653  
DB 601 YKSPFNHTTNTVTI-NSIH---SSVHEPLLIRMSKNVQETQI 640  
RESULT 40  
ABU69672  
ID ABU69672 standard; Protein; 640 AA.  
XX ABU69672;  
XX AC ABU69672;  
XX DT 05-JUN-2003 (first entry)  
XX XX Novel human secreted and transmembrane protein PRO331.

X Human; secreted and transmembrane protein; gene therapy; psoriasis;  
 W enterocolitis; gastrointestinal ulceration; skin disease;  
 W keratinocyte differentiation; epithelial cancer; Alzheimer's disease;  
 W squamous cell carcinoma; Parkinson's disease; inflammatory disease;  
 W amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;  
 W multiple sclerosis; organ failure; atherosclerosis; cardiac injury;  
 W infertility; birth defect; premature aging; AIDS; cancer;  
 W diabetic complication; wound repair; tissue re-growth.

Homo sapiens.

US2003017463-A1.

23-JAN-2003.

11-JUL-2001; 2001US-0903640.

10-SEP-1998; 98WO-US18824.

14-SEP-1998; 98WO-US19177.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

01-DEC-1998; 98WO-US25108.

08-SEP-1999; 98WO-US20594.

13-SEP-1999; 98WO-US20944.

15-SEP-1999; 98WO-US21090.

15-SEP-1999; 98WO-US21547.

05-OCT-1999; 98WO-US23089.

29-NOV-1999; 98WO-US28214.

30-NOV-1999; 98WO-US28313.

01-DEC-1999; 98WO-US28301.

02-DEC-1999; 98WO-US28564.

02-DEC-1999; 98WO-US28565.

16-DEC-1999; 98WO-US30095.

20-DEC-1999; 98WO-US30911.

20-DEC-1999; 98WO-US30999.

05-JAN-2000; 2000WO-US00219.

11-FEB-2000; 2000WO-US03565.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US05004.

02-MAR-2000; 2000WO-US05841.

20-MAR-2000; 2000WO-US07377.

30-MAR-2000; 2000WO-US08439.

22-MAY-2000; 2000WO-US14042.

02-JUN-2000; 2000WO-US15264.

28-JUL-2000; 2000WO-US20710.

24-AUG-2000; 2000WO-US23328.

17-SEP-1997; 97US-059113P.

17-SEP-1997; 97US-059115P.

17-SEP-1997; 97US-059117P.

PR 28-OCT-1997;

PR 28-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 29-OCT-1997;

PR 31-OCT-1997;

PR 31-OCT-1997;

PR 31-OCT-1997;

PR 03-NOV-1997;

PR 07-NOV-1997;

PR 12-NOV-1997;

PR 17-NOV-1997;

PR 18-NOV-1997;

PR 21-NOV-1997;

PR 21-NOV-1997;

PR 24-NOV-1997;

PR 24-NOV-1997;

PR 24-NOV-1997;

PR 24-NOV-1997;

PR 25-NOV-1997;

PR 12-DEC-1997;

PR 04-JUN-1998;

PR 10-SEP-1998;

PR 14-SEP-1998;

PR 17-SEP-1998;

PR 13-OCT-1998;

PR 20-NOV-1998;

PR 22-DEC-1998;

PR 07-JUL-1999;

PR 26-JUL-1999;

PR 28-JUL-1999;

PR 18-SEP-2000;

XX (GETH ) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Pilvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;

XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

97US-063550P.

97US-063564P.

97US-063435P.

97US-063704P.

97US-063732P.

97US-063734P.

97US-063735P.

97US-063738P.

97US-064215P.

97US-063870P.

97US-064103P.

97US-064248P.

97US-064809P.

97US-065186P.

97US-065846P.

97US-065893P.

97US-066120P.

97US-066364P.

97US-066453P.

97US-066466P.

97US-066511P.

97US-066709P.

97US-066722P.

97US-066840P.

97US-069425P.

98US-088026P.

98US-099803P.

98US-100262P.

98US-100858P.

98US-104080P.

98US-109304P.

98US-113296P.

98US-143048P.

99US-145698P.

99US-146222P.

2000US-0665350.

WPI; 2003-341586/32.

N-PSDB; ACA55048.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing

or treating inflammatory diseases, organ failure, atherosclerosis,

cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or

Parkinson's disease.

Claim 12; Fig 104; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides

(secreted and transmembrane). The PRO polypeptides and nucleic acids are

useful in diagnosing or treating enterocolitis, gastrointestinal

ulceration, skin diseases associated with abnormal keratinocyte

differentiation, e.g. psoriasis or epithelial cancers such as squamous

cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic

lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,

asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac

injury, infertility, birth defects, premature aging, AIDS, cancer,

diabetic complications, or mutations in general. The polypeptides are

also useful for wound repair and associated therapies concerned with

re-growth of tissue. The PRO polypeptides and nucleic acid molecules

are also useful in gene therapy, and as molecular weight markers for

protein electrophoresis purposes. The anti-PRO antibodies may be used

in diagnostic assays for PRO, or for the affinity purification of PRO

from recombinant cell culture or natural sources. This is the amino

acid sequence of a novel human PRO polypeptide.

XX

3Q	Sequence	640 AA;	
	Query Match	54.2%; Score 1865; DB 24; Length 640;	
	Best Local Similarity	56.4%; Pred. No. 1.6e-146;	
	Matches	363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;	
2Y	22	VYLTAQVWILCAIAAASAGPQNCPSVCSNPFQKVCWCTRRGLSEVPQIGIPSNTRYLN 81	
2b	29	VLLALQLLVAGLVRA-----QTCPSVCSNPFQKVCWCTRRGLSEVPQIGIPSNTRYLN 82	
2Y	82	LMENNIQWQADTRHLHLLEVLQSGNSRQTEVGFAGNGLASLNTLELPDNKLVTPISG 141	
2b	83	LEENQIQIKVNSPKHLRHLLEVLQSGNSRQTEVGFAGNGLASLNTLELPDNKLVTPISG 142	
2Y	142	AFYLSKLREZLWLNNEPTEGTPSYAFNRVPSLRDLGELKLEYISEGAFCELFNLYL 201	
2b	143	AFVLSKLREZLWLNNEPTEGTPSYAFNRVPSLRDLGELKLEYISEGAFCELFNLYL 202	
2Y	202	NLHCNFKDMNLTPLVGLSEHLENSGHPFIRPGSFHGLSSKLWVNSQVSLTERNA 261	
2b	203	NLWNCNLRSEIPLFKLDELDSGNHLGSAIRPGSFQGLMHQKLMQISQVQVTERNA 262	
2Y	262	FDGLASIVELNLAHNNLSLPHDLFTPLRYLVLELHLHNPWNCDCDILMLAWLREYIPT 321	
2b	263	FDNQLSVLEINLAHNNLSLPHDLFTPLHLERLHLHNPWNCDCDILMLAWLREYIPT 322	
2Y	322	NSTCGRCCHAPMHRGRLVVEVDQASTQCCGAPFMDAPRDNISSEGMAELKCR-TPPMS 380	
2b	323	NTACCARCNTPENLKGRYIGELDQNYFTCVAPVIVEPPADLVNTEGMAELKCRASSTLT 382	
2Y	381	SVKMLLPNGTVLSHARHPRTSVLNDGTLNPFVSHVLLSDTGVYTCWTVNAGNSNAGAYLN 440	
2b	383	SVSMITPNTGTVTHGAYKRVAVLSDGTLNFTVTVQDAGNYTCWVNSGVNTASATLN 442	
2Y	441	VSTAEINTNSYFTTIVTEVTEIISPD-----TTRKYKVP-----TTSTGYQAYTTSIT 492	
2b	443	VTAA--TTTPESTSTVETWETPESQDEARTDNNVGFPPVDWETTNV-----TTSLT 494	
2Y	493	VLIOTTR-VPKOVAPATDITDKMOTSIDEVMTKTKIIIGCFVAVTLLAAALIVPKLR 551	
2b	495	P--QSTRTEKTFIPIVTDINSIGI-PGIDEVMTKTKIIIGCFVAVTLLAAALIVPKLR 551	
2Y	552	KRHOORSTVTAARTVEIIOVDEPIDAATSAATAAPSGVSGGAVLPTI-HDHIN-YNT 609	
2b	552	KOHROHNEHAPTRVEIINVDDEITGTPM-----ESHLPMPAIEHEHLAHYNS 600	
2Y	610	YKPAHGAHWNTENSLGSLHPTVTIIESEPIIIOHTKDKVQETQI 653	
2b	601	YKSPFNHTTIVNTI-NSIH-----SSVHEPLLRMSKONVQETQI 640	
RESULT 41			
ID	ABU71495	ABU71495 standard; Protein; 640 AA.	
XX	AC	ABU71495;	
XX	DT	10-JUN-2003 (first entry)	
XX	DE	Human PRO polypeptide #51.	
XX	KW	Human; secreted and transmembrane protein; PRO polypeptide; cancer;	
KW	KW	Alzheimer's disease; ischaemia; cyostatic; nootropic; vasotropic;	
KW	KW	neuroprotective.	
XX	OS	Homo sapiens.	
XX	OS	US2002192659-A1.	
XX	PN	19-DEC-2002.	
XX	PD	10-JUL-2001; 2001US-0902853.	
XX	PF		
XX	XX		

PR	10-SEP-1998;	98WO-US18824.	
PR	14-SEP-1998;	98WO-US19177.	
PR	16-SEP-1998;	98WO-US19330.	
PR	17-SEP-1998;	98WO-US19437.	
PR	01-DEC-1998;	98WO-US25108.	
PR	08-SEP-1999;	99WO-US20594.	
PR	13-SEP-1999;	99WO-US20944.	
PR	15-SEP-1999;	99WO-US21090.	
PR	15-SEP-1999;	99WO-US21547.	
PR	05-OCT-1999;	99WO-US23089.	
PR	01-DEC-1999;	99WO-US28301.	
PR	02-DEC-1999;	99WO-US28564.	
PR	02-DEC-1999;	99WO-US28565.	
PR	16-DEC-1999;	99WO-US30035.	
PR	20-DEC-1999;	99WO-US30911.	
PR	20-DEC-1999;	99WO-US30999.	
PR	05-JAN-2000;	2000WO-US00219.	
PR	11-FEB-2000;	2000WO-US03565.	
PR	22-FEB-2000;	2000WO-US04414.	
PR	28-JUL-2000;	2000WO-US20710.	
PR	24-AUG-2000;	2000WO-US23328.	
PR	17-SEP-1997;	97US-059113P.	
PR	17-SEP-1997;	97US-059113P.	
PR	17-SEP-1997;	97US-059117P.	
PR	18-SEP-1997;	97US-059266P.	
PR	15-OCT-1997;	97US-062125P.	
PR	17-OCT-1997;	97US-062285P.	
PR	17-OCT-1997;	97US-062287P.	
PR	21-OCT-1997;	97US-063486P.	
PR	24-OCT-1997;	97US-062814P.	
PR	24-OCT-1997;	97US-062816P.	
XX	(GETH ) GENENTECH INC.		
XX	PA		
PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;		
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;		
PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KO, Kljavin LJ;		
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;		
PI	Williams PM, Wood WI;		
XX	WPI: 2003-361832/34.		
XX	N-PSDB; ACA59533.		
XX	New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or		
XX	PRO1866, useful in molecular biology, chromosome and gene mapping, in		
XX	generating antisense RNA and DNA, and in gene therapy		
XX	Claim 12; Fig 104; 474pp; English.		
XX	The present invention relates to the isolation of novel human secreted		
XX	and transmembrane proteins (PRO polypeptides), and the polynucleotide		
XX	sequences encoding them. The polynucleotide sequences are useful in		
XX	molecular biology, as hybridisation probes, in chromosome and gene		
XX	mapping, in generating antisense RNA and DNA, and in gene therapy. The		
XX	polynucleotide sequences may also be used in preparing PRO polypeptides		
XX	by recombinant techniques, and in generating either transgenic animals		
XX	or knock-out animals which, in turn, are useful in the development and		
XX	screening of therapeutically useful reagents. The PRO polypeptides or		
XX	their antibodies are useful in preparing a medicament for treating a		
XX	condition responsive to the polypeptide or antibody, such as cancer,		
XX	Alzheimer's disease or ischaemia, and in various diagnostic assays.		
XX	ABU71445-ABU71505 represent human PRO polypeptides of the invention.		
XX	Sequence 640 AA;		
XX	Query Match	54.2%; Score 1865; DB 24; Length 640;	
XX	Best Local Similarity	56.4%; Pred. No. 1.6e-146;	
XX	Matches	363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;	
QY	22	VYLTAQVWILCAIAAASAGPQNCPSVCSNPFQKVCWCTRRGLSEVPQIGIPSNTRYLN 81	
DB	29	VLLALQLLVAGLVRA-----QTCPSVCSNPFQKVCWCTRRGLSEVPQIGIPSNTRYLN 82	

Y 82 LMENNIQIADTFHLEHLVLQAGRNSIRQIEVGAENGLASLNTLELPDNLWLTVPSP 141  
b 83 LHENQIILKVSFHLRLHLELQSRHRTIEICAFNGLANLTLFELPRLTITPSP 142  
Y 142 APEYLSKLELRLNPIESIPSYAFNPVPSLMRLDLGELKKLYISGAFEGFLNKL 201  
C 143 AFVYLSKLELRLNPIESIPSYAFNPVPSLMRLDLGELKKLYISGAFEGFLNKL 202  
Y 202 NLGCMNKDMPNLTPLVLEELGEMSGNHPPEIRPGSFGLSLKKLVNNSQVSLIERNA 261  
C 203 NLAMCNLRPIPLTLFLKLELDELGLSNHLSAIRPGSFGLHQLKLMQIQIOVIERNA 262  
Y 262 FQGLASVLNLAHNLSSLPDLFTPLRYLVLLHLPNWCDCDILWLAWMLREYIPT 321  
C 263 FQGLASVLNLAHNLSSLPDLFTPLRYLVLLHLPNWCDCDILWLAWMLREYIPT 322  
Y 322 NTCCGRCAPHMGRYLVVVDQASFOCSAPFMDAPRLNISEGRVAELKCR-TTPMS 380  
C 323 NTACCARCNTPNLKGRIYGEIDQNYFTCYAEVVEPPADLNVTGMAELKCRASLT 382  
Y 381 SVKMLLPNGITVLSHSHRPRISVLNDGTLNFSHLLSDTGVVTCMTNVAAGNSASAYLN 440  
C 383 SVSWITPNTGTHGKRYKRIAVLDGTLNFINVTQTCMTNVAAGNSASAYLN 442  
Y 441 VSTAEINTSNYFFFTVTVETTEISPED---TTRKYKVP-----TSTGYQPAYTSTT 492  
C 443 VTA---TTPFSVSTVETVETMEPSQDEARTDNNVGPVVDWETINV-----TTSLT 494  
Y 493 VLQITR-VPKOVAVPATDTDKMOTSLDEVMKTKIIGCPVAVTLAAAMLVFKLR 551  
b 495 P--QSTRTEKFTTPTVDINGSI-PGIDEVMKTKIIGCPVAVTLAAAMLVFKLR 551  
Y 552 KRQQRSTVTAARTVEIIQVDBDIPAATSAAATAAPSGVSGEAVLPTI-HDHN-INT 609  
b 552 KQHRQNHAPRTVEIINVDBEITGDEM-----ESHLPMEALBHEHLNHYNS 600  
Y 610 YKPAHAHTENSLNSLHPTVTITSEPIIOTHKVKQVETOI 653  
b 601 YKSPFNHTTAVTI-NSIR---SSVHEPLIRMSKNVQETOI 640  
  
RESULT 42  
BUT1941  
D ABUT1941 standard; Protein; 640 AA.  
X C ABUT1941;  
X T 12-JUN-2003 (first entry)  
X E Human secreted/transmembrane protein PRO331.  
X W Human; secreted protein; transmembrane protein; PRO;  
W gene therapy; chromosome identification; chromosome marker.  
X S Homo sapiens.  
X N US2003003530-A1.  
X D 02-JAN-2003.  
X F 11-JUL-2001; 2001US-0904011.  
X R 10-SEP-1998; 98WO-US18824.  
R 14-SEP-1998; 98WO-US19177.  
R 16-SEP-1998; 98WO-US19330.  
R 17-SEP-1998; 98WO-US19437.  
R 01-DEC-1998; 98WO-US25108.  
R 08-SEP-1999; 99WO-US20594.  
R 13-SEP-1999; 99WO-US20944.  
R 15-SEP-1999; 99WO-US21090.  
R 18-SEP-1999; 99WO-US21547.  
R 05-OCT-1999; 99WO-US23089.  
R 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 02-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059115P.  
PR 17-SEP-1997; 97US-059117P.  
PR 17-SEP-1997; 97US-059119P.  
PR 17-SEP-1997; 97US-059121P.  
PR 17-SEP-1997; 97US-059122P.  
PR 17-SEP-1997; 97US-059184P.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 15-OCT-1997; 97US-062125P.  
PR 17-OCT-1997; 97US-062285P.  
PR 17-OCT-1997; 97US-062287P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-062814P.  
PR 24-OCT-1997; 97US-062816P.  
PR 24-OCT-1997; 97US-063045P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 24-OCT-1997; 97US-063127P.  
PR 24-OCT-1997; 97US-063128P.  
PR 27-OCT-1997; 97US-063327P.  
PR 27-OCT-1997; 97US-063329P.  
PR 28-OCT-1997; 97US-063341P.  
PR 28-OCT-1997; 97US-063342P.  
PR 28-OCT-1997; 97US-063344P.  
PR 28-OCT-1997; 97US-063549P.  
PR 28-OCT-1997; 97US-063550P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063704P.  
PR 29-OCT-1997; 97US-063732P.  
PR 29-OCT-1997; 97US-063734P.  
PR 29-OCT-1997; 97US-063735P.  
PR 29-OCT-1997; 97US-063738P.  
PR 29-OCT-1997; 97US-064215P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 03-NOV-1997; 97US-064248P.  
PR 07-NOV-1997; 97US-064809P.  
PR 12-NOV-1997; 97US-065186P.  
PR 17-NOV-1997; 97US-065846P.  
PR 18-NOV-1997; 97US-065693P.  
PR 21-NOV-1997; 97US-066120P.  
PR 21-NOV-1997; 97US-066364P.  
PR 24-NOV-1997; 97US-066453P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066511P.  
PR 24-NOV-1997; 97US-066770P.  
PR 24-NOV-1997; 97US-066772P.  
PR 18-SEP-2000; 2000US-0665350.  
  
( GETH ) GENENTECH INC.  
PA Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin ID;  
PI Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
XX  
DR WPI: 2003-329602/31.  
DR N-PSDB; ACA60240.  
XX

XX New transmembrane polypeptides and nucleic acids encoding the  
FT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, in generating probes and in tissue typing -  
XX  
XX Claim 12; Fig 104; 484pp; English.

XX The invention relates to an isolated nucleic acid with at least 80%  
XX nucleic acid sequence identity to a nucleotide sequence encoding one of  
XX 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a  
XX protein extracellular domain. Also included are a vector comprising a  
XX the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
XX polypeptide (by culturing the host cell for the expression of the PRO  
XX polypeptide, and recovering the PRO polypeptide from the cell culture),  
XX an isolated PRO polypeptide (having at least 80% sequence identity  
XX to: (a) an amino acid sequence selected from the 61 PRO proteins;  
XX (b) an amino acid sequence encoded by a nucleic acid molecule deposited  
XX with an ATCC number (detailed in the specification); or (c) an  
XX extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking  
XX its associated signal peptide), a chimeric molecule comprising a PRO  
XX polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
XX antibody, detecting a PRO245 or PRO1868 in a sample suspected of  
XX containing the polypeptide, linking a bioactive molecule to a cell  
XX expressing a PRO245 or PRO1868 and modulating at least one biological  
XX activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which  
XX encode PRO can be used to generate either transgenic animals or knock-out  
XX animals which may be used in the development and screening of  
XX therapeutically useful reagents. The nucleic acids may also be used in  
XX gene therapy, in chromosome identification, as chromosome markers, or in  
XX for protein electrophoresis, and the isolated nucleic acids may be used  
XX for recombinantly expressing those markers. The PRO polypeptides and  
XX nucleic acids may also be used in tissue typing. Anti-PRO antibodies  
XX are useful in diagnostic assays for PRO, and in affinity purification  
XX of PRO from recombinant cell culture or natural sources. The  
XX present sequence represents a PRO protein.

XX Sequence 640 AA;  
XX  
XX Query Match 54.2%; Score 1865; DB 24; Length 640;  
XX Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
XX Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;

QY 22 VYLAQVNLCAIAAASAGPQNCPSVCSCNQPSKVYCTERGLSEVPQGPISNRYLN 81  
DB 29 VLLALQLLVAGLVRA-----QTCSVCSCNQPSKVYCTERGLSEVPQGPISNRYLN 82  
QY 82 LKENNIQMIQADTFRHLHLEVLQGRNSIRQIRVGAFNGLASINTLELFDNWLTVIPSG 141  
DB 83 LHENQIQLKNSFKELRHLLEQLSRNIRTEIGAFNGLASINTLELFDNWLTVIPSG 142  
QY 142 AFYLSKLELWLNRPISISYAFNRPISYAFNRPISYAFNRPISYAFNRPISYAFNRPIS 201  
DB 143 AFYLSKLELWLNRPISISYAFNRPISYAFNRPISYAFNRPISYAFNRPISYAFNRPIS 202  
QY 202 NLQCMNCKMPNLTPLVGLLEEMSGNHFPEIRPGSPFGLSLKLLWYNSQVSLIERNA 261  
DB 203 NLQCMNCKMPNLTPLVGLLEEMSGNHFPEIRPGSPFGLSLKLLWYNSQVSLIERNA 262  
QY 262 FDGLSLVEINLANNLSSLPDLFTPLRYLVELHLHNPWNCDDILWLAWLREYIPT 321  
DB 263 FDNLSQVEINLANNLSSLPDLFTPLRYLVELHLHNPWNCDDILWLAWLREYIPT 322  
QY 322 NSTCCRCRCHAPMGRKYLVEVDQASFOQSPAPFMDAPDLNISGRMAELKCR-TPRMS 380  
DB 323 NTACCRCRCHAPMGRKYLVEVDQASFOQSPAPFMDAPDLNISGRMAELKCR-TPRMS 382

QY 381 SVKLLPENGTVLASHARPRISVLINDGTLPNSHLLSDTGVTCMTNVNAGNSAYLN 440  
DB 383 SVSMITPENGTVMTREGAYKVAIVLSDGTLPNFVTVODTGMVTCVNSVSGNTTASATLN 442  
QY 441 VSTAEIATNSVSPFTTFTVETTELSPED---TTRKYKPPV-----TSTGCVQPAYTTSTT 492  
DB 443 VTAA--TTTPESYFTVETMPEQSDEARTDNNVGTTPVVDKETTIV-----TTSILT 494  
QY 493 VLIOTTR-VPKQAVPAPADTDDKMQTSLDEVMKTKTKIIIGCFVAVTLLAAAMLIVFYKLR 551  
DB 495 P--QSTRSEKTFIPVTDINSGLPGIDEVMKTKTKIIIGCFVAVTLLAAAMLIVFYKMR 551  
QY 552 KRHOQRSTVTAARTVEIIQVDEIDIPATSAATAAPSGVSGEGAVLPTI-HDHIN-YNT 609  
DB 552 KQHRQNHAPTRTVEIINVDEITGTPM-----ESHLPMPALTEHEHMHFNS 600  
QY 610 YKPAHGAETWNSLGNLSLHPTVTIISPIYIIQTHTKDKVQETOI 653  
DB 601 YKSPNNHTTNTI-NSIH---SSVHEPLLIRMSKUNVQETOI 640  
RESULT 43  
ID AEU66753 standard; Protein; 640 AA.  
XX AEU66753;  
AC AEU66753;  
XX 23-MAY-2003 (first entry)  
DT Human PRO polypeptide #184.  
DE Human PRO polypeptide; secreted and transmembrane protein;  
XX Human: PRO polypeptide; secreted and transmembrane protein;  
XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
XX differentiation; chondrocyte; tumour; genetic disorder;  
XX cytostatic.  
XX Homo sapiens.  
XX OS  
XX US2003036180-A1.  
XX 20-FEB-2003.  
XX 09-MAY-2002; 2002US-0143114.  
XX 31-MAR-1997; 97WO-US05230.  
XX 12-JUN-1998; 98WO-US12456.  
XX 14-JUL-1998; 98WO-US14552.  
XX 28-AUG-1998; 98WO-US17888.  
XX 10-SEP-1998; 98WO-US18824.  
XX 14-SEP-1998; 98WO-US19093.  
XX 14-SEP-1998; 98WO-US19094.  
XX 14-SEP-1998; 98WO-US19177.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 29-OCT-1998; 98WO-US22991.  
XX 29-OCT-1998; 98WO-US22992.  
XX 20-NOV-1998; 98WO-US24855.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1999; 99WO-US05190.  
XX 20-APR-1999; 99WO-US08615.  
XX 14-MAY-1999; 99WO-US10733.  
XX 02-JUN-1999; 99WO-US12252.  
XX 01-SEP-1999; 99WO-US20111.  
XX 08-SEP-1999; 99WO-US20594.  
XX 13-SEP-1999; 99WO-US20944.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 05-OCT-1999; 99WO-US23089.  
XX 29-NOV-1999; 99WO-US28214.  
XX 30-NOV-1999; 99WO-US28313.



Db 495 P--QSTRSTKFTIPVDINSGLPGIDEVKTITKIIIGCFVAITLMAAVMLVIFKOR 551  
 Qy 552 KHQORSTVTAARTVEIIOVDEIPATSAATAAPSGVGEVAVLPTI-HOHIN-INT 609  
 Db 552 KQHQRNEHAPTRVEIINVDEITGTPM-----ESLHPFAIEHEHLNHS 600  
 Qy 610 YKPAHGAHWTSNLSHPTVTIISRPYIIQHTTKDKVQSTQI 653  
 Db 601 YKSPNHTTWNII-NSIH---SSVHEPLLIRMSKNVQSTQI 640

RESULT 44

ABU67029  
 ID ABU67029 standard; Protein; 640 AA.  
 XX  
 AC ABU67029;  
 DT 27-MAY-2003 (first entry)  
 DE Human secreted/transmembrane, PRO, protein SEQ ID 368.  
 DE  
 KW Human; secreted protein; transmembrane protein; PRO;  
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 KW infertility; birth defects; premature aging; AIDS; biosensor;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
 KW bio-reactor; tumour.

OS Homo sapiens.

XX US2003032155-A1.

PN 13-FEB-2003.

DD 03-MAY-2002; 2002US-0137865.

PF 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18924.

PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19094.

PR 14-SEP-1998; 98WO-US19177.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22991.

PR 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US24108.

PR 05-JAN-1999; 98WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 20-DEC-1999; 99WO-US30999.  
 PR 22-DEC-1999; 99WO-US30720.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 11-AUG-2000; 2000WO-US20710.  
 PR 28-JUL-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 18-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 01-JUN-2001; 2001US-0866034.  
 PR 05-JUN-2001; 2001US-0872035.  
 PR 14-JUN-2001; 2001US-0874503.  
 PR 19-JUN-2001; 2001US-0882636.  
 PR 21-JUN-2001; 2001US-0886342.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.

N-PSDB; ACA04207.

New secreted and transmembrane nucleic acids and polypeptides,

PT



T designated as PRO, useful for treating inflammation, organ failure,  
T atherosclerosis, cardiac injury, infertility, birth defects, premature  
T aging, AIDS, or cancer  
X Claim 12; Fig 368; 659pp; English.  
X The invention relates to an isolated nucleic acid comprising, or which is  
C at least 80% identical to, or the full-length coding sequence of, any of  
C the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
C (one of 275 secreted or transmembrane proteins). The nucleic acid  
C further comprises the full-length coding sequence of the DNA deposited  
C under American Type Culture Collection (ATCC) accession number in a list  
C given in the specification. Also included are vectors and host  
C cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
C antibodies, PRO extracellular domains and mature sequences, methods  
C of detecting PRO proteins, methods for stimulating the release of  
C TNF-alpha (tumour necrosis factor alpha) from human blood,  
C (and the proliferation of differentiation of chondrocyte cells, the  
C proliferation of, or gene expression in pericyte cells, the release or  
C proteoglycans from cartilage, proliferation of inner ear articular  
C supporting cells, the proliferation of T-lymphocyte cells, the release  
C of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
C proliferation of endothelial cells), a method for modulating the uptake  
C of glucose or free fatty acid (FFA) by skeletal muscle cells,  
C a method for inhibiting the binding of A-peptide to factor VIIA,  
C or the differentiation of adipocyte cells, a method for detecting the  
C presence of a tumour in a mammal and an oligonucleotide probe derived  
C from any of the nucleotide sequences cited above. The nucleic acids and  
C polypeptides are useful for treating inflammatory diseases, organ  
C failure, atherosclerosis, cardiac injury, infertility, birth defects, or  
C premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
C diabetic complications. The nucleic acids are useful as hybridisation  
C probes, in chromosome and gene mapping, and in generating antisense RNA  
C or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
C biosensors or bioreactors. Both are useful in tissue typing.  
C The present sequence represents a PRO protein of the invention.

X Q Sequence 640 AA;

Query Match 54.3%; Score 1865; DB 24; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
Y 22 VYLTAQWILCAIAAASAGPQCSQNSQPSKQVCTRGSEVPQGPSPNTRYLN 81  
b 29 VLLALQLLVAGLVRA-----QTCPSVCSQNSQPSKVICVRKLEVEDGISTWRLLA 82  
Y 82 LMENNIQMIQADTFRLHHLHLEVLQLGRNIRQIEVCAFNGLASLNTLEFDNLWLVPSG 141  
b 83 LHENQIQIKVNSFKHLRHLLEILQLSRNIRTIETIGAFNGLANLTLFDRNLATIPNG 142  
Y 142 AFVLSKRLRLRNPIESIPSYAFNRPVPSLMDLGLKXLEYISGAPFGLNLYL 201  
b 143 AFVLSKRLRLRNPIESIPSYAFNRPVPSLMDLGLKXLEYISGAPFGLNLYL 202  
Y 202 NLGMCNIDKPNLTPVLGLBELEMSGNHFFETPRGSGFHGLSSDKKLWVNSQVSLIERNA 261  
b 203 NLAMCNLREIPNLTPKLDLDELSDGNHLSAIPGSGFQGLHQLXLMQSQIQIERNNA 262  
Y 262 FDGLASVLELANHNLSSPHDLFTPLRYLVLHLPNPNPCDDILWLANWLEIYPT 321  
b 263 FDNQLSLEINLAFNLTLLPHDLFTPLHLEIRLHHPNPNPCDDILWLSWIKDMAPS 322  
Y 322 NSTCCGRCHAPMEMRGYLVVEVQAFQCSAPFMDAPDLNISEGRMAELKCR-TPPMS 380  
b 323 NTACCACNTPPNKGRIYIGELQNYFTCYAPVIVEPADLVNTEGAAELKCRASISIT 382  
Y 381 SVKLLPNGTVLGHASHPPISVLNGLNLSHVLSDGTGVTCWNTVAGNSNAYLN 440  
b 383 SVSMITNGTWTMGAYKVRIVLSDGLTNFTVQDTGMVTCWNSVGNVTASATLN 442  
Y 441 VSTAEALNTSNYSPTTVVETTESPED---TTRKYPVP-----TTSYGQPAYTSTT 492

Db 443 VTAA--TTTFVSFSTVTVETWEPESQDEARTTNNVGPVVDWMTTV-----TTSIT 494  
Qy 493 VLIQTR-VFKQAVADATDTDKWQTSLEWVKTKIILICCFVAVTLLAAAMLIVFYKLR 551  
Db 495 P-QSIFSTKFTTIPVDINSGL-FGIDEVWKTIIIGCFVAITLMAAVMLVIFYKMR 551  
Qy 552 KRUCQSRSTVTAARTVHIIQVDEDI PAATSAATAAPSGVSGEAVVLPYI-HDHIN-YMT 609  
Db 552 KQHRQNHAPPTVRIRIINVDDITGDTW-----ESHLPMPAIEHEHLNHYNS 600  
Qy 610 YKPAHGAAHTWENSLGNSLHPTVTITSEPVIIOTHTKDKVQETQI 653  
Db 601 YKSPFNHTTVNTI-NSIH---SSVHEPLLIRNWSKDNVQETQI 640  
RESULT 45  
ABU67395  
ID ABU67395 standard; Protein; 640 AA.  
XX ABU67395;  
AC ABU67395;  
XX  
DT 29-MAY-2003 (first entry)  
XX  
DE Human secreted protein PRO331.  
XX  
KW Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;  
KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;  
KW Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;  
KW atrophila areata; inflammatory disease; asthma; rheumatoid arthritis;  
KW ischaemia.  
XX  
OS Homo sapiens.  
XX  
XX US2003023054-A1.  
XX  
PD 30-JAN-2003.  
XX  
XX 16-JUL-2001; 2001US-0906742.  
XX  
PR 10-SEP-1998; 98WO-US18924.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23128.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059115P.  
PR 17-SEP-1997; 97US-059117P.  
PR 17-SEP-1997; 97US-059119P.  
PR 17-SEP-1997; 97US-059121P.

PR 17-SEP-1997; 97US-059122P.  
PR 17-SEP-1997; 97US-059184P.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 15-OCT-1997; 97US-062125P.  
PR 17-OCT-1997; 97US-062285P.  
PR 17-OCT-1997; 97US-062287P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-062814P.  
PR 24-OCT-1997; 97US-062816P.  
PR 24-OCT-1997; 97US-063045P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 24-OCT-1997; 97US-063127P.  
PR 24-OCT-1997; 97US-063128P.  
PR 27-OCT-1997; 97US-063327P.  
PR 27-OCT-1997; 97US-063329P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063542P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063549P.  
PR 28-OCT-1997; 97US-063550P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063435P.  
PR 29-OCT-1997; 97US-063704P.  
PR 29-OCT-1997; 97US-063732P.  
PR 29-OCT-1997; 97US-063734P.  
PR 29-OCT-1997; 97US-063735P.  
PR 29-OCT-1997; 97US-063738P.  
PR 29-OCT-1997; 97US-064215P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 03-NOV-1997; 97US-064248P.  
PR 07-NOV-1997; 97US-064809P.  
PR 12-NOV-1997; 97US-065186P.  
PR 17-NOV-1997; 97US-065846P.  
PR 18-NOV-1997; 97US-065893P.  
PR 21-NOV-1997; 97US-066120P.  
PR 21-NOV-1997; 97US-066364P.  
PR 24-NOV-1997; 97US-066453P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066770P.  
PR 24-NOV-1997; 97US-066772P.  
PR 25-NOV-1997; 97US-066840P.  
PR 12-DEC-1997; 97US-069425P.  
PR 04-JUN-1998; 98US-088026P.  
PR 10-SEP-1998; 98US-099803P.  
PR 14-SEP-1998; 98US-100262P.  
PR 13-OCT-1998; 98US-100858P.  
PR 20-NOV-1998; 98US-104808P.  
PR 22-DEC-1998; 98US-113296P.  
PR 07-JUL-1999; 98US-143048P.  
PR 26-JUL-1999; 98US-145698P.  
PR 28-JUL-1999; 98US-146222P.  
PR 18-SEP-2000; 2000US-0665350.  
PA (GETH ) GENENTECH INC.  
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WJ;  
XX WPI; 2003-331485/31.  
DR N-PSDB; ACA05578.

XX Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.  
XX PRO245 or PRO1868, useful in chromosome and gene mapping, in generating  
XX antisense RNA and DNA, and in treating cancer and Alzheimer's disease -

PS Example 43; Fig 104; 481pp; English.  
XX The invention relates to sixty one nucleic acids encoding PRO  
CC polypeptides (secreted and transmembrane). The polynucleotide is useful  
CC in molecular biology, including uses as hybridisation probes, in  
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in  
CC gene therapy. The polynucleotide may also be used in preparing PRO  
CC polypeptides by recombinant techniques, and in generating either  
CC transgenic animals or knock-out animals which, in turn, are useful in the  
CC development and screening of therapeutically useful reagents. The PRO  
CC polypeptide or the antibody is used in preparing a medicament for  
CC treating a condition responsive to the polypeptide or antibody, such as  
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.  
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease  
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,  
CC atrophla areata, angiogenesis, inflammatory disease e.g asthma and  
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The  
CC present sequence represents the amino acid sequence of a PRO polypeptide.  
XX  
SQ Sequence 640 AA;  
Query Match 54.2%; Score 1865; DB 24; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
QY 22 VYLTAQVILCAIAAASAGFQPCSVCSNCFKVCVCTRRGLSEVPQGIPTENTYLN 81  
DB 29 VLLALQLLVAGLVRA-----QTCPVCSNCFKVCVCTRRGLSEVPQGIPTENTLN 82  
QY 82 LMENNIOMIOADTFHLLHLEVLQIGRNSIRQIVGAFNGLASLNTLELFDNMLTVPISG 141  
DB 83 LHENQIQIKVNSPKLEHLEILQISRNHRTIIGAFNGLANLNTLELFDNRLTTPNG 142  
QY 142 AFEYLSKLELRLNNPIESIPSYAFNRVPSLMRLDGLGELKKLYISEGAFGLFNLYL 201  
DB 143 AFVYLSKLELRLNNPIESIPSYAFNRVPSLMRLDGLGELKKLYISEGAFGLFNLYL 202  
QY 202 NLGMCNIDKMPNLATPLVCLLEMSGNHFEIRPGSFGHLSLKKLVMSQVSLIERNA 261  
DB 203 NLAMCNLEIPNLTKLDELDSGNHLSAIRPGSFGHLSLKKLVMSQVSLIERNA 262  
QY 262 FDGLASVELNLAHNNLSLPHDLFTPLRYLVELLHNNPNCNCDILWLAWMLRYIPT 321  
DB 263 FDNLSQVLEINLAHNNLTLPHDLFTPLHLEIRHLEHNNPNCNCDILWLAWMLRYIPT 322  
QY 322 NSTCCGRCHAPMRGRYLVVDQASFOCSAPFTMDAPDLINISEGRMAELKCH-TPPMS 380  
DB 323 NTACCARGCNTPNLKGRIYIGELDQNYFTCYAPVIVEPPADLNVTGMAELKCHASLT 382  
QY 381 SVKLLPNTGTVLSHARHPRIISVLNDGTLPNSHVLSDTGVYTCVATNVAGNSASAYLN 440  
DB 383 SVSWITPNTGTVMHGAYKVRIVLSDGTLPNTVTVQDTGMYTCWNSVCGNTASATLN 442  
QY 441 VSTAEANTSNYSFFTTVTVETTEISPD-----TTRKYKVP-----TTSTGQPAYTSTT 492  
DB 443 VTAA--TTTPSYSTVTVTETMPSQDEARTDNNVGPFPVVDWETTNV-----TSTLT 494  
QY 493 VLIQOTR-VPKQVAVPATDITTKQMTSLDEVKTKTIIIGCFVAVTLLAAAMLVIFYKLR 551  
DB 495 P--QSTRTEKTFIPVTDINSGL-PCIDEVWTKTKIIIGCFVAILTMAAVMLVIFYKMR 551  
QY 552 KKHQRSTVTAARTVEIIOVEDIPATSAATAAPSGVSGEGAVLPTI-HDHN-YNT 609  
DB 552 KQHQRHNPATRTVEIINVDEITGDTM-----ESHLPMPAIEHEHLNHS 600  
QY 610 YKPAHGAHWNTSNGNSLHPTVTTISEPYIIQTHKKVQETOI 653  
DB 601 YKSPFNHTTTVNTII-NSIH---SSVHEPLLIRMSKNVQETOI 640  
RESULT 46  
ABU59834  
ID ABU59834 standard; Protein; 640 AA.





24-OCT-1997; 97US-062816P.  
 24-OCT-1997; 97US-063045P.  
 24-OCT-1997; 97US-063120P.  
 24-OCT-1997; 97US-063121P.  
 24-OCT-1997; 97US-063127P.  
 24-OCT-1997; 97US-063128P.  
 27-OCT-1997; 97US-063327P.  
 27-OCT-1997; 97US-063329P.  
 28-OCT-1997; 97US-063541P.  
 28-OCT-1997; 97US-063542P.  
 28-OCT-1997; 97US-063544P.  
 28-OCT-1997; 97US-063549P.  
 28-OCT-1997; 97US-063550P.  
 28-OCT-1997; 97US-063564P.  
 29-OCT-1997; 97US-063435P.  
 29-OCT-1997; 97US-063704P.  
 29-OCT-1997; 97US-063732P.  
 29-OCT-1997; 97US-063734P.  
 29-OCT-1997; 97US-063735P.  
 29-OCT-1997; 97US-063738P.  
 29-OCT-1997; 97US-064215P.  
 31-OCT-1997; 97US-063870P.  
 31-OCT-1997; 97US-064103P.  
 03-NOV-1997; 97US-064248P.  
 07-NOV-1997; 97US-064809P.  
 12-NOV-1997; 97US-065186P.  
 17-NOV-1997; 97US-065846P.  
 18-NOV-1997; 97US-065693P.  
 21-NOV-1997; 97US-066120P.  
 21-NOV-1997; 97US-066364P.  
 21-NOV-1997; 97US-066453P.  
 24-NOV-1997; 97US-066466P.  
 24-NOV-1997; 97US-066511P.  
 24-NOV-1997; 97US-066770P.  
 24-NOV-1997; 97US-066772P.  
 18-SEP-2000; 2000US-0665350.

(GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini ID;  
 Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D;  
 Williams PM, Wood WI;

WPI; 2003-288105/28.  
 N-PSDB; ABX96257.

New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)  
 and genes encoding them, useful for detecting or treating e.g.  
 hyperplasia, endometriosis, cancers, ischemia, coronary arterial  
 disease or inflammations -

Claim 12; Fig 104; 477pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides  
 and the nucleic acid encoding them. The polypeptides can be used to  
 raise antibodies that specifically bind to the PRO polypeptide, for  
 linking a bioactive molecule to a cell expressing a PRO protein and for  
 modulating at least one biological activity of a cell. The PRO  
 polypeptides or polynucleotides are also useful as pharmaceuticals,  
 diagnostics, biosensors or bioreactors, for detecting or treating e.g.  
 hyperplasia, endometriosis, cancers (e.g. those involving solid tumours),  
 ischaemia, coronary arterial disease, polycystic kidney disease, chronic  
 or acute renal failure, or inflammatory responses (e.g. asthma,  
 rheumatoid arthritis, psoriasis or multiple sclerosis). The  
 PRO genes may also be used in gene therapy, particularly for replacing a  
 defective gene. The sequences presented in ABU64499-ABU64559 are the  
 PRO polynucleotides of the invention.

Sequence 640 AA;

Query Match 54.2%; Score 1865; DB 24; Length 640;

Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
 Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;  
 QY 22 VYLTAQWILCAIAAAGAGPQNCPSVCSCNQSKVYCTRRGLSEVPGQIPSNRYLN 81  
 DB 29 VLLALQLLVAGLVRA-----QTCPSVCSCNQSKVICVKRLREVDPDGISTNRLIN 82  
 QY 82 LMENNTQMTQADTFHLLHLEVLQGRNSIROIFVGAENGLASLNTLELFDNWLTVPSG 141  
 DB 83 LHENQIITIKVNSFKLRLHLELQSRHIRTETGAFNGLANTLLELFDNRLTIPNG 142  
 QY 142 AFYLSKLRLRLNNPIESIPSYAFNRVPSLMRLDLGELKLEYISEGAFGLFLKYL 201  
 DB 143 AFYLSKLRLRLNNPIESIPSYAFNRVPSLMRLDLGELKLEYISEGAFGLFLKYL 202  
 QY 202 NLCWNIKOMPNTPLVGLLEBMSGNHPPETRPSFGLSSKLWNSQVSLIERNA 261  
 DB 203 NLAMCNLRREIPNLTLPLKDELDSLGNHLSAIRPSFQGLMELOKLMWISQIOIERN 262  
 QY 262 FDGLASIVELNLAHNNLSLPHDLFTPLRYLYVELHLHNNPNCDCDILWAWLREYIPT 321  
 DB 263 FDNLSQSLVEINLAHNNLTPLPHDLFTPLHLEHLHNNPNCDCDILWAWLREYIPT 322  
 QY 322 NSTCCORCHAPMRCRYLVEVDQASFOCSAPFIMDAPRDLMSGRMAELKCR-TPPMS 380  
 DB 323 NTACCACNTPPNLKRYIGELDQNYFTCYAFVIVEPPADLVNTEGMAABLKCRASST 382  
 QY 381 SVKWLPLNGTIVLSHSHRPRISVLNDGTILNFHLLSDTGVYTCMTNVAGNSNASAYLN 440  
 DB 383 SVSWITPNGTIVMTHGAYKRVIAVLSLGLTINFTVQDTGMYTCWNSVGNWTASATLN 442  
 QY 441 VSTAELNTSNYSFPTTIVTETTESPED---TTRKYKVPV-----TTSTGYQAPVTTSTT 492  
 DB 443 VTAA--TTTPFSYFSTVTVETMEPSQDEARTDNNVGP\*PVVDWETINV-----TISLT 494  
 QY 493 VLIQTR-VPKQVAVPATDTTDMQSLDVKMTKIIIGCVAVTLLAAAMLIVPKLR 551  
 DB 495 P--QSTRSTKTFITPVDINSGL-EGIDEVWKTIIIGCVAVTLLAAAMLIVPKLR 551  
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ABUS9185

ID ABUS9185 standard; Protein; 640 AA.

XX AC ABUS9185;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO331.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disease;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 XX chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

XX PN US2002132252-A1.

XX



Q Sequence 640 AA;		XX	
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		PR 08-MAR-1999; 99WO-US05028.	
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Query Match 54.2%; Score 1865; DB 24; Length 640;

Best Local Similarity 56.4%; Pred. No. 1.6e-146; Matches 363; Conservative 107; Mismatches 130; Indels 44; Gaps 14;

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 DB 443 VTAA--TTTPSYFSTVTVETNEPSCDEARTDNNNGPFPVVDWETINV-----TTSIT 494  
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RESULT 50
ABU59481
ID ABU59481 standard; Protein; 640 AA.
AC ABU59481;
CX 22-APR-2003 (first entry)
CX Novel human secreted or transmembrane protein PRO363.
CX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
CX cardiac insufficiency disorder; cancer; tumour; immune response;
CX adrenal cortical capillary endothelial growth; c-fos induction;
CX vascular endothelial growth factor inhibition; VEGF inhibition;
CX endothelial cell growth inhibitor; T-lymphocytes stimulation;
CX retinal neurons cell survival; rod photoreceptor cell survival;
CX retinal disorder; retinitis pigmentosa; kidney disease;
CX mammalian kidney mesangial cell proliferation; Berger disease;
CX dermatitis; herpiformis; Crohn's disease; chondrocyte proliferation;
CX chondrocyte redifferentiation; sports injury; arthritis.
CX Homo sapiens.
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PD 06-FEB-2003.
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PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095923P.  
PR 10-AUG-1998; 98US-096013P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096953P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 24-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.

Query Match 54.2%; Score 1865; DB 24; Length 640;  
Best Local Similarity 56.4%; Pred. No. 1.6e-146;  
Matches 363; Conservative 107; Mismatches 130; Indels 44; Caps 14;  
QY 22 VYLAQWILCAATAAASAGPQPCSVCSNQFSKVVCVTRGLSEVPQGISNTRYLN 81

Db 29 VLLAQLLVAVGLVRA-----QTCPSCVCSNQFSKVVCVTRGLSEVPDQIGISTNRYLN 82  
QY 82 LMENNTOIQADTFRHLHLVLVQLGRNSIROIEVCAFNGLASANTLELFDNMLTVIPSG 141  
Db 83 LHENQIQIKVNSFRHLRHLLEIQSRNHRIETIEGAFNGLANLNTLELFDNRLTIYNG 142  
QY 142 AFEYLSKRLRLMENNPIESIPSYAFNRVPSLMRLDGLGELKLEYISGAFGLNLYL 201  
Db 143 AFVYLSKRLMENNPIESIPSYAFNRIPSLRRLDGLGELKLEYISGAFGLNLYL 202  
QY 202 NLGCMNIKOMPILTPVGLERLEMSNHPETRPDSFGLSSLKXLMWNSOVSLIENA 261  
Db 203 NLAVCNLRPEIPNLPLIKLDELDSLGNHLSAIRPSFGELMHLQKLMLOSOIQVIERNA 262  
QY 262 FDGLASIVELNLAHNNLSLPHDLFTFLFYLVYELHLHNNPMNCDCDILMLAWLREYIPT 321  
Db 263 FDNLQSLVLEINLAHNNLTLLPHDLFTFLHLRIHLHNNPMNCDCDILMLWIKDMAPS 322  
QY 322 NSTCCGRCHAPMGRGYLVEVDQASPOCSAPFIMDAPEDLANISGRMAELKCR-TPPMS 380  
Db 323 NTACCARCNTPPNLKGRYIGELDPQNYFTCYAPVIEPPADLANTEGMAELKCRASSTUT 382  
QY 381 SVKMLLPNGTVLSHARRHPRISVLNDGTLNFSHVLSDTGVTTCMVTVNAGNSASAYLN 440  
Db 383 SVSWITENGTVMTHGAYKVRIAVLSDGTLNFTNTVTQDTGMVTCMVNSVGNVTASATLN 442  
QY 441 VSTAELNYSPPFTTVTVTFTHFISPD---TTRKYKVP-----TTSYGYPAYTTST 492  
Db 443 VTAA--TTTFYSYFTVTVETWEPQDEARTDNNVGPTEVVDWETNV-----TTSUT 494  
QY 493 VLIQTER-VPKQVAVPATDUTDKMOTSLDEVMKTKIIIGCFVAVTLAAAMLVIFYKLR 551  
Db 495 P--QSTRSTKTTTIPVTDINSOI--FGIDEVMKTKIIIGCFVAVTLAAAMLVIFYKLR 551  
QY 552 KRHQQRSTVTAARTVEIIQVDEDIIPAATSAATAAPSGVSGEGAVVLPPI-HDHIN-YMT 609  
Db 552 KQHRQRNHAPTRTVEIINVDEITGTPM-----ESHLEMPAIEHHLNHYNS 600  
QY 610 YKPAHGAHMTENSIGNSLHPTVTITISEPVIIQHTKDKVQETQI 653  
Db 601 YKSPFNHTTTVNTI-NSIH---SSVHEPLLIRMSKDNVQETQI 640

Search completed: February 5, 2004, 15:49:04  
Job time : 54 secs



103 180 5.2 656 2 AB1479 probable cell surf  
104 180 5.2 1007 2 C94668 probable receptor-  
105 178.5 5.2 943 2 E84429 probable receptor-  
106 178 5.2 549 2 T41744 hypothetical prote  
107 178 5.2 1039 2 T22117 hypothetical prote  
108 177.5 5.2 822 1 A56853 brain-derived neur  
109 177.5 5.2 1025 1 A57076 protein kinase Xa2  
110 177 5.1 338 2 S38030 suppressor protein  
111 177 5.1 696 2 A41344 lutropin-choriogon  
112 176.5 5.1 505 2 A41469 internalin like pr  
113 176.5 5.1 1256 2 T71436 probable resistanc  
114 176 5.1 790 1 TVRHTT nerve growth facto  
115 173 5.0 799 1 TVRHTT nerve growth facto  
116 172 5.0 800 2 AB1129 internalin A limpo  
117 171.5 5.0 1079 2 C96772 probable receptor  
118 171 5.0 821 1 S06943 brain-derived neur  
119 171 5.0 821 1 A39667 brain-derived neur  
120 170.5 5.0 477 1 I73631 brain-derived neur  
121 170 4.9 808 2 E97303 hypothetical prote  
122 169 4.9 800 2 S37387 internalin A precu  
123 168.5 4.9 1237 2 AC1583 internalin protein  
124 168.5 4.9 1257 2 A88536 protein B0523.5 [i  
125 168 4.9 813 2 T04313 protein kinase Xa2  
126 168 4.9 874 2 E97302 hypothetical prote  
127 168 4.9 1112 2 T10504 disease resistance  
128 167.5 4.9 548 2 AH1107 internalin H limpo  
129 167 4.9 1143 2 T10636 hypothetical prote  
130 166.5 4.8 700 2 I74633 lutetizing hormon  
131 166.5 4.8 700 2 A49744 lutropin-choriogon  
132 166 4.8 2145 2 J04747 adenylyate cyclase  
133 165.5 4.8 526 2 C94552 hypothetical prote  
134 164.5 4.8 499 2 A11107 internalin E limpo  
135 164 4.8 474 1 C39657 brain-derived neur  
136 164 4.8 476 1 A35104 brain-derived neur  
137 164 4.8 476 1 B39667 brain-derived neur  
138 163.5 4.8 821 2 AB1126 internalin, peptid  
139 163.5 4.8 1009 2 T45645 receptor kinase-11  
140 163 4.7 540 2 T12704 leucine-rich prote  
141 163 4.7 700 2 A42395 lutropin receptor  
142 163 4.7 1011 2 T45718 receptor-kinase li  
143 162.5 4.7 1064 2 B86465 probable Protein k  
144 162 4.7 717 2 T33295 hypothetical prote  
145 161.5 4.7 612 2 T10727 protein kinase Xa2  
146 161 4.7 853 2 T17461 disease resistance  
147 161 4.7 2493 2 A55481 adenylyate cyclase  
148 160.5 4.7 2088 2 E71436 hypothetical prote  
149 160 4.7 2222 2 T13924 skk protein - frui  
150 159.5 4.6 1045 2 T41119 internalin- relate

## ALIGNMENTS

RESULT 1  
T46266  
Hypothetical protein DKFp761A179.1 - human (fragment)  
C:Species: Hmo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46266

R.Blum, H.; Baverachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
Submitted to the Protein Sequence Database, January 2000

A:Reference number: 223034

A:Accession: T46266

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-421 <AAA>

A:Cross-references: EMBL:AL137451

A:Experimental source: adult amygdala; clone DKFp761A179

C:Genetics:

A>Note: DKFp761A179.1

Query Match 33.7%; Score 1158; DB 2; Length 421;

Best Local Similarity 53.6%; Pred. No. 1.9e-73;

Matches 225; Conservative 62; Mismatches 95; Indels 38; Gaps 5;  
QY 205 MCNIXDMPNLPLVCLGLEMSGNHFFPIRPGSGHEGLSSLKCLWVMSQVSLIERNAPDG 264  
DB 1 MCNIXDMPNLPLVCLGLEMSGNHFFPIRPGSGHEGLSSLKCLWVMSQVSLIERNAPDG 60  
QY 265 LASVELMLANNSSPHDLFTPLRYLVLELHHPNWCDCDILWLAWLREVIPTNST 324  
DB 61 LKSLFEELSHNNLSLPHDLFTPLRLERVLHHPNWCDCDILWLAWLREVIPTNST 120  
QY 325 CGGRCHAPMHRGVLVEVDQASFOCSAPFIMDAPRDNINSEGRMAELKCRTPPMSSVK 383  
DB 121 CACRCHAPAGLGRIGELDQSHFTCPAPVLEPTDINVEGMAELKCRTPGTSMTSVN 180  
QY 384 WLLPNTGYLSHASRPRISVNLDTLNFSHVLLSDTGYTCMTVNVAGNSNAGLAYLNST 443  
DB 181 WLPNTGYLSHASRPRISVNLDTLNFSHVLLSDTGYTCMTVNVAGNSNAGLAYLNST 240  
QY 444 AEL-----NTSNYSFFTTVTVEISPEDT-----TRKYKPV 476  
DB 241 VDPVAAAGTGGGGPGGG 300  
QY 477 PTT-----STGYOPAYTTSTTVLIQTR-VPKQVAVPAITDTTKMOTSLDEVNKT 526  
DB 301 PTTDGVWCGGPRGDAAGPSSSTTAPAPRSRPTKAPTIVTDTVENALKOLDVDVKT 360  
QY 527 KIIIGCFVAVTLLAAMLIYFKLRKHQBSTVTAARTVLIQVDEDIQAATSAATAA 586  
DB 361 KIIIGCFVAVTLLAAMLIYFKLRKHQBSTVTAARTVLIQVDEDIQAATSAATAA 420  
RESULT 2  
A58532  
glial cell membrane glycoprotein LIG-1 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 05-Nov-1999  
C:Accession: A58532  
R.Suzuki, Y.; Sato, N.; Toyama, M.; Wanaka, A.; Takagi, T.  
J. Biol. Chem. 271, 22522-22527, 1996  
A:Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in  
A:Reference number: A58532; MUID:96394313, PMID:8798419  
A:Accession: A58532  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1091 <SUZ>  
A:Cross-references: GB:D78572; MID:g1545806; PIDN:BAAL1416.1; PID:g1545807  
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-ter  
F:36-61/Domain: proteoglycan amino-terminal homology <PAH>  
F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F:385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F:440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 12.7%; Score 438; DB 2; Length 1091;

Best Local Similarity 21.0%; Pred. No. 1.8e-22;

Matches 196; Conservative 110; Mismatches 275; Indels 354; Gaps 26;

QY 28 WVILCAIAAASAGPQ-----NCFSVCSNCFKSVKVTCTRGISEVPGQIPSNTRYLNL 82

DB 20 LWLLLLLQWPESAGARPRAPCAACTCAG--NSLDCSGRGLATLPRLDLPWTRSLNL 77

83 M-----83  
 78 SYNRLSEIDSAPELDTNLQEVYNSNELTAIPSLGASIGVVSFLQHNKILSDGSOL 137  
 84 -----83  
 138 KSVLSLEVLDSNNITEIRSCPPNGLRIRLEINLASNRISLESAGFDGLSRSLTLRL 197  
 84 -----ENNIMQIADTFRLHLHLVLEVLQGRNSIRQIEVQAF 119  
 198 SKNRITQLPVKAPKPLRLTOLDLRNRIRLIEGLTFQGLDLSLEVLRLQNNISRLTDGAF 257  
 120 NGLASLNTLELFPNWLTVIPSGAFVLSKRLRLNPNIESIPS-----YA 166  
 258 WGSKRVHLEFYSLEVNSSGLYGLTALQHLSSNSISRIQDGSFOOKLHELILS 317  
 167 FNVPSLMRLDLCELKCL-----EYISGAPEGLFNKLYMLGMCNITKDMPLTP 216  
 318 FNNLTRLDSSLAELSLSLRLSHNAISHIABGAPKGLKSLRVL-----363  
 217 LVGLELEMGSNHFPPIRPGSHGLSLKLLWNNQSVSLIERNAPDGLASLVELNLNHN 276  
 364 ---LDHNEISGT--IDTSGAPTGLDNLKSLTLFGNKIKSVAKRAPSGLESLEHLNIGEN 418  
 277 NLSSLPHDLFTPLRYLVELLHNPWNCDDILWLAWMLR-----316  
 419 AIRSVQDPAKMKNLKELYISSPFLDCQLXWLPFLMGRMLQAFVATCAHPESLKG 478  
 317 ---EYIPNTSTC-----CGR-----CHA-----PM-----333  
 479 QSIPLVDFSDVCDPFPKQIITQPETWAVGVKDIRFTCSAASSSSPMPTFAWKDNREV 538  
 334 ---HMRG-----RYLVEVDQASFOC-----350  
 539 LANADMENFAHRAQDGEVMEYTLHLRITVFGHGRVQCIITNFGSTYSEKARLTWN 598  
 351 SAPFINDAPDLNISSEGRMAELKCRTP--PMSSVKMLLPNGTVLSHSHRPRISVLNDGT 408  
 599 VLPSTKIPHDIAIRGTGTARLECAARGHPNPQIAWCKDGGTDFP--AARERRMEVMPDD 657  
 409 LNF--SHVLSGDTGVTCVNTVAGNSASAVLVNSTASLTSNYP---PTTVTVETTEI 464  
 658 VFFITDKIDMGVYSCTAQSAGSVASATLTV---LETPLAVPLEDRVVTVGETVA 713  
 465 SPEDTRKRPVPTTSTGYOP-----AYTTSTTVLIQT 497  
 714 PQCATGSPTRITWLKGRPLSLTERHHTPGNQLLWQNVMDDAGRYTCXSNPLGT 773  
 498 TRVPQAVAPATDTDKQMSLDEVMKTKIIGCFVAVTLLAAAMLIVFYKLRKHQR 557  
 774 ERAHSQLSILPTPGCRKDGITVG----IPTIAVVCISIVLTSL--VWVCIIYQTRKXSEY 827  
 558 STVTAARTVEIIQVDEDI PAATSAATAAPSGVSGEGAVLPTIHDHINVTYKPAHGAH 617  
 828 SVTNTDETI-----VPPDVPSVLSQGT-----LSDROETVVRTEGGH-QANGHIESNGVC 877  
 618 WTENSLGNSLHPTTITISEPVIITHKTD--KYOE 650  
 878 LRDPFLRPEVDIHSTTCRQPKLCVGYTRPQKYTE 912

RESULT 3  
 T42218  
 N:Alternate names: MEQF4 protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2002  
 C:Accession: T42218  
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
 J:Genomics 51, 27-34, 1998  
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
 A:Reference number: Z14126; MUID:98360089; PMID:9693030  
 A:Accession: T42218

A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1531 <NAX>  
 A:Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290  
 A:Experimental source: strain Sprague-Dawley; brain  
 C:Genetics:  
 A:Gene: MEQF4  
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 12.0%; Score 414; DB 2; Length 1531;  
 Best Local Similarity 24.1%; Pred. No. 1.4e-20;  
 Matches 139; Conservative 69; Mismatches 166; Indels 202; Gaps 15;

QY 27 QVWLCAATAAASAGPQPCSVCSQNFQSVCTFRGLSEVPOQIPSNRYLMLNHN 86  
 DB 17 ELWEL--LWNAWRIGATACPALCTCTG--TTVDCHGTGLQAIIPKNIPTNTELELNGNN 72  
 QY 87 IQMIQADTFRLHLHLVLEVLQGRNSIRQIEVQAFNGLASLNTLELFDNMLTVIP-----139  
 DB 73 ITRIHKNDPAGLQALVQLMENOIGAVERGAPDDMKELERLARLNQQLVPELLFQNN 132  
 QY 140 -----SCAPEYLSKIRELMRNPP 158  
 DB 133 QALSRLDLSNSIQAVPRKAFRGATDLKNLDKNQISIEGAFALRGLEVLTLNHN 192  
 QY 159 IESIPSYAFNRVP-----SLMRLD 177  
 DB 193 ITTIPVSSFNHMPKGLRFRLESNHLFCDCHLAWLSQWLQRPTIGLFTQCSGSPASLRGLN 252  
 QY 178 LGEUKLEYSIGSAFE-----GLF-----NLK 199  
 DB 253 VAEQYSEFSCSQGGEAAQVPACTLSGSCPAMCSGNSIVDCRGLGTAIAPANLPETMT 312  
 QY 200 YLNLGMCNIDMP--NLTPLVGLEELEMNSGNHPEIRPFSFGLSLKLLWNNQSVSLI 257  
 DB 313 EIRLELNGIKSIIPGAFSPYKRLRIDLSNNQIAEAPDAFQGLRSLSNLSVLYGNKITDL 372  
 QY 258 ERNAPFDG-----LASVELNLNHNLSLPHDLFTPLRYLV 293  
 DB 373 PRGVFGLYTLQALLNANKINCIRPDADFQDLQNLSLSLYDNKIOSLAKGTTFTSLRAIQ 432  
 QY 294 ELHLHHPNWCDDILWMLKRLREYIPTN--STCCGRCHAPMEMGRYLVVEVDQAFQCS 351  
 DB 433 TLHLAQNPFFICDNKRLADPLR-----TNPIETGARCASPRRLANKRIGQIISKPRCS 498  
 QY 352 A--PFIMDAPRLNISSEGRMAEL-----KCRTP-----PMSVSKWLLP 387  
 DB 489 AKQYFIPGTEDYELNSETSDVACPKRCSEASVWECSGLKLSKIPERIPQSTTELRIN 548  
 QY 388 NGTV-----LSHNR-----HPRISVLNDGT 408  
 DB 549 NNEISILEATGLFKGLSHLKKLNLSNNKVSIEDGT 584

RESULT 4  
 JC7763  
 neuronal leucine-rich repeat protein-3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: JC7763  
 R:Fukamachi, K.; Matsuo, Y.; Kitanaka, C.; Kuchino, Y.; Teuda, H.  
 J:Biochem. Biophys. Res. Commun. 287, 257-263, 2001  
 A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene  
 A:Reference number: JC7763; PMID:11549284  
 A:Contents: Fibrosarcoma cells  
 A:Accession: JC7763  
 A:Molecule type: mRNA  
 A:Residues: 1-707 <PUK>  
 C:Cross-references: GB:AF291437  
 C:Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,  
 is in protein-protein interaction and functions as a cell adhesion molecule or soluble ligand  
 C:Genetics:  
 A:Gene: nlrr-3

C;Keywords: cell adhesion

Query Match 12.0%; Score 411.5; DB 2; Length 707;  
Best Local Similarity 24.0%; Pred. No. 7.3e-21;  
Matches 172; Conservative 103; Mismatches 267; Indels 175; Gaps 24;

2Y 30 ILCAIAAASAGPQ--NCPSCVCS-----NQSKVCTRGILSEVPGIPSN 76  
DB 11 LLGLAITALVAGDKVDCPOLCTCEIRPWTPTPSIYWEASTVDCNDLGLNLPALPAD 70  
2Y 77 TRYLMENNTQIQADTFRLHLEHLVQLGRNSIRQIEVGAENGLASLTLELFDNWLTL 136  
DB 71 TQILLQTNRIAREHSTDFEV-NLTGLDLSQNNLSVNTINQKMSQLLSVYLEENKLT 129  
2Y 137 VIPSGAFYLSKLRRLMNRNPISPSYAFNRVPSLRDLGLKELKLEVISSEGAEGFLP 196  
DB 130 ELPEKCLYGLSLQELYYNHLNLSAISGAFVGLHNLRLHLNS-NELQWINSKWFELP 188  
2Y 197 NLKYLNLG---MCNKKMP-----NLT-----PLVGLLEBLE----- 224  
DB 189 NLEILMGLDNPILRIKQNNFQELKLSRLVLAGINLIEVPDVALGLENLESISFYDNRL 248  
2Y 225 -----MSGNHPPEIRPGSHGLSLKLLWV----- 249  
DB 249 NKVPOVALQKAVNLKFLDLNKNPINRIRGDFSNMLHLKELGINNMPELVISIDSLAVDNL 308  
2Y 250 -----YKSOVSLIERNAPDGLASLVELNLAHNLSLSPHDLFTPLRYLVLEHLHN 300  
DB 309 PDLKIEATNPRLSYIHPNAPFLPKLESIMLSNLSALYHGTIESLPNLEKISIHNS 368  
2Y 301 PNKCDLILWL---AWMLREYIPNSTCCGRCHAPMHRGRYLVVDQASFO-----C--- 350  
DB 369 PIRCDVIRWNNKNTIRFMEPDLFCVD---PPEFQO---NVRQVHFRDMMEICLP 421  
2Y 351 -----SAPPIKADPLNLSEGRMAELKCR--TPMSSVKWLLPENGTVLSHASRHSISV 403  
DB 422 LIAPESFSLVDEADSVS-----LHCRTAPQPEIYIWTSGKLLPNTLREKFEV 475  
2Y 404 LNDGTLNFSVLLSDGYVTCMTNVNAGSNASVLYNVTAEIANTSNYSFPTTVVETTE 463  
DB 476 HSEGLTDIRGITPEKGGLYTCIATNLVAGDLKSIWKVGFVFPQDNNGS---LNKIRD 531  
2Y 464 ISPEUTTRYK---VPVPTISGYQPAYTSTVLIQITREVPKQAV-----PATD--- 510  
DB 532 IRANSLVSWKANSKILKSSVKWTAFVKTEDSQAAQSARISDVVKVYNLTHLKEPSTYKI 591  
2Y 511 -----TTDRKQTSLDVNMKTKIILICFCFVAVTLAAAMLIVF----- 547  
DB 592 CIDIPITYOKSRKQCVNVTKSLRHDGKNGKSHTVFVAC-VGGLGIIGWMLFCGVSQ 650  
2Y 548 -----YKLRGRHOORSTVTHAR-----TVELIQVDEDIRAATSARATA--APSGVS 591  
DB 651 EGCNENHSYTYNHCHKPTLAFSELYPLINLWESSKEKPLASLEVKATAGVPTSMS 707

RESULT 5  
MEGF5 protein - rat  
N;Alternate names: slit protein homolog  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2002  
C;Accession: T13953  
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
Genomics 51, 27-34, 1998  
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
A;Reference number: Z14126; MUID:98360089; PMID:9693030  
A;Accession: T13953  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1523 <NAK>  
A;Cross-references: EMBL:AB011531; NID:93449291; PIDN:BA032461.1; PID:G3449292  
C;Genetics:  
A;Gene: MEGF5

C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 11.4%; Score 391; DB 2; Length 1523;  
Best Local Similarity 24.3%; Pred. No. 5.6e-19;  
Matches 137; Conservative 56; Mismatches 171; Indels 200; Gaps 14;

QY 31 LCATAAASAGP-QNCPSCVCSNQSKVCTRGILSEVPGIPSNRYLNMENNIOQM 89  
DB 18 LALALASILSGPPAAACPTKCTCS--AASVDCHGLGLRAVPRGIPRANERLDLDRNNITR 75  
QY 90 IQADTFRLHLEHLVQLGRNSIRQIEVGAENGLASLTLELFDNWLTVIPSGAFYLSKL 149  
DB 76 ITKMDFTGLKRLVHLLEDNQSVIERGAFQDLKQLERLRLNKKQLQVLPPELLFQSTPKL 135  
QY 150 RELMTRNNPIESIPSYAFNRVPSLRDLGLKELKLEVISSEGAEGFLNKLKYLNMCMNI- 208  
DB 136 TRLDLSEHQIQIGIPKAPRGVTVGNLQL-DNNHISCIEDGAFRALDLBIITLNNNIS 194  
QY 209 -----KDMNLTPL-----VG----- 219  
DB 195 RILVTSFNHMKIRTLRLHNSHLYCDCHLAWLSDWLQRRTIGQFTLCMAPVHLRGFSVA 254  
QY 220 ----- 219  
DB 255 DVQKEYVCPGPHSEAPACNANSISCSACSNNIYDRCGKGLTEIPANLPEGIIVEIRL 314  
QY 220 -----LEELEMSGNHPPEIRPGSHGLSLKLLWVMSQVSLIERNA 261  
DB 315 EQNSIKSIPAGAFIQYKGLKIDISKQISDIADAPQGLKSLTSLVLYGNKITEIPKGL 374  
QY 262 FDLGLASLV-----ELNLAHNLSLSPHDLFTPLRYLVLEHL 297  
DB 375 FDLGLSLQLLLNANKINCLRVNFTQDLQNLNLSLDNKLQITISKGLFAPLQSIQITLHL 434  
QY 298 HNPWPNKCDLILWLAWLRYIPTN--STCCGRCHAPMHRGRYLVVDQASFOCSAP-- 353  
DB 435 AQNPFPVCDCHLWLA---DVLQDNPIETSGARSSPRRLANKRISOIKSKKFCSCSED 490  
QY 354 -----PIMDAPDLNLTSEGRMAELKCRTPPSSVKWLLPENGTVL-----SHASRH 398  
DB 491 YRNRFSSCFMDLVCP-----KCR-----EGTIVDCSNQKLSRIFSHUPEY 533  
QY 399 PRISVINDGTNFSHVLSDTGVY 422  
DB 534 TTDLRLNDNDI-----AVLEANTGIP 553

RESULT 6  
A53860  
chondroadherin precursor - bovine  
N;Alternate names: 38K leucine-rich protein  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 05-Nov-1999  
C;Accession: A53860  
R;Neame, P.J.; Sommarin, Y.; Boynton, R.E.; Heinigard, D.  
J. Biol. Chem. 269, 21547-21554, 1994  
A;Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated from b  
A;Reference number: A53860; MUID:94342341; PMID:8063792  
A;Accession: A53860  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-361 <NEA>  
A;Cross-references: GB:U08018; NID:9470671; PIDN:AAA21330.1; PID:9470672  
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carboxyl-  
C;Keywords: disulfide bond  
P;300-346/Domain; proteoglycan carboxyl-terminal homology <PCH>

Query Match 10.9%; Score 376; DB 2; Length 361;  
Best Local Similarity 28.3%; Pred. No. 9e-19;  
Matches 102; Conservative 67; Mismatches 152; Indels 40; Gaps 9;

QY 20 PFVYLTQAVWILCAIAAASAGPQPCFVCSNQSKVCTRGILSEVPGIPSNTRY 79  
DB 20 PFVYLTQAVWILCAIAAASAGPQPCFVCSNQSKVCTRGILSEVPGIPSNTRY 79



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b 4 PMLLSLSGLASLIPALAA-----CPNCHCHSDLOHVICDKVGLQKPK-VSEKTKL 57
y 80 LNLKNNIOMIQADTERHLEHLEVLQGRNSIRQIEVGAFNGIASLNTLELFDNLWITP 139
b 58 LNLQNNFPVLATNSFRAMPNLSHLQHCQIREVAAGAFGLKQLLYLISHNDIRVL 117
y 140 SGAFYLSKLRLEWLNNPIESTPSVAFNRVPSLRDLGLBLKLEIYSEGAFGLFMILK 199
b 118 AGAFDDLTELTYLYLOHNVKVTLPGLSPLVNLFILOLNN-NKIRELSGAFQAGKDLR 176
y 200 YLMGLMCNIK-----DMPN-----LTPVLGLELEMSGNHFFPEI 233
b 177 WLKLSNSLSLOPGALDDVENLAKYLDNRNQLSSVPSAALSGLRVVEELKLSHPLASI 236
y 234 RPSGFHGLSS-LKKLVWMSQVSLIERNAPDGLASLVELNLSLPHLFTPLRYL 292
b 237 PDNAFQSPGRYLETLMLDNTNLEKFSQDAGFLVTTILKHVLENNRLHQLPSNF--PPDSL 294
y 293 VELHLHNNPNCDDILNLAWLREVIPTNSTCCGCHAPMEMRGYLVVEVDQAFQCSA 352
b 295 EETLTNNPWKCTCQURGLRWLE---AKTSRDPATCASPFKRGQHINDTD-AFGCKF 350
y 353 P 353
b 351 P 351

RESULT 7
36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
;Species: Drosophila melanogaster
;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
;Accession: A36665
;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
;Title: slit: an extracellular protein necessary for development of midline glia and co
;Reference number: A36665; MUID:91099665; PMID:2176636
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-1469 <ROT>
;Cross-references: GB:X53959
;Genetics:
;Gene: FlyBase:sl
;Cross-references: FlyBase:FBgn0003425
;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
;347-376/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
;7846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
;1028-1061/Domain: EGF homology <EGF>
;1068-1099/Domain: EGF homology <EGF2>
;1115-1148/Domain: EGF homology <EGF1>

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Query Match 10.3%; Score 355.5; DB 2; Length 1469;
Best local similarity 25.0%; Pred. NO. 1.6e-16;
Matches 109; Conservative 53; Mismatches 137; Indels 137; Gaps 8;

QY 46 CPVCSQSNQFSKVVCTRRGLSEVPQGISNTRYLNLMENNIQMIOADTFREHLHLEVLQ 105
Db 73 CPVCSCTG--LNVDCSHRGLTSVPKISADVERLELQGNLTVIYETFORLTKRLMLQ 130
QY 106 LGRNSIRQIEVGAFNGIASLNTLELFDNLWITPISGAFYLSKLRLELWLNPIPSY 165
Db 131 LTDNQIHTIERNFQDLVSLERLDISNNVITTVGRVFKGQASERSLQDNNOITCLDEH 190
QY 166 AFRVPSLMDLGLKLEIYSSGAFEGLENLYLNLG----- 204
Db 191 AFKGLVELEILTNN--NLTSLPENIFGGLRLRALRLSDNPACDCHLSWLSRFLRSAT 249
QY 205 -----MC-----NTKD----- 210
Db 250 RLAPYTRCQSPSKQGNVADLHDQBFKSGLTEHAPMECGAENSCPHPCRCADGIVDCR 309
QY 211 -----MPNLTPVLGLE----- 222
Db 310 EKSLTSVFTLPDPTDTRVLRQNFITELPKSPSSFRRLRRDLNNSNISRHAHDSGL 369
QY 223 -----LEMSGNHFFEIRPGSFHGLSKLKLWVMSQVSLIERNAPDGLASLVELNLAHNN 277
Db 370 KQLTTLVLYGNKIKDLPSGVFKGLSLRLLLNANEISCIKDAFRLHSLSLSLYDNN 429
QY 278 LSSLPHLFTPLRYLVELHLHNNPNCDDILNLAWLREVIPTN--STCCSCHAPMEM 335
Db 430 IQSLANGTFDAMSKMTYHLAKNPFICDCNRLWA----DYLKHNPIETSGARCESPKKM 485
QY 336 RGRYLVEVDQAFQCS 351
Db 486 HRRRIESLREEFKCS 501

RESULT 8
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
;Species: Drosophila melanogaster
;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
;Accession: A36665; A31640; S33523
;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
;Title: slit: an extracellular protein necessary for development of midline glia and co
;Reference number: A36665; MUID:91099665; PMID:2176636
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-1480 <ROT>
;Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:g8615
;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
;Cell 55, 1047-1059, 1988
;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
;Reference number: A31640; MUID:89077533; PMID:3144436
;Accession: A31640
;Molecule type: DNA
;Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', <R02>
;Cross-references: GB:M23543; NID:g340939; PID:g514357
;Genetics:
;Gene: FlyBase:sl
;Cross-references: FlyBase:FBgn0003425
;Amino acids: 1351/3
;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
;347-376/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
;7846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
;1028-1061/Domain: EGF homology <EGF>
;1068-1099/Domain: EGF homology <EGF2>
;1115-1148/Domain: EGF homology <EGF1>

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F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>  
 F:288-313/Domain: proteoglycan amino-terminal homology <PAH2>  
 F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>  
 F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>  
 F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>  
 F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>  
 F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>  
 F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>  
 F:512-537/Domain: proteoglycan amino-terminal homology <PAH3>  
 F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>  
 F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>  
 F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>  
 F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>  
 F:651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>  
 F:708-733/Domain: proteoglycan amino-terminal homology <PAH4>  
 F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>  
 F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>  
 F:791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>  
 F:815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>  
 F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
 F:1028-1061/Domain: EGF homology <EGF>  
 F:1068-1099/Domain: EGF homology <EGF2>  
 F:1115-1148/Domain: EGF homology <EGF1>

Query Match 10.3%; Score 355.5; DB 2; Length 1480;  
 Best Local Similarity 25.0%; Pred. No. 1.6e-16;  
 Matches 109; Conservative 53; Mismatches 137; Indels 137; Gaps 8;

QY 46 CPSVCSNQSESKVCTRRGLSEVPGQIPSTRYLNLMENNIMQIADTFRLHLEVLQ 105  
 DB 73 CERVCSCTG--LNVDCHSRGLTSVPRKISADVERLEQGNLTIVYETDFORLTKRLMLQ 130  
 QY 106 LGRNSIROIEVGAENGLASINTLELFDNLTVIFSGAFYLSKRLRLMNRNPISPSY 165  
 DB 131 LTDNQIHTIERNFSQDLVSLERLDISNNVITVGRVFKQAQSLRSQLDNNQITCLDEH 190  
 QY 166 AFNRVPSLMRLDLGELKLEYISEGAFGLFNLYKMLG----- 204  
 DB 191 AFKGLVELEITLNN--NNLTSLPHNIFGGLGRALRLSDNPFACDCHLSWLSRFLRSAT 249  
 QY 205 -----MC-----NIKD----- 210  
 DB 250 RLAPYTRQSPSQLKGQNVADLHDEQFKCSGLTEHAFMECGAENSCPHPCRCADGVDCR 309  
 QY 211 -----MPLNLTPLGLEE----- 222  
 DB 310 EKSLSVPTVPTDDITDVLRLQNTITELPPKSPSSFRRLRIDLSNNISRIADHLSGL 369  
 QY 223 -----LEMSGNHFFPIRPGSPFHGLSSLKLVWNSQVSLIERNAFDGLASLVELNLAHN 277  
 DB 370 KQLTTLVLYGNKIKDLPQGVFKGLSLRLLLNANEISCIRKQAFRLHLSLSLYDNN 429  
 QY 278 LSSLPHDLFTPLRYLVELHLENPNKCCDILWLAWLREYIPN--STCCGRCCHAPMGM 335  
 DB 430 IGSILANGTFDAKSMKTVHLANKNPFICDNLRLWLA----DYLHKNPIETSGARCESPKGM 485  
 QY 336 RGRYLVEVDQASFQCS 351  
 DB 486 HRRRTESLREKFKCS 501

RESULT 9  
 T28714  
 hypothetical protein T21D12.9a - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T28714  
 R:Woessner, J.  
 submitted to the EMBL Data Library, August 1997  
 A:Description: The sequence of C. elegans cosmid T21D12.  
 A:Reference number: Z20514  
 A:Accession: T28714  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-789 <WOB>  
 A:Cross-references: EMBL:AF016687; PIDN:AAC48096.1; GSPDB:GN00022; CESP:T21D12.9a  
 A:Experimental source: strain Bristol N2; clone T21D12  
 C:Genetics:  
 A:Gene: CESP:T21D12.9a  
 A:Map position: 4  
 A:Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2

Query Match 9.8%; Score 335.5; DB 2; Length 789;  
 Best Local Similarity 23.7%; Pred. No. 1.8e-15;  
 Matches 142; Conservative 79; Mismatches 207; Indels 171; Gaps 20;

QY 78 RYLMNMENIUMIQADTFRLHLEVLQGRNSIROIEVGAENGLASINTLELFDNLTV 137  
 DB 58 RSVLSRLRLISYLPKPTTSKAVNTEKLDLASNITDGTDFHPSFNTLVTKLARNHIT 117  
 QY 138 IPSGAFYLSKRLRLMNRNPISPSYAFNRVPSLM-----RLDGL----- 179  
 DB 118 LNQFSRLKLESIDLTNRNIREVRFLAFNQLPSLQNVSLARNVYLDGMEFYACEGL 177  
 QY 180 -----ELKKLEYISEGAFGL-----FN-----LKYINLMGNMKD 210  
 DB 178 KHLNLTNRVQAVTEGWMFGLTSLVLDLSVNTQTSFPHSSWSHTPKLWLSLHNRIOQ 237  
 QY 211 MP--NLTPLVGLLELSEGNHFFPIRPGSPFHGLSSLAKLV----- 249  
 DB 238 LPSGSFRVLRQLEELIUSANSIDSLHKFALVGMSSLHKLDSNTLAVCVSDGAVLYNTS 297  
 QY 250 -----MNSQVSLIERNAFDGLASLVELNLAHNLSLPHDLFTPLRYLVELHLEHN 300  
 DB 298 MFPLRLSRLFTNNQLRVIPKRAFRFPALBELDLTDNPDIATIHPEAFEPLE-LKRLVNSS 356  
 QY 301 PNWCDDILWLAWLREYIPNITNSTCCGRCHAPMHMRGRLVYLVVDQASFQCSAPFMDAPR 360  
 DB 357 SILCQCQISWLASWIYRLKDKSIIAKCSYPPPLADLYVVAIDTANLTCH----NDSPR 412  
 QY 361 -----DLNLSGRMAELKCRTPPMS--SVKW-LLPNGTIVLSHSHRPRISVINDGT- 408  
 DB 413 AKIVRQPEVSTVLIGERKARFTCNVYGASPLSIENRWENG-----QERVLVQDSATF 464  
 QY 409 -----LNFSHVLLSDTGVTCMTNVNAGNSNAYLNVSIAEL 446  
 DB 465 LSINRTAVVNGTDFERELAAELLDNVAMTDNSYOCVARNRFG-SDFSTHVKLQVYQA 523  
 QY 447 NTSNYSPTTIVTETTSIPEDTTRKYKVPETSTGYQPAYTTSTT-VLIQTTRVPK--- 502  
 DB 524 PKFTY-----TPED-----MPLLVGQTAFLCAATGTPRPEI 555  
 QY 503 -----QVAVPATDTDKNQTSLDE---VMKTKIIIGCP-----VAVTLAAAMLIVP 547  
 DB 556 KWAPQIAPPAAEARLYVTPDDHIVIMNVTKEDQAYTCHATNVAGOTQASANLIVP 614

RESULT 10  
 T28715  
 hypothetical protein T21D12.9b - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T28715  
 R:Woessner, J.  
 submitted to the EMBL Data Library, August 1997  
 A:Description: The sequence of C. elegans cosmid T21D12.  
 A:Reference number: Z20514  
 A:Accession: T28715  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1355 <WOE>  
 A:Cross-references: EMBL:AF016687; PIDN:AAC48095.1; GSPDB:GN00022; CESP:T21D12.9b  
 A:Experimental source: strain Bristol N2; clone T21D12  
 C:Genetics:  
 A:Gene: CESP:T21D12.9b  
 A:Map position: 4

.; Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2; 786/3; 84/2

Query Match 9.8%; Score 335.5; DB 2; Length 1355;  
Best Local Similarity 23.7%; Pred. No. 3.7e-15;  
Matches 142; Conservative 79; Mismatches 207; Indels 171; Gaps 20;

Y 78 RYLNLENNIOMIQADTFRLHLEVLQGRNSIRQIEVGAENGLASLNTLELFDNWLTVI 138  
b 56 TLDLRFNHIEELPAN-----AFSLAQITLFLINDLAVL 91

Y 139 PSQAFYLSKRLRLWLNPNPIESIPYAFNRVPSLMRLDLGLXKLEYISEGAFGLFNL 198  
b 92 QDGAINGLTALRPVYLNLRSLRSLPATIIFORMPL-----EGIP-- 130

Y 199 KYLNLCNCKIDPNLTPVLGLEELMSGNHPEIRPGSFHGLSSLKLVWNSOVSLIE 258  
b 131 -----LENDIWLQIP 140

Y 259 RNADFGLIASIVELNLAHNLSSLPDHLFTPLRYLVELHLHNPWNCDDI-----LWLAWM 314  
b 141 AGLFDNLPLRLNLIIMYNNKLTQLFVDPGNELNKLKELRLDGNALDIDCNGVYSLWRWH 200

Y 315 L-----REVIPNTSCCGRCHAPMGRYLYVEDQASFOCSAPFIMDAPDLNISSEGMAS 371  
b 201 LDVQRLVSLTCA-----APQMLQNGQSSLGEHFKCAKFOFLVAPQDAQVAGEQVE 256

Y 372 LKCRTPFM--SSVKMLLPNGTVLSHASRHRISVLDGTLNFSHVLLSDTVYTCWTVV 429  
b 257 LSCVTVCLHRPQITWM--HNTQELGLEBQTAELLPSGSLHRSADTSDMGIYQCIARNE 314

Y 430 AGNSASAYINVTABLNTSNYSFFTVTVTETTESPEDTTRY--KPVPTTSTGYQAPY 487  
b 315 MGAIRSQPVRLV-----VNGGNHPLDSPIDARSNQVWADAGTTHGATPLPSPSPSHSPH 370

Y 488 TT 489  
b 371 FT 372

RESULT 12  
JG0193  
G protein-coupled receptor FEX - mouse  
C; Species: Mus musculus (house mouse)  
C; Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-May-2000  
C; Accession: JG0193  
R; Hervey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.  
Biochem. Biophys. Res. Commun. 254, 273-279, 1999  
A; Title: Identification of a novel seven-transmembrane receptor with homology to glycophorin A  
A; Reference number: JG0193; MUID: 99121227; PMID: 9920770  
A; Accession: JG0193  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-907 <HER>

Query Match 9.3%; Score 321.5; DB 2; Length 907;  
Best Local Similarity 25.2%; Pred. No. 2e-14;  
Matches 108; Conservative 64; Mismatches 155; Indels 101; Gaps 10;

Y 22 VYLTAAQVWILCAIAAASAG-----PQNCPSVCSC---SNQFSKVCTRGUSEVPGQIP 74  
b 6 VHMLLSLLALLQVAAAGSSPGPDAPRPGCPCHCELDGRMLLRVDCSLGSLSELPSNL 65

Y 75 SNTRYLNLENNIOMIQAD-----TFRHLHLEVLQGRNS 110  
b 66 VFTSYLDLNNNISQPLASLHRLHLELRLAGNATHIPKGAFTGLSLKVLMLQNNQ 125

Y 111 IRQIEYGAENGLASLNTLELFDNWLTVIPSGAFYLSKRLRLWLNPNPIESIPYAFNRV 170  
b 126 LRKVPBEALQNLRLSLQSLRLDANHISYVPPSCFSLHSLRLHLDNALTDPVQAFSL 185

Y 171 PSLMRLDLGLKLEYISEGA-----FEGFLNLYKYLNLGMC 206  
b 186 SALQAMTLA-LANKIHADIYAFGNLSSLVVHLHNNRHSLGKKCFDGLHSLTDLNLYN 244

Y 207 NIKDMFN-LTPVLGLEELMSGNHPEIRPGSFHGLSSLKLVWNSOVSLIERNAFD-- 263  
b 245 NLDEPTAKTLNLKELGPHSNNIESIPERAFVGNPSLITTHFYDNPFIQFVGSVAFQHL 304

RESULT 11

46224  
eroxidase - fruit fly (Drosophila sp.)  
; Species: Drosophila sp.  
; Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000  
; Accession: S46224  
; Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.P.; Parker, MBO J. 13, 3438-3447, 1994  
; Title: Peroxidase: a novel enzyme-matrix protein of Drosophila development.  
; Reference number: S46224; MUID: 94341255; PMID: 8062820  
; Accession: S46224  
; Status: preliminary  
; Molecule type: mRNA  
; Residues: 1-1535 <NEL>  
; Cross-references: GB:U11052; NID:G531384; PID:AAA61568.1; PID:G531385  
; Superfamily: peroxidase; myeloperoxidase homology; proteoglycan amino-terminal homology  
; 13-44/Domain: proteoglycan amino-terminal homology <PAH4>  
; 161-1350/Domain: myeloperoxidase homology <MPX>

Query Match 9.6%; Score 331.5; DB 2; Length 1535;  
Best Local Similarity 23.2%; Pred. No. 8.3e-15;  
Matches 112; Conservative 72; Mismatches 173; Indels 125; Gaps 14;

Y 21 FVYLTAAQVWILCAIAAASAGPON--CPSVCSCNQFSKVCTRGUSEVPGQIPSNTR 78  
b 3 FMEMLQLLGLLELLLA-----GGVQSVYCPAGCTCLER--TVRCIRAKUSAVPK-LPQDTQ 55

QY 264 -----GLASVELNLAHNNLSLPHDLFTPLRYLVELHLHNPW 302  
Db 305 PEERITLNGASHITEPHLTGATLESITGAKISLPQAVCDQPLNQVLDLSYH-- 362  
QY 303 NCCDILMLAWMLREYIPNFTSCGRCCHAPMGRYLVVDQASQFASPPIMDAPRDL 362  
Db 363 -----LLEDPSLSGC--QKLQKIDLRHNEIYEIKGSTFQ-----QLFNLRSL 403  
QY 363 NISEGRMA 370  
Db 404 NLAWNKIA 411

RESULT 13  
JC6128  
insulin-like growth factor binding complex acid labile chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 05-Nov-1999  
C:Accession: JC6128  
R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.  
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996  
A:Title: Organization and chromosomal localization of the gene encoding the mouse acid labile chain of the insulin-like growth factor binding complex  
A:Reference number: JC6128; MUID:96413591; PMID:8816745  
A:Accession: JC6128  
A:Molecule type: DNA  
A:Residues: 1-603 <BOI>  
A:Cross-references: GB:U66900; NID:G1621612; PIDN:AA817270.1; PID:G1621613  
C:Comment: This protein is a serum protein and it is of the ternary complex in the phys  
A:Gene: als  
A:Map position: 17

Query Match 9.3%; Score 321; DB 2; Length 603;  
Best Local Similarity 24.5%; Pred. No. 1.3e-14;  
Matches 131; Conservative 69; Mismatches 162; Indels 172; Gaps 16;  
QY 36 AAAAGAPQNCVSCS-----NQFSKVCTRGSLSEVPGQIPSNR----- 78  
Db 32 ASADAEQPQ-CPVCTCSDYDDYDELS-VFCSSRLTQDPGIPVSTRALMDGNLSSI 89

QY 79 -----YLMNENNIQIADTFPHLHLE 102  
Db 90 PSAAFONLSSLDPLNLQGSWLSRLPQALLGLVHLRLHRLNLLSLAAGLFRHTPSLA 149

QY 103 VLQIGNSRQIEVAFNGLASLNTLELFDNLTWIPSGAFB----- 144  
Db 150 SLGLNLLGRLEEGFLRGLSHLDNLGWSLVLPDTPVFGLGNDHELVLGAKTYL 209

QY 145 -----VLSKRELWLRNPIESIPSYAFNRVPSLMLRLDGE-----LKKLE 185  
Db 210 QPALLCGLGSELRLDLSRNALSXYANVFIHLPRQLYLDENLITAVAPRAFLGMKALR 269

QY 186 YIS-----EGAFGLFMKYLINLGMCMKMPNLT--PLVGLBELEMSGNHFFPEI 233  
Db 270 WLDLSHNRVAGLLEDTFPGLLGLHLVRLAHNAITSRLRPTTKDLHFLBEELQGHNRIRQL 329

QY 234 RGSFHLGLSSKLKLVWNSQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLV 293  
Db 330 GEKTFEGLQLVFLINDQIHEVKGAFPGFLPNVAVMLSGNCLRSLEPHVFGGLGLH 389

QY 294 EHLHNPWNCDCILMLAWLREVIPNSTCCGCHAPM-----MCRGYLVVEVDQA 346  
Db 390 SLFLEH-----SCLGRIR--LHTFAGLSGLRLFL----- 417

QY 347 SPQCSAPPIMDAPRLNIS---EGMAELKCHTTPMSSVKMLLPNGTVLSHSHRPRISV 403  
Db 418 -----RNSISIEQSLAGI-----SLELDLDTANQLTHLPHQ----- 452

QY 404 LNDGTLNPSHVLSDTGVTVMVNVAGNSASAYLANVSTABLNTSNYSFTTV 457  
Db 453 LFGQLQLEVLISNNQL-TMISEDVLGFLQAFWLDLSHNRLETAPAGLFSFL 505

RESULT 14  
JC5239  
insulin-like growth factor acid-labile chain - baboon  
C:Species: Papio sp. (baboon)  
C:Date: 17-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-May-1997  
C:Accession: JC5239  
R:Delhanty, P.; Baxter, R.C.  
Biochem. Biophys. Res. Commun. 227, 897-902, 1996  
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like growth factor  
A:Reference number: JC5239; MUID:97040714; PMID:8886027  
A:Contents: liver  
A:Accession: JC5239  
A:Molecule type: mRNA  
A:Residues: 1-605 <DEL>  
C:Comment: This factor is structurally related to proinsulin and have insuline-like met.

Query Match 9.2%; Score 315; DB 2; Length 605;  
Best Local Similarity 32.4%; Pred. No. 3.4e-14;  
Matches 94; Conservative 44; Mismatches 118; Indels 34; Gaps 7;  
QY 42 GPQNCVSCS-----NQFSKVCTRGSLSEVPGQIPSNRYLNMENNIQIADTFR 96  
Db 38 GPA-CPATCACSYDDVENVLS-VFCSSRLTQDPGIPGTOALWLDNSLSSIPAAFR 95

QY 97 HLHLEVL-----QLG-----RNSIRQIEVGAENGLASLNTLELFD 132  
Db 96 NLSSLAFLNLQGGQIGSLPQALLGLENLCHLHRLNQLRSLAVGTTFAYTPALALGLSN 155

QY 133 NMLTVIPSGAFYLSKRELWLRNPIESIPSYAFNRVPSLMLRLDGLGELKLEYISEGAF 192  
Db 156 NLSRLDGLFEGGLNLDNLGWSLAVLPDAFRLGGLRELVLG--NRLAYLQPALF 214

QY 193 EGLFMKYLINLGMCMKMPN--LTPLVGLBELEMSGNHFFPEIRPGSPHGLSSKLKLVW 250  
Db 215 SGLAELRLSDLSRNALRAKANVPAQLPRQLYLDENLITAAVAPRAFLGMKALRWLDLS 274

QY 251 NQVSLIERNAPDGLASLVELNLAHNNLSLPHDLFTPLRYLVELHLHNN 300  
Db 275 NNRVAGLLEDTFPGLLGLVRLHRLNLAISLRPTFEDLHFLBEELQGHN 324

RESULT 15  
JC1282  
insulin-like growth factor-binding protein acid labile chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jul-2000  
C:Accession: JC1282  
R:Bai, J.; Baxter, R.C.  
Biochem. Biophys. Res. Commun. 188, 304-309, 1992  
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth factor  
A:Reference number: JC1282; MUID:93038676; PMID:1384485  
A:Accession: JC1282  
A:Molecule type: mRNA  
A:Residues: 1-603 <DAL>  
A:Cross-references: GB:S46785; NID:G258002; PIDN:AA823770.2; PID:G5705934  
A:Experimental source: liver  
A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205  
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status  
F:287-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 9.0%; Score 310; DB 2; Length 603;  
Best Local Similarity 31.2%; Pred. No. 7.5e-14;  
Matches 92; Conservative 48; Mismatches 123; Indels 32; Gaps 5;  
QY 36 AAAAGAPQNCVSCS-----QFSKVCTRGSLSEVPGQIPSNRYLNMENNIQI 91  
Db 32 ASADAEQPQ-CPVACTCSDYDDYDELSVFCSSKNLTHLPDIPVSTRALMDGNLSSIP 90

QY 92 ADTFRHLHLE-----VLQIGNSRQIEVGAENGLASLNT 127  
Db 91 SAAPQNLSSLDPLNLQGSWLSRLPQALLGLQNLVYHLERNLNLAVGLFTHTPSLAS 150

Y 128 LEFDNWLTVIPSGAPEYISKLELRLNRPPIESIPSAFNRVPSIMRLDGLGELKLEYI 187  
b 151 LSSNLLGLRLEBGLFQGLSHLWDLNGLWNSLVLPDVTFFQGLGHLHVLVLAG-NKLTYL 209  
Y 188 SCGAPFGLFNLYLNTGCMYKDMFN--ITPLVGLSELEMSGNHFPPIRPSFHLSSLYK 245  
b 210 QPALFQGLGELRDLRSNALRSVKANVFVHLPRQKLYLDRNLITAVAPGAFGLGMKALR 269  
Y 246 KLMWMSQVSLIERNAFDGLASIVELNLAHNLSLPHDLFTPLRYLVVELHLHN 300  
b 270 WLDSLNRVAGLMEDTFGLGLGLHVLRLAHNAIASLRPTFTKDLHFLBELQLGHN 324  
RESULT 16  
41915  
;Title: Structure and functional expression of the insulin-1  
;Reference number: A41915; MUID:92357025; PMID:1379671  
;Accession: A41915  
;Status: preliminary  
;Molecule type: mRNA; protein  
;Residues: 1-605 <EO>  
;Cross-references: GB:M86926; NID:G184807; PIDN:AAA36047.1; PID:G184808  
;Experimental source: liver  
;Note: sequence extracted from NCBI backbone (NCBIP:110171)  
;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
;75-92/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>  
;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>  
;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>  
;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>  
;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>  
;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>  
;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>  
;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>  
;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>  
;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>  
;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>  
;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>  
;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>  
;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>  
;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>  
;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>  
Query Match 9.0%; Score 309; DB 2; Length 605;  
Best Local Similarity 23.8%; Pred. No. 8.9e-14;  
Matches 121; Conservative 69; Mismatches 154; Indels 168; Gaps 16;  
Y 42 GPQNCPSVSCS-----NPFKVVCTRRGLSEVPQIPSENTR----- 78  
b 38 GPA-CPAACVSYDDADELS-VFCSSRLNLPDGVPGTQALWLDGNLSSVPPAAAFQ 95  
Y 79 -----YNLMENNTQADTFPHLHLEVLQLGR 108  
b 96 NLSSGLFLNQGGQLSLFPQALLGLLENLCHLERNQRLSALGTFPAALASGLSN 155  
Y 109 NSIRQIEVGAFNGLASLNTLELFDNWLTVIPSGAPEYISKLELRLNRPPIESIPSAFN 168  
b 156 NRIURLLEDGLFEGSLGWDNLNGLWNSLAVLPDAAFRGLGSLRELVLNAGNLAYLQPALFS 215  
Y 169 RVPSIMRLDGL-----ELKGL-----EYISGAPFGLFNLYLNT-- 203  
b 216 GLAELRELDLSRNAIRAIKANVFVQLFRQKLYLDRNLITAAVAPGAFGLKALRLDLSH 275

QY 204 -----GMCNIK-----DMPNLTP-----LVGLEELMSGNHFPPIRPSGFH 239  
Db 276 NRVAGLELDTFPGLLGLRLVLRSLHNAIASLRPTFTKDLHFLBELQLGHNRIQLAERSFE 335  
QY 240 GLSSAKKLWMSQVSLIERNAFDGLASIVELNLAHNLSLPHDLFTPLRYLVVELHLHH 299  
Db 336 GIGQLVFLIDHQLQEVVAGAFGLGTVAVWNLGNCNLRNLPQVFRGLGKLHSLHL-- 393  
QY 300 NPWNCDDILWLAWMLREYIPTNSTCCGRCH-----APMEMRGYLVVEVDQASFQ 349  
Db 394 -----EGSLGRIRPHFTFTGLSGRLRLFLKONGLVGIBEQSLW 431  
QY 350 CSAPPI-MDAPRD-----LNISGRMARLKC-RTPPMSSVKYL----- 385  
Db 432 GLAELLELDLTSNQLPHLPHRLFQGLGKLEYLLGRNRLALPADALGQLQAFWLVDVH 491  
QY 386 -----LPNGTVLSHASRHRPRISVLDNGTINFS 412  
Db 492 NRLEALPN-SLLAPGLRLAYLSLRNLSLTFT 522  
RESULT 17  
T42626  
;Title: secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  
;Alternate names: neurogenic extracellular slit protein  
;Species: Mus musculus (house mouse)  
;C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 16-Aug-2002  
;Accession: T42626  
;R:Holmes, G.P.; Negus, K.; BurrIDGE, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.  
;Mech. Dev. 79, 57-72, 1998  
;A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in  
;A:Reference number: 222177; MUID:9929238; PMID:10349621  
;Accession: T42626  
;A:Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: mRNA  
;A:Residues: 1-1025 <HOL>  
;A:Cross-references: EMBL:AF074960; NID:G4151258; PID:G4151259; PIDN:AAD04345.1  
;C:Genetics:  
;C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein  
Query Match 9.0%; Score 309; DB 2; Length 1025;  
Best Local Similarity 23.7%; Pred. No. 1.8e-13;  
Matches 111; Conservative 60; Mismatches 155; Indels 142; Gaps 15;  
QY 46 CPBVCSCSNQFSKVCVTRGLSEVPQIPSNTRYLNLMENNTQADTFPHLHLEVL 104  
Db 2 CPBKCCEG--TVDCSNQRLNKIPDHIPQYTAELRLNNEFTVLEATGIPKLPQLRXI 59  
QY 105 QLGRNSIRQIEVGAFNGLASLNTLELFDNWLTVIPSGAPEYISKLELRLNRPPIESIPS 164  
Db 60 NFGNNKITDIEGAFEGASGVNEILLTSNRLNENVOHMKPKGLESLKTLMLRSNRISCVGN 119  
QY 165 YAFNRVPSIMRLDGLGKLEYISGAPFGLFNLYLNT-----GMCN----- 207  
Db 120 DSFIGLSVRLSLYD-NQITTVAPGAFDXLSLSTLNLANLPNCNCHLAWLGEWLARK 178  
QY 208 -----IKMP-----NLTPL----- 217  
Db 179 RIVTGNPRCKPKPYFLKEIRIQDVAIQDFTCDGNDNDSCLSPSCFSECTCLDTXVRCN 238  
QY 218 VGLS-----ELEMGNHF-----PEIRPGSPHGLSS 243  
Db 239 KGUKVLPGIKDVLTLYDGNQFTLVPKELSNYKHLTIDLSNNRISTLSNOXFSNWTQ 298  
QY 244 LKKLWMSQVSLIERNAFDGLASIVELNLAHNLSLPHDLFTPLRYLVVELHLHHPN 303  
Db 299 LLTLILSYNLRICIPRTFTDGLKSLRLSLHNGDISVVPFEGAFNDLSALSHLAGNPLY 358  
QY 304 CUCDILWLAWLR-EYIPTNSTCCGRCHAPMEMRGYLVVEVDQASFQSPFIMDAPDL 362  
Db 359 CDCNMQLSDWVKSEY---KPGIARFACGAGEMADKLLLTTPSKKFTQCPM-----DI 409

QY	363	NISEGRMAELKCRTPPMSSVKVLLPNGTVLHSHSRHPRISVLNDGTLN	410
DB	410	TI-----QAK-NPCLSN-----PCKNDGTGN	430
RESULT 18			
A3531			
oncofetal trophoblast glycoprotein ST4 precursor - human			
N:Alternate names: oncofetal antigen ST4			
C:Species: Homo sapiens (man)			
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999			
C:Accession: A3531; S40087			
R:Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.			
J. Biol. Chem. 269, 9319-9324, 1994			
A:Title: Isolation of a cDNA encoding ST4 oncofetal trophoblast glycoprotein. An antigen			
A:Reference number: A3531; MUID:94179356; PMID:8132670			
A:Accession: A3531			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-420 <MEY>			
A:Cross-references: EMBL:Z29083; NID:G435654; PIDN:CAA82324.1; PID:G435655			
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homolog			
C:Keywords: duplication; glycoprotein; transmembrane protein			
F:1-31/Domain: signal sequence #status predicted <SIG>			
F:32-420/Product: oncofetal trophoblast glycoprotein ST4 #status predicted <MAT>			
Query Match 9.0%; Score 308.5; DB 2; Length 420;			
Best Local Similarity 29.5%; Pred. No. 5.9e-14;			
Matches 98; Conservative 47; Mismatches 136; Indels 51; Gaps 9;			
QY	35	IAAASAG---PQNCPSVCSNQPSKVCTRGSLSEVQGPISNRYLNLXENNIQMIQ	91
DB	48	LASVASQPLPDQCFALCECEAAARTKCVNRNLTEVTPDLPAYVNLFLTGNQLAVLP	107
QY	92	ADTFRLHHLHLEVLQGRNSIRQIEGAF---NGLASMTLELFNMTLTPSGAFYLSK	148
DB	108	A-----GAFARPPILAEALNLSGRLDEVRAGAFELPS	143
QY	149	IRELMRNPNPISPSYAFN-----RVPS-LMRDLGELKKLYISEG-AFEGFLNLY	200
DB	144	LRQLDLSNPLADLSPFAFGSNASVASPSPLVELILNHIVPEDEPQRNSFGMW-VAA	202
QY	201	LNLEGNCKMDNPLVGLGLELESGNHFPEIRPGSPHGLSSLKLVWMSQVSLERN	260
DB	203	LLAGRA-----LQGRLELASHNHLFPLRDVLAQLPSLRHLDLSNLSVSTYV	252
QY	261	AFDGLASIVELNAHNLSLPHDLFTPLRYL--VELHLHNPWNCDDILMLAWLREY	318
DB	253	SPFNLTLESLEHLDNALKVLHNGTLAEQLGLPHIRVFLDNNPNVWCDCHMADMTWLKET	312
QY	319	IFTNSTCCGRCHAPNMRGRVLYVEDQASFOC	350
DB	313	EVVQKORLTCAYPEKMRNRVLELNSADLDC	344
RESULT 19			
A60164			
platelet membrane glycoprotein V precursor - human			
C:Species: Homo sapiens (man)			
C>Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 05-Nov-1999			
C:Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329			
R:Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.			
J. Biol. Chem. 268, 20801-20807, 1993			
A:Title: Cloning and characterization of the gene encoding the human platelet glycoprotein			
A:Reference number: A48030; MUID:94012616; PMID:8407908			
A:Accession: A48030			
A:Molecule type: DNA			
A:Residues: 1-560 <LA2>			
A:Cross-references: EMBL:Z23091; NID:G312501; PIDN:CAA80637.1; PID:G312502			
R:Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama,			
Blood 75, 2349-2356, 1990			
A:Title: Rapid purification and characterization of human platelet glycoprotein V: the a			
A:Reference number: A60164; MUID:90275263; PMID:2350580			



F;189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F;211,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.8%; Score 303.5; DB 1; Length 359;  
Best Local Similarity 31.9%; Pred. No. 1.1e-13;  
Matches 84; Conservative 45; Mismatches 123; Indels 11; Gaps 7;

QY 40 SAGPQNCPSVCSNQPSKYVCTRRLGSEVPGIPSNTRYLNLMENNTQMCAQDFRHLH 99  
DB 49 SLGFW-CPERCQC---HLRVQCSDLGLDKVPKLPDFTLLDLQNNKITEIKDGFKNLK 105  
QY 100 HLEVLQLGNSIRQIEVGAFNGLASLNTLELFDNWLFTVPSGAFYLSK-LFEELWRNP 158  
DB 106 NLHALLVNNKLSKVPSPGFTPLVKLERLYLSKNQLKEP---EKPKTLQELRAHENE 161  
QY 159 ISSIPSYAFNRVPSLWRDLGL-ELKKLEYISGAFEGFLPNLYKLANLGMCNIKDMPNLPL 217  
DB 162 ITKRVKVTFGNLQMWIVIELGTPNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPOGLP- 220  
QY 218 VGELEHMGSGNHFPRICSGFHLGSLSKLWYNNQSVLSIRNAPDGLASLVELMLANN 277  
DB 221 PSLTEHLQNGKISRVDAASLKLNNLAKLGLSFNSISAVDNGSLANTPHLRBELHDNKK 280  
QY 278 LSSLPHDLFTPLRYLYVELHLEN 300  
DB 281 LFRVPGGL-AEHKYIQVVYLHNN 302

RESULT 21  
JB0176  
orphan G protein-coupled receptor precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 21-Jul-2000  
C;Accession: J00176  
R;McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q.  
Biochem. Biophys. Res. Commun. 247, 266-270, 1998  
A;Title: Identification and cloning of an orphan G protein-coupled receptor of the glyco-  
A;Reference number: JB0176; MUID:98308104; PMID:9642114  
A;Accession: J00176  
A;Molecule type: mRNA  
A;Residues: i-907 <MCD>  
A;Cross-references: GB:AF062006; NID:g3366801; PIDN:AAC28019.1; PID:g3366802  
C;Comment: This protein is a receptor for a novel class of glycoprotein ligands.  
C;Genetics:  
A;Gene: HG38  
A;Map position: 12q22-23  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;562-583/Domain: transmembrane #status predicted <TM1>  
F;594-616/Domain: transmembrane #status predicted <TM2>  
F;639-660/Domain: transmembrane #status predicted <TM3>  
F;681-701/Domain: transmembrane #status predicted <TM4>  
F;725-744/Domain: transmembrane #status predicted <TM5>  
F;768-791/Domain: transmembrane #status predicted <TM6>  
F;803-824/Domain: transmembrane #status predicted <TM7>

Query Match 8.8%; Score 303.5; DB 2; Length 907;  
Best Local Similarity 26.1%; Pred. No. 3.7e-13;  
Matches 111; Conservative 60; Mismatches 156; Indels 99; Gaps 10;

QY 22 VYLTAQVWILCAIAAASAGP--QNCPSVCSG---SNQFSKVCTRGRLSEVPGIPSN 76  
DB 8 VLILSLPVLQLATGGSSPRSGVLLRGCPTHCEPDGRMLLRVDCSLGSELSPNLSVP 67  
QY 77 TRYLNLMENNIO-----MIQADTPR 96  
DB 68 TSYDLSMNNI SOLPLNPUPSURFLEELFAGNALSNTLELFDNWLTVPSGAFYLSK 127  
QY 97 H-----LHEVLQLGNSIRQIEVGAFNGLASLNTLELFDNWLTVPSGAFYLSK 148  
DB 128 HYPEALQNLRSLSQSLRDANHSYVPPSCFSGLSLRHLWDDNALTEIPVQAFRESLSA 187  
QY 149 LRELWRNPPIESIPSYANRVPSLWRDLGLKKLEYISGAFEGFLPNLYKLANLGMCN 208  
DB 149 LRELWRNPPIESIPSYANRVPSLWRDLGLKKLEYISGAFEGFLPNLYKLANLGMCN 208



Db 188 LOAMTALNKXIHHPDYAFGNLSLVLHLHN-NRIHSIGKKCFDGLHSLTLDLNNYL 246  
 Qy 209 KMPN-LPIVGLBLENSGNFPEIRPGSHGLSSLKLLWVMSQVSLIERNAD---- 263  
 Db 247 DEFFPAITRLNKLGHSHNNIRSIPEKAFVGNPSLITTHFYDNPLOFVGRGAFQHLPE 306  
 Qy 264 -----GLASIVELNLAHNNLSLPHDLFTPLRYLVLHHLHHPNWC 304  
 Db 307 LRTEFLNGASQITTEPDTGTANLESULTCAQISLSPQVTCNQLPNQLVLDLSYN--- 362  
 Qy 305 DCDILNLAWLREVITYPTNSTCGRCHAPMHRGRLVVEVDQSCAPIMDAPROLNI 364  
 Db 363 -----LLEDLPFSVC--QKLOKIDURHNEIYEIKVDTFQ-----QLLSRLSLNL 405  
 Qy 365 SEGRMA 370  
 Db 406 ANWKIA 411.

RESULT 22  
 decorin precursor - bovine  
 N:Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text\_change 20-Aug-1999  
 C:Accession: S06280; B31430; A26545; A20935  
 R:Day, A.A.; McQuillan, C.I.; Termini, J.D.; Young, M.R.  
 B:Chem. J. 248, 801-805, 1987  
 A:Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan II c  
 A:Reference number: S06280; MUID:80133946; PMID:3435485  
 A:Accession: S06280  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <DAY>  
 A:Cross-references: EMBL:Y00712; NID:9618; PIDN:CAAG8702.1; PID:9619  
 A:Experimental source: bone  
 R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.  
 J. Biol. Chem. 264, 2876-2884, 1989  
 A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, fro  
 A:Reference number: A31430; MUID:89123388; PMID:2914936  
 A:Accession: B31430  
 A:Molecule type: protein  
 A:Residues: 31-33, X', 35-54 <CHO>  
 A:Experimental source: cartilage; fetal skin  
 R:Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.  
 J. Biol. Chem. 262, 3809-3812, 1987  
 A:Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship to b  
 A:Reference number: A26545; MUID:87137687; PMID:3818667  
 A:Accession: A26545  
 A:Molecule type: protein  
 A:Residues: 31-50 <COS>  
 A:Experimental source: sclera  
 R:Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.  
 J. Biol. Chem. 258, 15101-15104, 1983  
 A:Reference number: A20935; MUID:84087911; PMID:6654908  
 A:Accession: A20935  
 A:Molecule type: protein  
 A:Residues: 31-54 <PEA>  
 A:Experimental source: skin  
 R:Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.  
 Biochem. J. 232, 277-279, 1985  
 A:Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulphate  
 nes around glycosylation sites in different proteoglycans.  
 A:Reference number: A4700; MUID:86103195; PMID:3936484  
 A:Contents: annotation; glycosylation  
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
 F:1-15/Domain: signal sequence #status predicted <PRO>  
 F:16-30/Domain: propeptide #status predicted <PRO>  
 F:31-360/Product: decorin #status predicted <NAT>  
 F:49-73/Domain: proteoglycan amino-terminal homology <PAH>  
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:223-245/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:309-360/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:334/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
 F:190-326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
 F:212,263,304/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.7%; Score 298; DB 2; Length 360;  
 Best Local Similarity 30.1%; Pred. No. 2.6e-12;  
 Matches 84; Conservative 49; Mismatches 12; Indels 24; Gaps 7;

Qy 38 AASAGPQN-----CPSCVSCSNQFQKVVCTRRGLSEVPQGPSPNRYLNLM 83  
 Db 33 ASGIGPEHPFVPEIPEPMGVCFPRQC--HLRVVQCSDLGLEKVPKDLPPDTALLDLQ 90  
 Qy 84 ENNIQMIQADTFRHLHLHLEVLQGRNSIRQIEVCAPNGLASLNTLELFDNHLTVIPSGAF 143  
 Db 91 NKKITEIKDGFKNLKNLHTLILNNKISKISPGAPAPLVKLERLYLSKNQKELP---- 146  
 Qy 144 EYLSK-LRELRLNNPIESIPSYAFNRVPSLMRLDLG-ELKKLEYISGGAPEGLFNLYL 201  
 Db 147 EKPKTLQELAVHENEITKVKSVFNGLNQMIIVELGTNPKSSGIENGAFQGMKLSYI 206  
 Qy 202 NMGCMNKDMNLTPLVQLELEMSGHFFPEIRPGSHGLSSLKLLWVMSQVSLIERN 261  
 Db 207 RIADTNITTIPOGLP-FSLTEHLDCGKTKTKVDAASLKLNLAKGLSFNSISAVDNGS 265  
 Qy 262 PDGLASLVELNLAHNNLSLPHDLFTPLRYLVLHHLHNN 300  
 Db 266 LANTHLRELHNNLAKVPGCV-ADHKYIQVYVLENN 303

RESULT 23  
 I47020  
 decorin - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 20-Aug-1999  
 C:Accession: I47020  
 R:Zhan, Q.; Burrows, R.; Cintron, C.  
 Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995  
 A:Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.  
 A:Reference number: I47020; MUID:95122319; PMID:7822148  
 A:Accession: I47020  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <ZHA>  
 A:Cross-references: GB:S76584; NID:913374; PIDN:AAB33083.1; PID:9913375  
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:223-245/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 8.5%; Score 293.5; DB 2; Length 360;  
 Best Local Similarity 32.2%; Pred. No. 5.3e-13;  
 Matches 84; Conservative 44; Mismatches 122; Indels 11; Gaps 7;

Qy 42 GPQNCPSVSCSNQFQKVVCTRRGLSEVPQGPSPNRYLNLMENNIOIQAQTFRHLHL 101  
 Db 52 GPV-CFFRCQC--HLRVVQCSDLGLEKVPKDLPPDTLLDLQNNKITEIKDGFANLNL 108

Y 102 EVLQGRNSIRQIEVGAFNGLASLNTLEFDNMLTVIPSGAFYLSK-LRELWLRNNPTE 160  
b 109 HALILVNNKLSKISPGAFPLVLERLYLSKXHLKELP-...EKWPKSQELRAHENEIT 164  
Y 161 SIFSYPANRVPVSLMRLDLG-ELKKLEYISEGAFEGFLNLYNLGNMCNKDKMPNITPLVG 219  
b 165 KVRKSVFSGNMQIVIELGTNPVLSKSGIENGAFQGMKKLSYIRIADTNTITITPQGLP-PS 223  
Y 220 LBELEMSGNHFFPIRPGSPHGLSSLLKLLWMNSQVSLIERNAPFDGLASIVELNLAHNL 279  
b 224 LTELHLDGNKIKIDASSLKLNNLAKLGLSFNDISAVDNGSLANAPHLRELHLDNKL 283  
Y 280 SLPHDLFTPLRYLVVELLHNN 300  
b 284 RVPQGL-ADHKYIQVVYLHNN 303  
RESULT 24  
24317  
ecorin precursor - chicken  
;Alternate names: corneal chondroitin/dermatan sulfate proteoglycan  
;Species: Gallus gallus (chicken)  
;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 20-Aug-1999  
;Accession: S24317, S58474, S22197  
;Ref: Li, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.  
rch. Biochem. Biophys. 296, 190-197, 1992  
;Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals  
;Reference number: S24317; MUID:92296755; PMID:1605630  
;Accession: S24317  
;Molecule type: mRNA  
;Residues: 1-357 <LIW>  
;Cross-references: EMBL:X63797; NID:G62887; PIDN:CAA45318.1; PID:G62888  
;Accession: S58474  
;Molecule type: protein  
;Residues: 31-33, 'X', 35-39, 'X', 41-48, 'X', 50-51 <LIA>  
;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
;Keywords: Collagen binding; extracellular matrix; glycoprotein  
;1-16/Domain: signal sequence #status predicted <SIG>  
;17-30/Domain: propeptide #status experimental <PRO>  
;31-357/Product: decorin #status experimental <MAT>  
;46-70/Domain: proteoglycan amino-terminal homology <PAH>  
;80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
;128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
;199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
;220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
;244-267/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
;268-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
;291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
;306-357/Domain: proteoglycan carboxyl-terminal homology <PCH>  
Query Match 8.4%; Score 287.5; DB 2; Length 357;  
Best Local Similarity 32.2%; Pred. No. 1.4e-12;  
Matches 84; Conservative 43; Mismatches 123; Indels 11; Gaps 7;  
Y 42 GPQNCPSVCSNQPSKVCTRGSLSPVQGISNRYNLNLMNNIQLQADTFRHLL 101  
b 49 GPV-CPPRCQC--HLRVQCSDLGLRVPKDXPDFTLLDQNNKITEKSGDFNKL 105  
Y 102 EVLQGRNSIRQIEVGAFNGLASLNTLEFDNMLTVIPSGAFYLSK-LRELWLRNNPTE 160  
b 106 HALILVNNKLSKISPAFAFLKLERLYLSKXHLKELP-...ENWPKSQELRAHENEIT 161  
Y 161 SIFSYPANRVPVSLMRLDLG-ELKKLEYISEGAFEGFLNLYNLGNMCNKDKMPNITPLVG 219  
b 162 KLRXAVENGLNQIVIELGTNPVLSKSGIENGAFQGMKKLSYIRIADTNTITPQGLP-PS 220  
Y 220 LBELEMSGNHFFPIRPGSPHGLSSLLKLLWMNSQVSLIERNAPFDGLASIVELNLAHNL 279  
b 221 LTELHLDGNKISKIDAGLSGLNTLAKLGLSFNSISSVNGSLNNVPHLRELHLDN 280

Qy 280 SLPHDLFTPLRYLVVELLHNN 300  
Db 281 RVPQGL-GEHKYIQVVYLHNN 300  
RESULT 25  
259145  
decorin precursor - rat  
;Alternate names: dermatan sulfate proteoglycan-II  
;Species: Rattus norvegicus (Norway rat)  
;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 20-Aug-1999  
;Accession: S29145; I60238; S28517  
;Ref: Abramson, S.R.; Woessner Jr., J.F.  
Biochim. Biophys. Acta 1132, 225-227, 1992  
;Title: cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).  
;Reference number: S29145; MUID:93003331; PMID:1390895  
;Accession: S29145  
;Status: preliminary  
;Molecule type: mRNA  
;Residues: 1-354 <ABR>  
;Cross-references: EMBL:Z12298; NID:G57549; PIDN:CAA78170.1; PID:G57550  
;Ref: Asundi, V.K.; Dreher, K.L.  
Eur. J. Cell Biol. 59, 314-321, 1992  
;Title: Molecular characterization of vascular smooth muscle decorin: deduced core prot  
;Reference number: I60238; MUID:93154359; PMID:1493796  
;Accession: I60238  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: mRNA  
;Residues: 11-354 <RES>  
;Cross-references: EMBL:X59859; NID:G56056; PIDN:CAA42519.1; PID:G56057  
;Genetics: DCN  
;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
;Keywords: collagen binding; extracellular matrix; glycoprotein  
;F1-354/Product: decorin #status predicted <MAT>  
;F43-67/Domain: proteoglycan amino-terminal homology <PAH>  
;F77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
;F101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
;F125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
;F146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
;F170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
;F196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
;F217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
;F241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
;F265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
;F288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
;F303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>  
Query Match 8.3%; Score 286.5; DB 2; Length 354;  
Best Local Similarity 31.3%; Pred. No. 1.6e-12;  
Matches 83; Conservative 44; Mismatches 123; Indels 15; Gaps 7;  
Qy 43 PQN-----CPSCVCSNQPSKVCTRGSLSPVQGISNRYNLNLMNNIQLQADTFRH 97  
Db 41 PDNPLTSMCPYRCQC--HLRVQCSDLGLRVPKDXPDFTLLDQNNKITEKSGAFKN 98  
Qy 98 LHELEVLQGRNSIRQIEVGAFNGLASLNTLEFDNMLTVIPSGAFYLSK-LRELWLRNN 156  
Db 99 LKDLHTLILVNNKLSKISPAFAFLKLERLYLSKXHLKELP-...EKLPTKLQELRLHD 154  
Qy 157 NPSTPSYAFNRPVSLMRLDLG-ELKKLEYISEGAFEGFLNLYNLGNMCNKDKMPNIT 215  
Db 155 NEITKLKSVFNGLNRMIVIELGTNPVLSKSGIENGAFQGMKKLSYIRIADTNTITPQGL 214  
Qy 216 PLVGLBELEMSGNHFFPIRPGSPHGLSSLLKLLWMNSQVSLIERNAPFDGLASIVELNLAH 275  
Db 215 P-TSISELHLDGNKIKAVDASLKGNSLKLGLSFNSITVVENGLANVPHLRELHLDN 273  
Qy 276 NNLSLSPHDLFTPLRYLVVELLHNN 300  
Db 274 NKLLRVPAGL-AQHKYIQVVYLHNN 297

RESULT 26

A55454  
 A:Accession: A55454  
 A:Title: The mouse decolin. Complete cDNA cloning, genomic organization, chromosomal as  
 A:Reference number: A55454; MUID:95050610; PMID:7961765  
 A:Accession: A55454  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <SCH>  
 A:Cross-references: GB:X53668; PIDN:CRAA37876.1; PID:G53669  
 A:Naitoh, Y.; Suzuki, S.  
 submitted to the EMBL Data Library, July 1990  
 A:Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGII.  
 A:Reference number: S20811  
 A:Accession: S20812  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <NAI>  
 A:Cross-references: EMBL:X53668; PIDN:CRAA37876.1; PID:G53669  
 A:Superfamily: decolin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
 C:Keywords: collagen binding; extracellular matrix; glycoprotein  
 F:1-16/Domain: signal sequence #status predicted <Sig>  
 F:17-30/Domain: propeptide #status predicted <Pro>  
 F:43-67/Domain: proteoglycan amino-terminal homology <PAH>  
 F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
 F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 8.1%; Score 279.5; DB 2; Length 354;  
 Best Local Similarity 30.7%; Pred. No. 5e-12;  
 Matches 81; Conservative 45; Mismatches 125; Indels 13; Gaps 6;  
 QY 43 PON-----CPVCSGCSNQSFKVCTRRGLSEVPQGISFNTRYLNLMENNIMQIQADTPRH 97  
 DB 41 PDNPLISMCPYRCQC--HLRVVQCSGLGDKVPWDFPDPTLLDLQNNKITEIKGAFKN 98  
 QY 98 LHLLEVLQGRNSIQIEVGAFNGLASLNTLELFDNNLTVIPSGAFYLSKLRRLMNN 157  
 DB 99 LKDLHTLLVNNKISKISPEAFKPLVKLERLYLSKNQLKSLPE---KMPPTLOELRVHEN 155  
 QY 158 PIESTPSVAENRVPSLMDL-GEKKLEYISGAFGLFNKLYNLGCMCNKIDMENLTP 216  
 DB 156 EITKLRKSDFNGLNNVLVIELGNNPLKNGIENGAFQGLKSLSYIRISDNTNIAIPQGLP 215  
 QY 217 LNLGLEELSGNHPPIRPSFGHLSLKLKLVNNSOVSLIERNAPDGLASLVELMLAEN 276  
 DB 216 -TSLTEVHLDGNTKTVDPAPLSKGLNLSKLGISFNITWNGSLANVPHLRHLDDNN 274  
 QY 277 NLSSLPDLPFTPLRYLVHLLHNN 300  
 DB 275 KLLRVPAGL-AQHKYIQVYVLLHN 297

RESULT 27

T13852  
 A:Accession: T13852  
 A:Title: gene wheeler protein - fruit fly (Drosophila melanogaster)  
 A:Reference number: T13852  
 A:Accession: T13852  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-536 <TAN>  
 A:Cross-references: GB:J05158; NID:gl79935; PIDN:AAA51921.1; PID:gl79936  
 C:Genetics:  
 A:Gene: GDB:ACBP  
 A:Cross-references: GDB:127893  
 A:Map position: eq25.3-6q26  
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
 C:Keywords: hydrolase; metallo-carboxypeptidase

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000

A:Accession: T13852  
 R:Eldon, E.; Kooyer, S.; D'aveilyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.  
 Development 120, 885-899, 1994  
 A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking similitude  
 A:Reference number: T13852; MUID:95324375; PMID:7600965  
 A:Accession: T13852  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1389 <ELD>  
 A:Cross-references: EMBL:L23171; NID:gl415682; PID:gl019104; PIDN:AAA79208.1  
 C:Genetics:  
 A:Gene: wheeler  
 A:Cross-references: FlyBase:FBgn0004364

Query Match 7.8%; Score 268.5; DB 2; Length 1389;  
 Best Local Similarity 24.3%; Pred. No. 1.9e-10;  
 Matches 103; Conservative 62; Mismatches 161; Indels 97; Gaps 11;  
 QY 80 LNLNENNIQIADTFERHLHLEVLQGRNSIQIEVGAFNGLASLNTLELFDNNLTVIP 139  
 DB 338 LNLNENNIQIADTFERHLHLEVLQGRNSIQIEVGAFNGLASLNTLELFDNNLTVIP 139  
 QY 140 SGAPEYLSKLRRLMNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISGAFGLFNK 199  
 DB 398 NRIFNGLVLTCLTLNNLVSVESQAFRCNSDLKELDLSS-NQLTEVPE-AVQDLMLK 455  
 QY 200 VNLGCMNIXDMP-----NLTPLVGLLEELSGNHPPIRPSFGHLSLKLKLVNNSOV 254  
 DB 456 TLDLGENQISFKNNTFRNLNQLTGLRLD---NRIGNITVGHFQDLPLRSLVNLAKNRI 512  
 QY 255 SLIERNAFDGLASLVELMLAHNNLSLPHDLFTPLRYLVHLLHNNPNCDDILMAW 314  
 DB 513 QSIKRGAPDKNTEIARLDKCNFLTDI-NGIFATLASLLMLNSEN-----HLVMP 562  
 QY 315 LREVIPTNSTCCGCHAPMGRGYLVEVQASQCSAPFIMDAPRLNISEGMAELKC 374  
 DB 563 DYAFIPSN----- 570  
 QY 375 RTPPMSSVKWLLPNGTVLSHARHPRI-SVLNGLTNFNSHVLSDTGVYTC-----M 425  
 DB 571 -----LKWLDHSGNYEALGNYVKLQEEIRVTVTLDSHNRIEIGAMSVPSIELLFI 623  
 QY 426 VTNVAGNSNAYLN---VSTAEIANTSNYSFPTTVVETTEISPEITRKYKVPPTSTG 482  
 DB 624 NNNIIGQIQANTFVDKTRARVDLYANVLSKISLNALRVAPVSAE-----KPVPEPYLG 677  
 QY 483 YQP 485  
 DB 678 GNP 680

RESULT 28

A34901  
 A:Accession: A34901  
 A:Title: lysine carboxypeptidase (EC 3.4.17.3) 83K chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 05-Nov-1999  
 C:Accession: A34901  
 R:Tan, F.; Weerasinghe, D.K.; Skidgel, R.A.; Tamei, H.; Kaul, R.K.; Roninson, I.B.; Schi  
 J. Biol. Chem. 265, 13-19, 1990  
 A:Title: The deduced protein sequence of the human carboxypeptidase N high molecular wei  
 A:Reference number: A34901; MUID:90094386; PMID:2378615  
 A:Accession: A34901  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-536 <TAN>  
 A:Cross-references: GB:J05158; NID:gl79935; PIDN:AAA51921.1; PID:gl79936  
 C:Genetics:  
 A:Gene: GDB:ACBP  
 A:Cross-references: GDB:127893  
 A:Map position: eq25.3-6q26  
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
 C:Keywords: hydrolase; metallo-carboxypeptidase

[illegible]

Query Match 7.6%; Score 262.5; DB 2; Length 369;  
Best Local Similarity 31.9%; Pred. No. 8.2e-11;  
Matches 82; Conservative 40; Mismatches 124; Indels 11; Gaps 7;  
QY 46 CPSVCSNQSKVYCTRRGLSEVPGQIPSNRYLNLMENNIMQIADTFRLHLEVLQ 105  
Db 64 CPGCHC--HLRVVQCSDLGLKTVKPEISPDITLDDQNNDISELRKDDPKGLQHLVALV 121  
QY 106 LGRNSIRQIEVGAFNGLASLNTLELFDNMLTVIPSGAFEYLSKLRELWLNPNPIPSY 165  
Db 122 LVNNKISKIHEKAFSPRLKOKLYISKHLVEIPP--NLPSSSLVELRIHDNRIRKVPKG 178  
QY 166 AFNRPVSLARLDLGLKLEY--ISEGAFEGFLKYLKYNLMCMNKMDPNLTPVLGUEL 223  
Db 179 VFSGLRNWNCIEMGG-NPLENSGFPGAFDGL-KLNYLRISSEAKLTGTPKDLPET-LNEL 235  
QY 224 ENSGNHFEIRPGSPHGLSSLLKLVWMSOVSLEARNAFDGLASIVELNLAHNNLSLPH 283  
Db 236 HLDHNKIQAIIELEDLLRYSKYLRGLGHQIRMIENGSLSPFLTIRELHLDNKLKSRVPA 295  
QY 284 DLFTPLRYLVELHLHNN 300  
Db 296 GL-PDLKLVVYVLSN 311  
RESULT 32  
S32793  
biglycan precursor - rat  
N;Alternate names: dermatan sulfate proteoglycan I (DS-PG1); proteoglycan I core protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
C;Accession: S32793  
R;Dröher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.  
A;Title: Vascular smooth muscle biglycan represents a highly conserved proteoglycan with  
A;Reference number: S32793; MUID:91184222; PMID:2081545  
A;Accession: S32793  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-369 <DRE>  
A;Cross-references: GB:U17834; NID:G600497; PIDN:AAA58797.1; PID:G600498  
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C;Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; extracellular matrix; 9  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-37/Domain: propeptide #status predicted <PRO>  
F;38-369/Product: biglycan #status predicted <MAT>  
F;58-82/Domain: proteoglycan amino-terminal homology <PAH>  
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LI  
F;317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F;42,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F;271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 262.5; DB 2; Length 369;  
Best Local Similarity 31.9%; Pred. No. 8.2e-11;  
Matches 82; Conservative 40; Mismatches 124; Indels 11; Gaps 7;  
QY 46 CPSVCSNQSKVYCTRRGLSEVPGQIPSNRYLNLMENNIMQIADTFRLHLEVLQ 105  
Db 64 CPGCHC--HLRVVQCSDLGLKTVKPEISPDITLDDQNNDISELRKDDPKGLQHLVALV 121  
QY 106 LGRNSIRQIEVGAFNGLASLNTLELFDNMLTVIPSGAFEYLSKLRELWLNPNPIPSY 165  
Db 122 LVNNKISKIHEKAFSPRLKOKLYISKHLVEIPP--NLPSSSLVELRIHDNRIRKVPKG 178  
QY 166 AFNRPVSLARLDLGLKLEY--ISEGAFEGFLKYLKYNLMCMNKMDPNLTPVLGUEL 223  
Db 179 VFSGLRNWNCIEMGG-NPLENSGFPGAFDGL-KLNYLRISSEAKLTGTPKDLPET-LNEL 235  
QY 224 ENSGNHFEIRPGSPHGLSSLLKLVWMSOVSLEARNAFDGLASIVELNLAHNNLSLPH 283  
Db 236 HLDHNKIQAIIELEDLLRYSKYLRGLGHQIRMIENGSLSPFLTIRELHLDNKLKSRVPA 295  
QY 284 DLFTPLRYLVELHLHNN 300  
Db 296 GL-PDLKLVVYVLSN 311  
RESULT 32  
S32793  
biglycan precursor - rat  
N;Alternate names: dermatan sulfate proteoglycan I (DS-PG1); proteoglycan I core protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
C;Accession: S32793  
R;Dröher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.  
A;Title: Vascular smooth muscle biglycan represents a highly conserved proteoglycan with  
A;Reference number: S32793; MUID:91184222; PMID:2081545  
A;Accession: S32793  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-369 <DRE>  
A;Cross-references: GB:U17834; NID:G600497; PIDN:AAA58797.1; PID:G600498  
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C;Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; extracellular matrix; 9  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-37/Domain: propeptide #status predicted <PRO>  
F;38-369/Product: biglycan #status predicted <MAT>  
F;58-82/Domain: proteoglycan amino-terminal homology <PAH>  
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LI  
F;317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F;42,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F;271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Y 166 AFNRVSLKRLDGLGKLEY--ISGAFEGFLNLYLNGMNCNIDKPNLTPVGLREL 223  
b 179 VFSGLENNMCIEGG-NPLENGFEGAFDGL-KNLYLSISAKUTGPKOLFET-LNEL 235  
Y 224 EMSGNFPPRPGSPHGLSLKLMWNSQVSLIERNAPDGLASIVELNLAHNNLSLPH 283  
b 236 HLDENKIQALEDLARYSKVLGGLGHQIRMIENGSLSFPTREHLHNNKLSRYP 295  
Y 284 DLFTPLRYLVELHLHN 300  
b 296 GL-PDLKLLQVVYLSN 311  
  
**RESULT 33**  
1938  
Ypothetical protein C44H4.2 - *Caenorhabditis elegans*  
;Species: *Caenorhabditis elegans*  
;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
;Accession: T1938  
;Smye, R.  
;Submitted to the EMBL Data Library, August 1996  
;Reference number: Z19200  
;Accession: T1938  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: DNA  
;Residues: 1-738 <WIL>  
;Cross-references: EMBL:Z79598; PIDN:CAB01864.1; GSPDB:GN00028; CESP:C44H4.2  
;Experimental source: clone C44H4  
;Genetics:  
;Gene: CESP:C44H4.2  
;Map position: X  
;Introns: 30/3; 89/3; 125/3; 168/1; 327/3; 453/3; 524/3; 612/2; 680/2  
  
Query Match 7.6%; Score 262.5; DB 2; Length 738;  
Best Local Similarity 23.4%; Pred. No. 2.1e-10;  
Matches 141; Conservative 79; Mismatches 232; Indels 151; Gaps 22;  
  
Y 71 QGIPSTRYLNLMENNIOIADTFRHLHELEVLQGRNIRQIVGAFNGLASLNTL 130  
b 145 QNVKSIQITNLGHNNNTAVPSSAIRGLQQLSLHKNRIEQLDALNPLNPLVNL 204  
Y 131 FDNWLTVPISGAPEYLSKRLWLRNPIETSPVAFNRVPSLMRLDGLGKLEYSEG 190  
b 205 AGNOIHELNRQAPNVPISRYLYLSGNKTKTAVQVQTFQLEMLDITN-NEIGAI 263  
Y 191 AFEGFLNLYLNGMNCNIDK-PNLFPLVLELEMSGNHFFPIRPGSFHGLSLKLV 249  
b 264 SLSELQALQLYLAHKNISNNAFTNSSIVVVLSSNELKTLTAGIISGLPNLQV 323  
Y 250 MNSQVSLIERNAPDGLASIVELNLAHNNLSLPHDLFTPLRYLVELH- 296  
b 324 RENQIKTINRNFADYDAASLVMLDLAKXQLTEI-----APTFLAQNLNLLV 378  
Y 297 -----LHNPWNCDDILMAWMLREYI-PTNSTCCGR----- 328  
b 379 TPYSAFNSRVGTLLKENFLVCTENLHMLQOQGVYVRDSPDIIICGRPTKPEV 438  
Y 329 -----CHAPMH-MGRVLYVEVDQASFQ-----CSAP-----FI 355  
b 439 VTDSLSTQRPALVQIPKQIHRNVHTTGDQAPQIPSGAFQOQDLGKRSILPRG 498  
Y 356 MDAPRLNINSEGRMAELKCRTPMSSVKVLLNGTVLSHSHRPRI--SVLNDGTL 413  
b 499 LDKPSTREQSVEFTEL---TPIQI---ILP-----SREDIRQSSWEAGT---SQ 541  
Y 414 VLLSDTGVTCTMVTNAGNSASAYLNVSTABLNTSNYSFFTTVTVETETISPE 473  
b 542 ESVEATSKIPSTTDIDRPNVVLPPVPFLKRGPP--NLSESKVVESTD----- 588  
Y 474 KPVPTSTGQPAYTSTTVLIQCTVPKQVAPADTTDK-----M 515  
b 589 --NPSTS--QVZHTLPLPSILIEPGSTPK-VAQPSSTEAINKSEHIDFALASSN 642

QY 516 QTSLEDEWMTKTI--IGCFVAVTLAAAMLVVFLYKLRHQO-----RSTVTAARTV 566  
Db 643 QPRLKSFFTTIIIFICVGTAVILVWVIAGLCI-----SKRQLQFENTYSDSSAARTS 697  
  
QY 567 EII 569  
Db 698 EYI 700  
  
**RESULT 34**  
BGHUN  
biglycan precursor - human  
N:Alternate names: cartilage proteoglycan I; dermatan sulfate proteoglycan I (DS-PGI); p  
C:Species: Homo sapiens (man)  
C:Date: 21-Apr-1992 #sequence\_revision 26-May-1995 #text\_change 28-Jan-2000  
C:Accession: A40757; I38706; A32458; S14349; S05639; A28457  
R:Fisher, L.W.; Heegaard, A.M.; Vetter, U.; Vogel, W.; Just, W.; Termine, J.D.; Young, M.  
J. Biol. Chem. 266, 14371-14377, 1991  
A:Title: Human biglycan gene. Putative promoter, intron-exon junctions, and chromosomal  
A:Reference number: A40757; MUID:91317791; PMID:1860845  
A:Accession: A40757  
A:Molecule type: DNA  
A:Residues: 1-368 <FIS1>  
A:Cross-references: GB:M65151; NID:gl79428; GB:M65152; NID:gl79429; GB:M65153; NID:gl794  
A:Note: The translated sequence in Genbank entry HUMBGN3, release 113.0, (PIDN:AAA52287;  
d not the DNA) and 26 residues inserted after residue 80 (apparently from a misread sp1  
R:Just, W.; Rau, W.; Muller, R.; Gearkens, C.; Vogel, W.  
Hum. Mol. Genet. 3, 2268, 1994  
A:Title: Dinucleotide repeat polymorphism at the human biglycan (BGN) locus.  
A:Reference number: I38706; MUID:95187185; PMID:7881444  
A:Accession: I38706  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 361-368 <JUS>  
A:Cross-references: EMBL:U11686; NID:g607862; PIDN:AAC50117.1; PID:g619663  
R:Fisher, L.W.; Termine, J.D.; Young, M.F.  
J. Biol. Chem. 264, 4571-4576, 1989  
A:Title: Deduced protein sequence of bone small proteoglycan I (Biglycan) shows homology  
A:Reference number: A32458; MUID:89174714; PMID:2647739  
A:Accession: A32458  
A:Molecule type: mRNA  
A:Residues: 1-138, 'DV', 141-162, 'DV', 165-368 <FIS2>  
A:Cross-references: GB:J04599; NID:gl84339  
A:Note: Parts of this sequence, including the amino end of the mature protein, were dete  
R:Stoecker, J.; Meyer, H.E.; Wagener, C.; Greiling, H.  
Biochem. J. 274, 415-420, 1991  
A:Title: Purification and N-terminal amino acid sequence of a chondroitin sulphate/derma  
A:Reference number: S14349; MUID:91174749; PMID:1848758  
A:Accession: S14349  
A:Molecule type: protein  
A:Residues: 38-57 <STO>  
A:Experimental source: aorta  
R:Roughley, P.J.; White, R.J.  
Biochem. J. 262, 823-827, 1989  
A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of  
A:Reference number: S05639; MUID:90073579; PMID:2590169  
A:Accession: S05639  
A:Molecule type: protein  
A:Residues: 38-41, 'X', 43-46, 'X', 48-57 <ROU>  
R:Fisher, L.W.; Hawkins, G.R.; Turose, N.; Termine, J.D.  
J. Biol. Chem. 262, 9702-9708, 1987  
A:Title: Purification and partial characterization of small proteoglycans I and II. bone  
A:Reference number: A92656; MUID:87250639; PMID:3597437  
A:Accession: A28457  
A:Molecule type: protein  
A:Residues: 38-41, 'X', 43-62, 'X', 64-66 <FIS3>  
A:Experimental source: bone  
C:Genetics:  
A:Gene: GDB:BGN  
A:Cross-references: GDB:119727; OMIM:301870  
A:Map position: Xq28-Xq28  
A:Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3



C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C:Keywords: chondroitin sulfate proteoglycan, dermatan sulfate; duplication; extracellular  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-37/Domain: propeptide #status predicted <PRO>  
F:38-369/Product: biglycan #status predicted <MAR>  
F:57-81/Domain: proteoglycan amino-terminal homology <PAH>  
F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:115-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:139-159/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:184-207/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:209-229/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:230-253/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:254-277/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:301-315/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR  
F:316-369/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F:42,47/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F:180,198/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F:270,311/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 261.5; DB 1; Length 369;  
Best Local Similarity 31.5%; Pred. No. 9.6e-11;  
Matches 81; Conservative 41; Mismatches 124; Indels 11; Gaps 7;

QY 46 CPSVCSNQSKVCTRGSLSEVPGIPSNTRYLNLMENNIQMIQADTFRLHLEVLQ 105  
DB 63 CPFGCHC-HLRVQCSDGLKAVPKISPTTLQNDISELRKDDFKGLQHLVALV 120  
QY 106 LGRNSIRQIEVGAFNGLASINTLEFDNWLTVIPSGAFYLSKRELWLRNPIESPSY 165  
DB 121 LVNKKISKIHEKAFSPRLKQLYISKHLEVIP--NLPSLVELRIHNRIRKVPKG 177  
QY 166 AFNRVPSLMRLDGLGELKLEY--ISEGAFEGFLNKLNGMCNKDMNPITLVGLLEL 223  
DB 178 VFGSLGNMNCIEMGG-NPLENGSGFPGADGL-KENYLRISEAKLTGPKLPET-LNEL 234  
QY 224 EMSGNHFPPIRPGSPFGLSSLLKLVWMSQVSLIERNAFDGLASIVELNHNLSLPH 283  
DB 235 HLDHNKIQALEEDLLRYSKLYGLGHNQIRMIENGSLPFLTRELHLDNNKLSRVP 294  
QY 284 DLFTPLRYLVELLHN 300  
DB 295 GL-PDLKLLQVYVLTN 310

RESULT 35  
S32559  
biglycan precursor - bovine  
N:Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin core prot  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 03-May-1994 #sequence revision 20-Feb-1995 #text change 07-May-1999  
C:Accession: S32559; S34229; A33701; A31430; FT0078; S55673; A33337  
R:Torok, M.A.; Evans, S.A.S.; Marcum, J.A.  
Biochim. Biophys. Acta 1173, 81-84, 1993  
A:Title: cDNA sequence for bovine biglycan (PGI) protein core.  
A:Reference number: S32559; MUID:93250052; PMID:8485158  
A:Accession: S32559  
A:Molecule type: mRNA  
A:Residues: 1-369 <TOR>  
A:Cross-references: EMBL:L07953; NID:g162746  
A:Experimental source: aortic smooth muscle  
R:Marcum, J.A.; Torok, M.; Evans, S.  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S34229  
A:Accession: S34229  
A:Molecule type: mRNA  
A:Residues: 1-250, 'V', 252-369 <MAR>  
A:Cross-references: EMBL:L07953  
R:Neame, P.J.; Choi, H.U.; Rosenberg, L.C.  
J. Biol. Chem. 264, 8653-8661, 1989  
A:Title: The primary structure of the core protein of the small, leucine-rich proteoglyc  
A:Reference number: A33701; MUID:89255324; PMID:2656687

A:Accession: A33701  
A:Molecule type: protein  
A:Residues: 35-187, 'E', 189-367, 'Y' <NEA>  
A:Experimental source: cartilage  
R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.  
J. Biol. Chem. 264, 2876-2884, 1989  
A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, fr  
A:Reference number: A31430; MUID:89123388; PMID:2914936  
A:Accession: A31430  
A:Molecule type: protein  
A:Residues: 38-41, 'X', 43-47, 'X', 49-63 <CHO>  
A>Note: sequences from skin and cartilage were identical  
R:Marcum, J.A.; Thompson, M.A.  
Biochem. Biophys. Res. Commun. 175, 706-712, 1991  
A:Title: The amino-terminal region of a proteochondroitin core protein, secreted by aor  
om human bone.  
A:Reference number: PT0077; MUID:91207372; PMID:2018513  
A:Accession: PT0078  
A:Molecule type: protein  
A:Residues: 17-24, 'F', 26-30 <MA2>  
A:Experimental source: aortic smooth muscle  
R:Scott, P.G.; Nakano, T.; Dodd, C.M.  
Biochim. Biophys. Acta 1244, 121-128, 1995  
A:Title: Small proteoglycans from different regions of the fibrocartilaginous temporoma:  
A:Reference number: S55673; MUID:95284073; PMID:7766647  
A:Accession: S55673  
A:Molecule type: protein  
A:Residues: 38-41, 'X', 43-47, 'X', 49-53 <SCO>  
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan  
C:Keywords: cartilage; chondroitin sulfate proteoglycan; dermatan sulfate; extracellular  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-37/Domain: amino-terminal propeptide #status predicted <PRO>  
F:38-369/Product: biglycan #status predicted <MAR>  
F:58-82/Domain: proteoglycan amino-terminal homology <PAH>  
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LI  
F:317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>  
F:42,48/Binding site: dermatan sulfate (Ser) (covalent) #status experimental  
F:181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  
F:271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 261.5; DB 2; Length 369;  
Best Local Similarity 31.9%; Pred. No. 9.6e-11;  
Matches 82; Conservative 40; Mismatches 124; Indels 11; Gaps 7;

QY 46 CPSVCSNQSKVCTRGSLSEVPGIPSNTRYLNLMENNIQMIQADTFRLHLEVLQ 105  
DB 64 CPFGCHC-HLRVQCSDGLKAVPKISPTTLQNDISELRKDDFKGLQHLVALV 121  
QY 106 LGRNSIRQIEVGAFNGLASINTLEFDNWLTVIPSGAFYLSKRELWLRNPIESPSY 165  
DB 122 LVNKKISKIHEKAFSPRLKQLYISKHLEVIP--NLPSLVELRIHNRIRKVPKG 178  
QY 166 AFNRVPSLMRLDGLGELKLEY--ISEGAFEGFLNKLNGMCNKDMNPITLVGLLEL 223  
DB 179 VFGSLGNMNCIEMGG-NPLENGSGFPGADGL-KENYLRISEAKLTGPKLPET-LNEL 235  
QY 224 EMSGNHFPPIRPGSPFGLSSLLKLVWMSQVSLIERNAFDGLASIVELNHNLSLPH 283  
DB 236 HLDHNKIQALEEDLLRYSKLYGLGHNQIRMIENGSLPFLTRELHLDNNKLSRVP 295  
QY 284 DLFTPLRYLVELLHN 300  
DB 296 GL-PDLKLLQVYVLTN 311



## RESULT 36

T23395  
hypothetical protein K07A12.2 - Caenorhabditis elegans  
;Species: Caenorhabditis elegans  
;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
;Accession: T23395  
;McLay, K.  
submitted to the EMBL Data Library, October 1996  
;Reference number: Z19735  
;Accession: T23395  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: DNA  
;Residues: 1-961 <WIL>  
;Cross-references: EMBL:Z81098; PIDN: CAB031182.1; GSPDB: GN00019; CESP: K07A12.2  
;Experimental source: clone K07A12  
;Genetics:  
;Gene: CESP: K07A12.2  
;Map position: 1  
;Introns: 33/3; 97/3; 137/3; 167/2; 285/3; 325/3; 548/3; 898/2

Query Match 7.5%; Score 256.5; DB 2; Length 961;  
Best Local Similarity 21.8%; Pred. No. 7.8e-10;  
Matches 87; Conservative 63; Mismatches 120; Indels 129; Gaps 11;  
29 WILCAATA---AAASAGPQCPS-----VCSNQFQKVVCTRRGLSEVP- 70  
3 WLTIAVAHLIAFLSSAETCPRIPEKCDCKISKSMILSCNGEDVKTIAQTGTGQIDE 62  
71 -----QGIPSN-TRYLNLMXNNIOMIQADTERHLK-HLEVLQGRNSIROIEVG 117  
63 LHINGTGVKIESLFFNGRLTIALNSTLOSFTSWARHVEATIEHITNGELKTPV- 121  
118 AFNGIASLNTLEFDNMLTVIPSGAFYLSKRLRLMNNPI-----ELKKLWISE- 159  
122 -FGNLSTLMNLSNQISSIPDKAFNGLSALTQLRLNNAICDPPEKSLDAVKASLVLL 180  
160 -----ESIPSYAFNRVPSLMDLIG-----ELKKLWISE- 189  
181 DVSGNCLDAIPAQILRNAANLMDLGSNISEINNFELMNLPHRELVRQNNLTERRHP 240  
190 -----GAFGLFNKLKYL-----GMCNKKDMFNLTF- 217  
241 MAFNVNPOQLVLYQDNIISTLDGNRLQGFNLEVDVSNALVALPSLKLNLQAVRV 300  
218 -----VGLBLESGNHFPFIRPGSPHGLSSLKKLWVNSQVSLIERNA 261  
301 DGNLITKTIETLAFSNNPNLQIISVQNNNIVQISRNFSFSLDKLWLLVAGNNSLAKIERGM 360  
262 FDGLASLVELMLAHNLSLPHDLFTPLRVLVELHLHN 300  
361 PDGKNLQQLSIRNNLTALDASSPAQLAHLTTLDLGN 399

## RESULT 37

T24315  
hypothetical protein T01G9.3 - Caenorhabditis elegans  
;Species: Caenorhabditis elegans  
;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
;Accession: T24315  
submitted to the EMBL Data Library, July 1996  
;Lennard, N.  
;Reference number: Z19874  
;Accession: T24315  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: DNA  
;Residues: 1-603 <WIL>  
;Cross-references: EMBL:T275713; PIDN: CAB00050.1; GSPDB: GN00019; CESP: T01G9.3  
;Experimental source: clone T01G9  
;Genetics:  
;Gene: CESP: T01G9.3  
;Map position: 1  
;Introns: 68/3; 346/1; 407/3; 450/3; 486/3

## Query Match 7.4%; Score 254; DB 2; Length 603;

Best Local Similarity 20.2%; Pred. No. 6.2e-10;  
Matches 128; Conservative 81; Mismatches 188; Indels 238; Gaps 21;  
17 ILDPFVYLTAAQWILCAIAAASAGPQCPSVCS- SNQFSKVWCTRRGL-----SEV 69  
5 ILLFL-----SFLVLCISI-----ALPSSCNLCECDNDSSMSVYCRKAIINDTIYAEI 54  
70 FQGIPTNTRYLNLM-----ENNIQHIQADTER-----HLHLE 102  
55 LNQLPLTLRLSHIOPPSNRIGSNKLRWNNINPAQRVLRLINCOIPAMRSIRLPSLE 114  
103 VLQGRNSIROIEVGAFLASLNTLEFDNMLTVIPSGAFYLSKRLRLMNNPIES 162  
115 VLDLHNSNIEHATNSFGMPKLRVLDLSSNHLNLTPTGVFTYLRALRSLSLGNNTISDL 174  
163 PSYAFNRVPSL--MRDLGELKLEIYSE-----GAFGLFN 197  
175 STNLLRGLNSLRVLRLDRNPI-PIEHINELFTVDSQDLDELVLNHCNLSIYSLALDRIPQ 233  
198 LKYLNLGMCNIKOMP--NLTPLVGLLELEMSGNHFPFIRPGSF-----HGLSSL 244  
234 LRQLGIGGNLKVPTKEKLSLPOLSVLDLSHNSIQEITACAFCTNISKLDLSHNLGI 293  
245 KK-----LWVNSQVSLIERNAFQ----- 264  
294 SKDSPFNEDAFRTMPLRHLDLSEFNHNDPDSKWLGAQBELTSIALSGNFLKNFESWTY 353  
265 -LASLVELNLAHNLSLPHDLFTPLRY----- 291  
354 TKSLIHLELAYNHKIPVQL--PSRYHLSINISGNELTYLPDNINTLLPNVKTFDI 411  
292 -----LVLEHLHNPNCDCILWMLWMLREYIPTNSTCCGRCHAPM 333  
412 TANRFTPTSHDLAFLNNVBOVYVGNPWCSCAIQGL-----QV 451  
334 HMRGYLVE--VDQASQCSAPFTMDAPRDINISEGRMABLKCRTPPMSSVKWLLPNGTV 391  
452 HRRDYAMRHILYDNRVCATPSLVEGHSVALTD-----VNDCA 491  
392 LSHASRH-----PRISVLNDGTINFSHVLLSDTG-VYTCMTVNVAGNSASAYLNVTAE 445  
492 VLGARYGLTQTSMLILLAGVLLFAALLMILGCIYFLRERQYKGSYVTRHSRTPLTM 551  
446 LNTSNYSFPT-----VTVETEISP 466  
552 ANTHSCSSTNDTRGPLSPPPDFPLVSTETEKATP 586

## RESULT 38

T23841  
hypothetical protein M88.6b - Caenorhabditis elegans  
;Species: Caenorhabditis elegans  
;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
;Accession: T23841  
R;Sulston, J.  
submitted to the EMBL Data Library, June 1994  
;Reference number: Z19806  
;Accession: T23841  
;Status: preliminary; translated from GB/EMBL/DBJ  
;Molecule type: DNA  
;Residues: 1-594 <WIL>  
;Cross-references: EMBL:Z34802; PIDN: CAB54282.1; GSPDB: GN00021; CESP: M88.6b  
;Experimental source: clone M88  
;Genetics:  
;Gene: CESP: M88.6b  
;Map position: 3  
;Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 361/1; 411/3; 455/1; 544/3

Query Match 7.3%; Score 252.5; DB 2; Length 594;  
Best Local Similarity 25.1%; Pred. No. 7.8e-10;  
Matches 94; Conservative 50; Mismatches 117; Indels 113; Gaps 11;

Qy	252	SQVSLIERNAPDGLASIVELNLAH-----NNVLSLPHOLEFT	287
Dd	292	TPISVIPNNAFMHPINLIIRLEMSEAAVDIERGAFORTQIOAIVLNKNRSLQSRAADFFE	351
Qy	288	PLR--YLVEL-----HLH-----	298
Dd	352	GLANDLYSIDLGNRIDNVQPLGFANLPALSHLDISYNLLQTNPVSFNQNSFLQPNDREV	411
Qy	299	-----HNPNWCCDDILMAWLRYI-----PNNSTCCGRCHAPMHRGRVYAVEVDQASF	348
Dd	412	IYACGNPMYCSELEMFRTLLRNLDIDVEKPGCTAVCTSSNGCPVEGTPLRSVDFPCQN	471
Qy	349	QCSCA-PFINDAPRLNTISEGRMAELKCRTPPMSSVXWLLPNCTVLASHSRHPRISVLNDG	407
Dd	472	NEEAQFLV-----GR-----ALSMVGWII-----	490
Qy	408	TLNTHSVLLSDTYTTCMVNTVA-GMSNASAYLVNSTAEINTSNYSFFTTVT-VETTEIS	465
Dd	491	----LAVINTILLISIICLANVYGMSHQEK--KQYDAEVAAREETHHTQTATSIYNAPIS	544
Qy	466	PEDTTRKYKPVPTTSTCYQPAYT	488
Dd	545	VVD--RPYSTVPVNLDLPAAYT	565

```

RESULT 40
T19939
hypothetical protein C44H4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19939
R:Smyle, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19200
A:Accession: T19939
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-680 <WIL>
A:Cross-references: EMBL:Z79598; PIDN: CAB01865.1; GSPDB: GNO0038; CESP: C44H4.3
A:Experimental source: clone C44H4
C:Genetics:
A:Gene: CESP:C44H4.3
A:Map position: X
A:Introns: 26/3; 74/3; 122/3; 216/3; 364/3; 589/3

```

Query Match	7.34	Score 250;	DB 2;	Length 680;
Best Local Similarity	25.0%	Pred. No. 1.4e-09;		
Matches 126;	Conservative	64;	Mismatches 185;	Indels 128; Gaps 21;
Qy	54	NQPSKVVCIRGLSEVPGQIPSNTRYLNWE---	NNIQMIQADTRHLLHLEVLQLGNS	110
Db	108	NVMQELSUSENNKEVPTSAALGRVLNLSLCKNKIENITTKAFVNMTSLIDVNLGCQ	167	
Qy	111	IRQIEVGAF-NGLASLNTLBEIFONWLTIPVSGAFYLSKRLBLWRNPNPIESPSYAFNR	169	
Db	168	ICSMADTFANVMSLQWLILDNNKCTEPPSKAVRMWNLIALHIKYKINAIRQNDPVN	227	
Qy	170	VPSLMRLDLGLSKLEYISGSAFEGHFNLYKMLMGMCNTKOMP-N	LTPLVGLELEENSG	227
Db	228	LTSLSMLSLNG-NMISEIKGALQNTPNLHYLYLNENNLQTLDNGVLGQFQKQLQVLDSL	286	
Qy	228	NHFFPIRPGSGHGLSSLKLLWVMSQVSLIERNAPDGLASLVELNLAHNLSSLPHDLFT	287	
Db	287	NNFTDITKEMFEGLESIOHNLNLSNRISAVAPGAFAG-----	T	324
Qy	288	PURYLVELHLHNPWNCDCDILMLAWLREYIPTNSTCCGRCHAPMHRGRYLVEDQAS	347	
Db	325	PIL-----LLMW-----PNN-----C-----	LTEVSQQT	343
Qy	348	FOCSAFFINDAPRLNISTEGRMAELK-----CRTPPMSSVKMLLPNGTVLS	393	
Db	344	LX-GAPFL---RMVLSNNIRREVHLSFDHLPNLTLD---LANNKIMSQNTKLSGPE	396	

QY	16	A	I	L	L	P	P	V	T	L	T	R	A	O	W	I	L	C	A	I	A	A	A	S	A	G	P	Q	-----	N	C	P	S	V	C	S	C	N	Q	F	S	K	V	C	T	R	G	L	S	E	68			
DB	5	A	I	L	L	T	L	V	T	-----	V	Y	Q	C	P	A	L	S	G	A	C	R	A	P	S	V	T	P	V	A	I	C	N	A	G	L	Q	A	I	Q	A	R	-----	57										
QY	69	V	P	Q	P	S	N	T	R	Y	L	N	L	M	N	N	I	Q	A	D	T	F	R	L	H	L	E	V	L	Q	L	G	N	S	I	R	Q	E	V	G	A	F	N	G	-----	126								
DB	58	-----	D	I	P	I	D	S	-----	L	T	I	D	T	A	I	P	A	N	A	F	Q	S	T	I	R	-----	L	V	L	N	E	N	T	I	Q	N	D	D	Q	A	F	P	L	L	S	E	111						
QY	127	T	L	E	F	D	N	M	L	T	I	P	S	G	A	F	Y	L	K	R	E	L	M	R	N	P	N	I	E	S	I	E	S	A	F	N	V	P	S	-----	179													
DB	112	E	L	D	L	N	D	N	I	G	O	T	P	O	T	G	I	P	R	L	N	L	K	L	Y	N	R	I	N	Q	L	S	T	A	F	N	A	F	E	R	D	L	L	K	L	E	A	G	N	R	L	171		
QY	180	-----	E	L	K	L	E	I	S	E	G	A	F	E	G	L	F	N	-----	L	K	L	M	E	N	C	N	D	K	M	P	-----	212																					
DB	172	T	D	A	T	L	G	D	A	T	V	F	R	P	L	T	L	Q	E	L	S	I	E	T	S	I	T	S	I	P	S	A	L	V	N	Q	R	N	T	L	N	L	G	L	S	I	N	E	V	P	G	A	L	231
QY	213	-----	N	L	T	P	-----	L	V	G	E	E	L	E	M	S	G	N	H	F	P	E	I	P	G	S	F	H	G	L	S	S	K	L	K	L	W	N	251															
DB	232	I	D	P	V	I	S	S	I	E	N	G	I	T	V	I	P	O	A	F	O	G	V	N	O	F	I	V	T	G	N	K	F	S	W	A	P	E	R	V	I	T	O	L	K	I	G	E	291					

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394 -----HASRHPRIIVLNDGTLNFSHVLLSDTGYVTOMVTNAGNSASAVLNVTAEI--- 446
397 NLAVRLQENPVCVKKG-----PHVLNAGEAIW---LITNEA-NTICKGEWQATADLCPK 447
447 -----NTSNYSPTFTVIVETTBISPDTRKYPVPTSTTGQPAYTSTTTLVLOT 497
448 AQRPPIRPVCCSNEITTTTTTTTT-----FTL-----APTITTBEEKETETTE--KV 495
498 TRVPKQVAVPATDTTKMQTSLD 520
496 TTVGKSKTKATTTTBEPEDDD 518

RESULT 41
23836
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
;Accession: T23836
;Sulston, J.
;Submitted to the EMBL Data Library, June 1994
;Reference number: Z19806
;Accession: T23836
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-610 <WIL>
;Cross-references: EMBL:Z34802; PIDN:CAA84337.1; GSPDB:GN00021; CESP:M88.6a
;Experimental source: clone M88
;Genetics:
;Gene: CESP-M88.6a
;Map position: 3
;Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 427/3; 471/1; 560/3

Query Match 7.3%; Score 249.5; DB 2; Length 610;
Best Local Similarity 22.7%; Pred. No. 1.3e-09;
Matches 121; Conservative 75; Mismatches 172; Indels 165; Gaps 20;

29 WILCAIAAASAGPNC-----PSVCSNQ--PSKV-----VCTRGL 66
7 FVLLALARIAISBTRKSCIDIEKGFEEFNAHQPVCIADNGIPSTVKGFTIECESASI 66
67 SEYPOGIPS-----NTRVNLNLEN-----NIQMIQADTFRL- 98
67 ASVSENLASLNGTGLTTRDSTVNVLPQDLFENVFAQVKLGRGLSTLQPSFQSIG 126
99 HHEVLQGRNSIRQIEVGAFNGASLNTLELFDNMLTVIPGAFEYLSKLELMRNRP 158
127 GSAELLSLRNRIKLEKGLFTGLSKLTLDLAWNKIQIDVGAFEEELKVKVELLNEND 186
159 IESTPSVAFNRVPSLMLDGLBELKLEYISEGAFGLFNLKYLNGMGNK--DMPNLTTP 216
187 IRVLKGTTPGKMKLKLTLQNC-NLEIQGAFGLNSLEQLILSNLENIDWTIFSA 245
217 LVGLEELMSGNHPFPIRPGSPFGLSLKXKLWYNNSQ-----VSLIER 259
246 LKNLRVLDLGSKISNVEMKSPFKLEKL-----VLNNNTIDSMKSKLDPLSLVALFDR 301
260 NAFDGLASL-----VE-LNLANNLSSLPDLPFTPLRVLVELHLHHPNWCDDCI 308
302 NKIESIGDMDFGLTRSDRIETLSLARNLSQISPKAFORTNLTLLQYN----- 353
309 LNLAWMLREIPTNSTCCGRCHAFMNRGRLVVEVDQAS-----FQCSAPPFMDAPR 360
354 -----QIEELSSRKLTHTPIFKKLIFFPDSPS 380
361 DLNISBGRMAELKCRTPPMSSVKKLLPNGTIVLSHSHPRISVLNDGTL--NPSVLLSD 418
381 QV-----RTFPLASKLV-----TLQLSSNN--LSVIRSDGLPKSLSLALDH 422
419 TGYVTOMVTNAGNSASAVLNVTAEI---FTVIVETTETS 465
423 NVISKIARALEGMEIKULYH-----SNKLVLYQGTDSFSPKSVAEVDVS 470
```

## RESULT 42

## NEHUIA

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Platelet glycoprotein Ib alpha chain precursor - human
N:Alternate names: membrane glycoprotein Ib alpha chain
N:Contains: Glycocalicin
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C:Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102
R:Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A:Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p
A:Reference number: A94174; MUID:87289655; PMID:3303030
A:Accession: A94174
A:Molecule type: mRNA
A:Residues: 1-626 <LOP>
A:Cross-references: GB:J02940; NID:G183499; PIDN:AAA52595.1; PID:G306793
R:Wicki, A.N.; Walz, A.; Garber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.
Thromb. Haemost. 61, 448-453, 1989
A:Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A:Reference number: A60435; MUID:90020160; PMID:2799758
A:Accession: A60435
A:Molecule type: mRNA
A:Residues: 207-467 <WIC>
R:Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A:Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem
A:Reference number: S16945; MUID:91301149; PMID:2070794
A:Accession: S16945
A:Accession: A94173
A:Molecule type: protein
A:Residues: 17-315 <TIT>
R:Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A:Title: Identification of the disulphide bonds in human platelet glycoscalicin.
A:Reference number: S16945; MUID:91301149; PMID:2070794
A:Accession: S16945
A:Status: preliminary
A:Molecule type: protein
A:Residues: 224-227/262-270; 277-282 <HES>
R:Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
ations.
A:Reference number: I55355; MUID:92250564; PMID:1577776
A:Accession: I55355
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 412-427 <RES>
A:Cross-references: GB:S34436; NID:G249176; PIDN:AAB22152.1; PID:G249177
A:Note: variant D
C:Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C:Comment: Platelet activation apparently involves disruption of the macromolecular comp
C:Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un
C:Comment: Glycocalicin, which is approximately coextensive with the extracellular part
C:Genetics:
A:Gene: GDB:GPIBA; GPIB
A:Cross-references: GDB:118806; OMIM:231200
A:Map position: 17pter-17p12
C:Complex: heterodimer with platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
C:Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>
F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:379-430/Region: proline/threonine-rich 9-residue repeats
F:502-540/Domain: transmembrane #status predicted <TRM>
```

F;541-626/Domain: intracellular #status predicted <INT>  
F;37,175/Binding site: carbohydrate (Aen) (covalent) #status experimental  
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 7.2%; Score 248.5; DB 1; Length 626;  
Best Local Similarity 23.2%; Pred. No. 1.6e-09;  
Matches 128; Conservative 66; Mismatches 203; Indels 155; Gaps 22;

QY 49 VCSCNQFS--KVVCTRGSLSEVPGIPSNTRYLMNENNIQIADTFRLHLEVLQ 106  
DB 19 IEVSVASHLEWVNCRNLTALPPDPKDTILHLSNLTTFSLATMPYTRLTQNL 78  
QY 107 GRSISQIEVGAFNGLASNTLELFNMTLTPSGAFYLSKRLWLNRPISPSYA 166  
DB 79 DRCELTQIQVD--GTUPLVGLDLSHQQSIP-----LLQGTLPALTVDVS 124  
QY 167 FRVPSPMLDLGELKLEYISEGAFEGFLNLYLNGMNCIKOMP--LTPLVGLELE 224  
DB 125 ENRLTSL-----PLGALRGELGELQELYKGNELKTLPPGLTPTPKLELS 170  
QY 225 MSCGHPEIRPGSFHGLSSIKKLWVNSQVSLIERNAPDGLASVELAHNLSLPHD 284  
DB 171 LANNLTLPAGLNGLENDTL-----LOENSLYTIIPKG 206  
QY 285 LP-----TSLRYLVELHLHNPNCDCDILWLAWLKLEYIPTNSTCCGRCHAPMHRGRYL 340  
DB 207 FFGSHLLPFAF-----LHGNPMLCNCEILYFRRLQD-----NAENVYV 245  
QY 341 -----VEV-----DQAFQF-----SAPPIND-APRDL-----NISEGRMA 370  
DB 246 WKQGVDPKAMTSVAVSQCDNSKFPVYKPGKCTGLDGBDGLDYVPEDETEGKV 305  
QY 371 E-----LKCRTPMS--SVKWLFPNGTIVLASHRHRPRISVLMDG-----TL 409  
DB 306 RATRVTVKFTKATTPWGLFYSWSTASLDSQMPSSLHTQSTKEQITFPFRWTPNFTL 365  
QY 410 NFSHVLLSDGVVTCMVTVNAGNS--ASAYLVNSTAEINTNYGFTTVVETTEISPE 467  
DB 366 HMEISGFTKPKSTTEPTSPPTSEVPSPAPNMTLETPS-----PTTPEPTSEPA2S 420  
QY 468 DTRKYKVPVTTGTGQVATTTTTLQTRV--PQVAVPAT-----DPTDKQVQSL 519  
DB 421 PTPPEPTPIPIA-----TSFTILVSAFSLITKSTFLITTKPVSLLESTKTIPEL 472  
QY 520 DEVMKTKIIIG 531  
DB 473 DQPPKLRGVLOQ 484

## RESULT 43

A:Title: Toll protein precursor - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 02-Jun-2000  
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.  
Cell 52, 269-279, 1988  
A:Title: The Toll gene of *Drosophila*, required for dorsal-ventral embryonic polarity, and for the formation of the dorsal midline.  
A:Reference number: A29943; MUID:88135760; PMID:2449285  
A:Accession: A29943  
A:Molecule type: DNA  
A:Residues: 1-1097 <HAS>  
A:Cross-references: GB:M19969; GB:J02682; NID:G158640; PIDN:AAA28941.1; PID:G158641  
C:Genetics:  
A:Gene: FlyBase:Ti  
A:Cross-references: FlyBase:FBgn0003717  
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
C:Keywords: transmembrane protein  
Z:1-17/Domain: signal sequence #status predicted <SIG>  
Z:18-1097/Product: Toll protein #status predicted <MAT>

Query Match 7.2%; Score 247.5; DB 2; Length 1097;  
Best Local Similarity 20.6%; Pred. No. 4e-09;

Matches 121; Conservative 98; Mismatches 225; Indels 143; Gaps 20;  
QY 69 VPGQPSNTRYLN--LMENNI-----QMIQADTFRLHH 100  
DB 284 LPQGLFDHKKHLNVRKNNRVPLATPSRUFANQPEQLLEABQLSLPGDFUHFSTQ 343  
QY 101 LEVLQGRNSIQIEVGAFNGLASNTLELFNMTLTPSGAFYLSKRLWLNRPISPSYA 160  
DB 344 ITNISGLDNLKTLPATLLEHQVNLSDLSNRLTHLPDSLPFAHTTNLTDLREDNLT 403  
QY 161 SPSYAFNRPVPSMLRDLGELKLEYISEGAFEGFLNLYLNGMNCIKOMPNTPLVGL 220  
DB 404 GISGDIFPSNLGNLTVLWMSR--NRLRTIDSRFVSTNGRLHLHL-----DHNDIDLOQPLDI 459  
QY 221 BELEMSGHPEIRPGSFHGLSSIKKLWVNSQVSLIERNAPDGLASVELAHNLSL 280  
DB 460 MEQTQINSPP-----GYEGELTIN--LRNNSIIFVNDKNTMLQLRELDLSYNNIS 511  
QY 281 -----LPHDLFTPLRY-----LVELHLHNPNCDCDILM 310  
DB 512 LGYEDLAPLSQNRHLHVNMTNKKIRRIALPEDVHLGEGYNNNLVHVDLNDNPLVCDCTILM 571  
QY 311 LAWLIR-----EY-----IPTNSTCCGRCHAPMHRGRYLVEVDQASFCSCSAPPIMDAPR 360  
DB 572 FQQLVRGVHKPQSRQFKLRTDLVCSQ---ENVLEGTPPVROIEPQTLCPLDF--SDDER 627  
QY 361 DLNISEGRMAELKCRTPPMSVVKWLLPNGTIVLASHRHRPRISVLMDGTLNFSHV----- 414  
DB 628 -----ERKC-----PRG--CNCHVRTYDKALVINCHSGLNTHVPRPLNL 664  
QY 415 -----LLSDT-----GVYTCMTNVAGNSAYLVNSTAEINTNYGFTTVVETTEISPE 454  
DB 665 HKMQLMELHLENLTLRLPSANTPGYESVTSILHAGNLTSDVDQLPNTLHIDISWN 724  
QY 455 TTVTVETTEISPEPTTKYKVPVTTGTGQVATTTTTLQTRVPK-----QVAVPA 508  
DB 725 HLQWLARTVLGFLNRTMKRSVKLSGNPMWCDTAKFLILFTQDNFERIGDRNEMCVNA 784  
QY 509 TDTDKMQVSLDEVMKTK---IIICCFVAVT--LLAAMLIIVFYKLR 551  
DB 785 EMPTRMVSLTNDICPAERGVFIALAVVIALTGGLAGFTAALYYKFK 831

## RESULT 44

I73633  
gene trkC protein - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
C:Accession: I73633  
R:Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.  
J. Neurosci. 15, 477-491, 1995  
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extracellular matrix receptors.  
A:Reference number: I56557; MUID:95123473; PMID:7823156  
A:Accession: I73633  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-612 <RES>  
A:Cross-references: GB:S76476; NID:G913723; PIDN:AAB33112.1; PID:G913724  
C:Genetics:  
A:Gene: trkC  
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein repeat homology  
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <IRR>

Query Match 7.1%; Score 244; DB 2; Length 612;  
Best Local Similarity 23.6%; Pred. No. 3.2e-09;  
Matches 124; Conservative 64; Mismatches 198; Indels 140; Gaps 24;

QY 206 CNIKOMPNTPLV-GLSELEMSQN-----HPFEIRPGSGFLSS----- 243  
DB 45 CRPDGCLPGLLEGQDSGNSGNANINITDSRNTSIHIENWR--SLFTLNAVDMELY 102  
QY 244 --LKKLWVNSQVSLIERNAPDGLASVELAHNLSLPHDLFTPLRYLVELHLHNP 301

```
103 TGLQKLTIKNSGLRSTQPRAPAKNPHLRVINSSNRLTTLTSLWOLFQTLTSLRELELQNF 161
302 WNCDCDILWLAWLREYIPNTSTCCGRCHAPMHMRGRYVEVDQASF-----QCSAP 353
162 FNGSCDIRWQLWQEQ-----GEAKLSQNLICINADGSQLPLFRWNISQCDLP 210
354 FINDAPRLNISEGRMAELKCR--TPPMSSVVKWLPNGTYLASHSRH-----PRISVLN 405
211 ETSVSHVNLTVRGDNVAVITCNGSGPLDPDVIV---TGLQSINTHONLNTWNTVHAIN 267
406 DGTINFSHVLLDTG-VYTCMTNVNAGNSNAYLNVSTAEINTSNYSFFTTVTVEITEI 464
268 ---LTVAVTSEDNGTFLCIAENVVGMNASVALTV-----YPPRVSLEBEEL 315
465 SPB---DTRKKKVPVPTS-----TGYPQAVTTTTLVIQT----- 497
316 RLEHCIEFVVRGNPPPTLWHLNGOPLRESKIIHVEYIQEISRGCLLFNKPTHYNNGN 375
498 -TRVPKQ-----VAVPADTDTKMTQSLDEVMKTKI11-----GCFV 534
376 YTLIAKNPGLTANOTINGHFLKEPPPESTDNP-ILFDEVSPTPTVTVTHKPEEDTFGUSI 434
535 AVTLIAAA--MLIVFYKLRKHQRQSTVTAARTVEIIQVDEIPA-----ATSA 583
435 AVGLAFAFACVLLVWLFWMINKYGRSKFGKMGFPVAVISGEEDSASPLHINEGITTS 494
584 TAAPSGVSGEGAVLPTIHDHINYNKYKPAHGAH---WTENSLGN 625
495 DKGEDTVV-IGMTPIPVIE---NPQFROGHCHKRPDPTWVFSNIDN 536

RESULT 45
34319
Vpothetical protein K03A1.2 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
;Accession: T34319
;Nhan, M.
;Description: The EMBL Data Library, November 1995
;Reference number: Z21505
;Accession: T34319
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-562 <NHA>
;Cross-references: EMBL:U41625; PIDN:AAA83325.1; CESP:K03A1.2
;Gene: CESP:K03A1.2
;Introns: 113/3; 132/3; 171/3; 221/2; 269/2; 301/2; 332/2; 465/2; 497/2; 530/3

Query Match 7.0%; Score 242.5; DB 2; Length 562;
Best Local Similarity 28.9%; Pred. No. 3.6e-09;
Matches 85; Conservative 50; Mismatches 104; Indels 55; Gaps 12;

76 NTFY-LNTAKNNIQLQADTFPHLHLEVLQGRNISQIEVGAFNGLASLNTLEFDNW 134
229 NTLRLDLGYNRIKVVSDSFSLSKLVLDGNGPIKAWRKEMPKGLDLSLEELSDNCN 288
135 LTVIPSGAFYLSKLRFLWRNPIESPSYAFNRVPSLMRLDLGELKKLEYISEGAPEG 194
289 IENLPADIEFYLKVLKLSRENPLEEIPAVVAH--LKSLOIDL--SVTNLTETIRHAPAG 346
195 LFMVKYLYNIGMCKMPNLTPL-----VGLLEEM-----SGNHPEPTPGSP----- 238
347 DSDLEBIIL-----EKMPFETVVRDGGFCGLPOLKTLILNDKNYQLQLHPNAPGYIKSQP 401
239 -HGLSSKLLKLVNNSQVSLIERNAPGLASVELNLAHNNLSLPHDLFTPLRYLVELHL 297
402 GHKSAITSLQIHNSNISTISEHVD-----YDNLKT-----FQV 436
298 HNNPWNCCDILWLAWLRE-YIPTNSTCCGRCHAPMHMRGRYVEVDQASFQC 350
437 GGNPWNCCDQTFM---LEEKFAFKQDSVAPKCTSPAGLNGRLVTV-RASDAC 486
```

## RESULT 46

T19941

hypothetical protein C44H4.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C;Accession: T19941

R;Smye, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z19200

A;Accession: T19941

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-458 &lt;WIL&gt;

A;Cross-references: EMBL:279598; PIDN:CAB01867.1; GSPDB:GN000028; CESP:C44H4.1

A;Experimental source: clone C44H4

C;Genetics:

A;Gene: CESP:C44H4.1

A;Map position: X

A;Introns: 24/3; 157/1; 257/3; 372/3; 425/1

Query Match

Best Local Similarity 28.7%; Score 240; DB 2; Length 458;

Matches 92; Conservative 39; Mismatches 102; Indels 88; Gaps 13;

QY 69 VPQ---GIPSTRYLNLMENNLIQMIQADTFERLH---HLEVLQLGENSEIROIEVGAENGL 122

Db 139 IPQSGVSIILKQKILSLPONLIEYVQDNAFSLYSRDSLLKLDLSANNLTAIHTPTGLLGL 198

QY 123 ASLNTLEFDNMLTVPISGAFYLSKLRFLWL-----RN-----NPI 159

Db 199 ENLSQLSLDKNLSRIPSOALENIPSLDLSLGVNRIHTISRNLSPLPLNLSLEVAQI 258

QY 160 ESIPSVAFNRVPSLMRLDLGELKKLEYISEGAPEGLFMKLYLNIGMCKMPNLT----- 214

Db 259 RLIPSDSFSETFLLSYLYLGN-NLETSIDASFLHIGGLKVLN--MSNNKDTITSQANGK 315

QY 215 -----TPLVGLLEEMSGNHPEIRPGSHGLSSLKLVNNSQVSL 256

Db 316 LSVQPFKLCICILAFQHPAPSLIRLELFDCS---ISRIEP-----KSLQK--VQHIQVIL 364

QY 257 IERN-----AFDGLASVELNLAHNNLSLPHDLF-----TPRLRYLVELH 296

Db 365 LSRNQITQINAVDDPAFSQPLMTSLDLSNRLSPNVIYDLSLMQKKTSPQR--RLS 422

QY 297 LHEHPWNCCDILWLAWLRE 317

Db 423 IQNPWRCDKDLNLRKWLKD 443

## RESULT 47

A55178

neurotrophin receptor trkC precursor - human

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 18-Jun-1999

C;Accession: A55178

R;McGregor, L.M.; Baylin, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.

Genomics 22, 267-272, 1994

A;Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, a

A;Reference number: A55178; MUID:95104834; PMID:7806211

A;Accession: A55178

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-825 &lt;MCG&gt;

A;Cross-references: GB:U05012; NID:G442389; PIDN:AAA75374.1; PID:G442390

C;Genetics:

A;Gene: GDB:NTRK3

A;Cross-references: GDB:127899; OMIM:191316

A;Map position: 15q24-15q25

C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr

C;Keywords: alternative splicing; ATP; growth factor receptor

F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR1&gt;

F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:536-817/Domain: protein kinase homology <KIN>  
F:544-552/Region: protein kinase ATP-binding motif

Query Match 6.9%; Score 239; DB 2; Length 825;  
Best Local Similarity 23.7%; Pred. No. 1.1e-08;  
Matches 122; Conservative 61; Mismatches 195; Indels 136; Gaps 23;

206 CNIKMPNLTPLV-GLLEEMSGN-----HFEIRPGSFHGLSS----- 243  
45 CRPPDGNLFLLEEGQDSNGNGNANITDISNITSIHENWR--SLHTLNADVMEY 102  
244 --LKKLWYNSQVSLIERNAFDGLASVELNLAHNLSSLPDLPFTPLRYLVELLHHNP 301  
103 TGLQKLTIKNSGLRSIQPAPAKNPHLYINLSSNRLTSLWQLFQTLT-LRELQLEQNF 161  
302 WNCDDIILWAWLREYIPTNSTCCGRCHAPMGRGYLVEVDQASF-----QCSAP 353  
162 FNCSCDIRWQLWQEQ-----GEAKLNSQLYICINADGSQPLFRMNISQCDLP 210  
354 FMDAPRINISGEEMAEKCR--TPPMSSVKLLPNGTIVLSHARH-----PRISVLN 405  
211 ELSVSHVNLTVREGDNAVITCNGSGSLPDPVDWIV---TGLQINTHTQNLNWTNVHAIN 267  
406 DGTLPFSVLLSDTG-VYTCMTNVAGNSASAVLNSTABELNTSNYSFFTTVETTEI 464  
268 ---LTLVNTSDNGFTLTCAENYVGNASVALTV-----YPPRVWSLESPEL 315  
465 SPE---DTRKYKVPPTTS-----TGQPAYTTSITVLIQT----- 497  
316 RUEHCIEFVVRGNPPTLHNLHGQPLRESKLIHVEYQGEISEGCLLKNKPTHYNGN 375  
498 -TRVPKQ-----VAVPATDTRDMQTSLEDEWMTTKIII-----GCYV 534  
376 YTLIAKNPLGTANQINGHFLKEPPESTDNF-ILFDEVSPPTPIVTHKPEEDTFGVI 434  
535 AVTLAA--MLIVFYKLRKHQRSTVTAARTVEIIQVDEDIPA-----ATSA 583  
435 AVGLAFAFACVLLWLVFWINKYGRSKFGMKGPVAVISGEEDSASPLHHNHGITTPESSL 494  
584 TAAPSGVSGEAVLPTIHDHINYNKYKPAHGAH 617  
495 DAGPTTVV-IGWTRIPVIE---NPQYFRQGHCH 524

RESULT 48  
173632  
neurotrophin-3 receptor precursor - human  
N:Alternate names: receptor tyrosine kinase trkC  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 11-Jun-1999  
C:Accession: I73632  
R:Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.  
J. Neurosci. 15, 477-491, 1995  
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extracellular  
A:Reference number: I56557; MUID:95123473; PMID:7823156  
A:Accession: I73632  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-839 <RES>  
A:Cross-references: GB:576475; NID:g913721; PIDN:AB33111.1; PID:g913722  
C:Genetics:  
A:Gene: GDB:NTRX3; TRXC  
A:Cross-references: GDB:127899; OMIM:191316  
A:Map position: 15q24-15q25  
C:Function:  
A:Description: regulation of nervous system development; receptor for neurotrophin-3  
A:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop  
C:Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phosph  
F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-839/Product: neurotrophin-3 receptor #status predicted <MAT>  
F:32-436/Domain: extracellular #status predicted <EXT>  
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F:536-817/Domain: protein kinase homology <KIN>  
F:544-552/Region: protein kinase ATP-binding motif

Query Match 6.9%; Score 239; DB 1; Length 839;  
Best Local Similarity 23.7%; Pred. No. 1.1e-08;  
Matches 122; Conservative 61; Mismatches 195; Indels 136; Gaps 23;

206 CNIKMPNLTPLV-GLLEEMSGN-----HFEIRPGSFHGLSS----- 243  
45 CRPPDGNLFLLEEGQDSNGNGNANITDISNITSIHENWR--SLHTLNADVMEY 102  
244 --LKKLWYNSQVSLIERNAFDGLASVELNLAHNLSSLPDLPFTPLRYLVELLHHNP 301  
103 TGLQKLTIKNSGLRSIQPAPAKNPHLYINLSSNRLTSLWQLFQTLT-LRELQLEQNF 161  
302 WNCDDIILWAWLREYIPTNSTCCGRCHAPMGRGYLVEVDQASF-----QCSAP 353  
162 FNCSCDIRWQLWQEQ-----GEAKLNSQLYICINADGSQPLFRMNISQCDLP 210  
354 FMDAPRINISGEEMAEKCR--TPPMSSVKLLPNGTIVLSHARH-----PRISVLN 405  
211 ELSVSHVNLTVREGDNAVITCNGSGSLPDPVDWIV---TGLQINTHTQNLNWTNVHAIN 267  
406 DGTLPFSVLLSDTG-VYTCMTNVAGNSASAVLNSTABELNTSNYSFFTTVETTEI 464  
268 ---LTLVNTSDNGFTLTCAENYVGNASVALTV-----YPPRVWSLESPEL 315  
465 SPE---DTRKYKVPPTTS-----TGQPAYTTSITVLIQT----- 497  
316 RUEHCIEFVVRGNPPTLHNLHGQPLRESKLIHVEYQGEISEGCLLKNKPTHYNGN 375  
498 -TRVPKQ-----VAVPATDTRDMQTSLEDEWMTTKIII-----GCYV 534  
376 YTLIAKNPLGTANQINGHFLKEPPESTDNF-ILFDEVSPPTPIVTHKPEEDTFGVI 434  
535 AVTLAA--MLIVFYKLRKHQRSTVTAARTVEIIQVDEDIPA-----ATSA 583  
435 AVGLAFAFACVLLWLVFWINKYGRSKFGMKGPVAVISGEEDSASPLHHNHGITTPESSL 494  
584 TAAPSGVSGEAVLPTIHDHINYNKYKPAHGAH 617  
495 DAGPTTVV-IGWTRIPVIE---NPQYFRQGHCH 524

RESULT 49  
139068  
proline- arginine-rich end leucine-rich repeat protein PRELP precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 24-Sep-1999  
C:Accession: I39068  
R:Bengtsson, E.; Neame, P.J.; Heinigard, D.; Sommarin, Y.  
J. Biol. Chem. 270, 25639-25644, 1995  
A:Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found in  
A:Reference number: I39068; MUID:96029653; PMID:7592739  
A:Accession: I39068  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-382 <RES>  
A:Cross-references: EMBL:U29089; NID:g886135; PIDN:AA050230.1; PID:g886136  
C:Genetics:  
A:Gene: GDB:PRELP





GenCore version 5.1.1-6  
Copyright (c) 1993 - 2004 Compugen Ltd.

XM protein - protein search, using sw model

run on: February 5, 2004, 15:46:09 ; Search time 17 Seconds

(without alignments)

1806.379 Million cell updates/sec

title: US-09-989-279-229

effect score: 3440

sequence: 1 MKLLAQVTHVHTWNAILLP.....ISEPYIIQHTXKRVQETQI 653

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 127863 seqs, 47026705 residues

total number of hits satisfying chosen parameters: 127863

linimum DB seq length: 0

laximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	390	11.3	713	1	GAMP HUMAN
2	389	11.3	646	1	FLRI HUMAN
3	385	11.2	649	1	FLR3 HUMAN
4	380.5	11.1	358	1	CHAD MOUSE
5	379.5	11.0	358	1	CHAD RAT
6	379	11.0	581	1	LR15 HUMAN
7	375.5	10.9	1504	1	SLIT DROME
8	375	10.9	361	1	CHAD BOVIN
9	372.5	10.8	473	1	RT4R MOUSE
10	371.5	10.8	578	1	LR15 RAT
11	370	10.8	473	1	RT4R RAT
12	368	10.7	473	1	RT4R MACFA
13	365.5	10.6	359	1	CHAD HUMAN
14	364	10.6	473	1	RT4R HUMAN
15	356.5	10.4	660	1	FLR2 HUMAN
16	338.5	9.8	951	1	LGR4 RAT
17	337	9.8	567	1	GPV RAT
18	334.5	9.7	951	1	LGR1 HUMAN
19	321.5	9.3	907	1	LGR5 MOUSE
20	321	9.3	567	1	GPV MOUSE
21	321	9.3	603	1	ALS MOUSE
22	320	9.3	481	1	NYX HUMAN
23	315	9.2	605	1	ALS PAPA
24	310	9.0	603	1	ALS RAT
25	309	9.0	605	1	ALS HUMAN
26	305.5	8.9	560	1	GPV HUMAN
27	303.5	8.8	359	1	PGS2 HUMAN
28	303.5	8.8	907	1	LGR5 HUMAN
29	302	8.7	360	1	PGS2 HORSE
30	300	8.7	360	1	PGS2 PIG
31	298	8.7	360	1	PGS2 BOVIN
32	298	8.7	360	1	PGS2 SHEEP
33	297	8.6	360	1	PGS2 CANFA

34	293.5	8.5	360	1	PGS2 RABIT
35	287.5	8.4	357	1	PGS2 CHICK
36	286.5	8.3	354	1	PGS2 RAT
37	284.5	8.3	356	1	PGS2 COIJA
38	281.5	8.2	1050	1	TLR7 MOUSE
39	279.5	8.1	354	1	PGS2 MOUSE
40	277	8.1	966	1	Y918 HUMAN
41	275.5	8.0	369	1	PGS1 CANFA
42	268	7.8	905	1	TLR3 MOUSE
43	267	7.8	381	1	PRLP BOVIN
44	267	7.8	536	1	CBP8 HUMAN
45	267	7.8	904	1	TLR3 HUMAN
46	263.5	7.7	423	1	OMD RAT
47	262.5	7.6	369	1	PGS1 MOUSE
48	262.5	7.6	369	1	PGS1 RAT
49	262	7.6	1049	1	TLR7 HUMAN
50	261.5	7.6	368	1	PGS1 HUMAN
51	261.5	7.6	369	1	PGS1 SHEEP
52	261.5	7.6	757	1	LGR7 HUMAN
53	260.5	7.6	369	1	PGS1 BOVIN
54	260.5	7.6	372	1	PGS1 HORSE
55	259.5	7.5	368	1	PLIB XENLA
56	259	7.5	331	1	PLIB AKBL
57	259	7.5	423	1	OMD MOUSE
58	255	7.4	353	1	KERA CHICK
59	255	7.4	353	1	KERA COIJA
60	254	7.4	977	1	Y848 HUMAN
61	253	7.4	352	1	KERA BOVIN
62	253	7.4	352	1	KERA HUMAN
63	251.5	7.3	422	1	OMD BOVIN
64	248.5	7.2	373	1	ASPN MOUSE
65	248.5	7.2	626	1	GPBA HUMAN
66	247.5	7.2	1097	1	TOLL DROME
67	244.5	7.1	351	1	KERA MOUSE
68	242	7.0	421	1	OMD HUMAN
69	240.5	7.0	347	1	A2GL HUMAN
70	240.5	7.0	754	1	LGR8 HUMAN
71	239.5	7.0	379	1	ASPN HUMAN
72	239	6.9	839	1	TRKC HUMAN
73	238	6.9	382	1	PRLP HUMAN
74	237	6.9	378	1	PRLP MOUSE
75	236	6.9	377	1	PRLP RAT
76	234.5	6.8	440	1	OMGP HUMAN
77	233.5	6.8	1032	1	TLR8 MOUSE
78	233	6.8	825	1	TRKC PIG
79	231	6.7	737	1	LGR6 MOUSE
80	229.5	6.7	782	1	CHAO TRICA
81	229	6.7	828	1	LGR6 HUMAN
82	228.5	6.6	661	1	C180 HUMAN
83	227	6.6	827	1	TRKC CHICK
84	225.5	6.6	380	1	FMOD CHICK
85	225.5	6.6	661	1	C180 MOUSE
86	225	6.5	1041	1	TLR8 HUMAN
87	220.5	6.4	375	1	FMOD BOVIN
88	220.5	6.4	1315	1	CHAO DROME
89	220	6.4	864	1	TRKC RAT
90	219	6.4	440	1	OMGE MOUSE
91	215.5	6.3	695	1	FSHR HUMAN
92	215.5	6.3	695	1	FSHR MACFA
93	215.5	6.3	740	1	CT75 HUMAN
94	214.5	6.2	376	1	FMOD HUMAN
95	214.5	6.2	826	1	TLR4 PAPAN
96	213	6.2	843	1	TLR4 HORSE
97	212.5	6.2	376	1	FMOD MOUSE
98	211.5	6.1	376	1	FMOD RAT
99	211.5	6.1	858	1	TLR5 HUMAN
100	209.5	6.1	859	1	TLR5 MOUSE
101	207.5	6.0	582	1	SHO2 HUMAN
102	207.5	6.0	582	1	SHO2 MOUSE
103	207.5	6.0	781	1	TL22 CHICK
104	206	6.0	662	1	GARP HUMAN
105	205.5	6.0	343	1	LUM CHICK
106	205.5	6.0	343	1	LUM COIJA

028888	oryctolagus
028675	gallus gall
001129	rattus norv
09de68	coturnix co
058681	mus musc
028654	mus musc
094991	homo sapien
002678	canis fami
099mb1	mus musc
09gkn8	bos taurus
022792	homo sapien
015455	homo sapien
092187	rattus norv
028653	mus musc
047853	rattus norv
09nyk1	homo sapien
021810	homo sapien
046390	ovis aries
09hbx9	homo sapien
021809	bos taurus
046403	equus cabal
091b75	xenopus lae
093233	agkistrodon
035103	mus musc
042235	gallus gall
09d666	coturnix co
094933	homo sapien
062702	bos taurus
060938	homo sapien
077742	bos taurus
099mq4	mus musc
07359	homo sapien
008953	drosophila
035367	mus musc
099983	homo sapien
02750	homo sapien
08wxd0	homo sapien
09bxn1	homo sapien
016288	homo sapien
051888	homo sapien
09jk53	mus musc
09eqp5	rattus norv
023515	homo sapien
058682	mus musc
024786	sus scrofa
091225	mus musc
082963	tribolium c
09hbx8	homo sapien
099467	homo sapien
091044	gallus gall
051887	gallus gall
062192	mus musc
09nr97	homo sapien
013605	bos taurus
012024	drosophila
003351	rattus norv
063912	mus musc
023945	homo sapien
032212	macaca fasc
08wxd4	homo sapien
006828	homo sapien
09tsp2	papio anubi
09myw3	equus cabal
050608	mus musc
050609	rattus norv
060602	homo sapien
09jlf7	mus musc
09ug13	homo sapien
088520	mus musc
09dgb6	gallus gall
014392	homo sapien
014390	gallus gall
09de67	coturnix co

107 205.5 6.0 582 1 CONN DROME Q01819 drosophila  
 108 205.5 6.0 841 1 TLR4\_BOVIN Q91655 bos taurus  
 109 204.5 5.9 699 1 ECM2\_HUMAN Q94769 homo sapien  
 110 203.5 5.9 695 1 FSHR\_BOVIN P35376 bos taurus  
 111 201.5 5.9 694 1 FSHR\_HORSE P47799 equus caball  
 112 201.5 5.9 695 1 FSHR\_PIG P49059 sus scrofa  
 113 201.5 5.9 733 1 C775\_MOUSE P59383 mus musculu  
 114 200 342 1 LUM\_BOVIN Q05443 bos taurus  
 115 199.5 5.8 338 1 LUM\_HUMAN P21884 homo sapien  
 116 198.5 5.8 1032 1 TLR5\_HUMAN Q9NR96 homo sapien  
 117 198 5.8 1115 1 GPCR\_LYMET P46023 lymnaea sta  
 118 196 5.7 835 1 TLR4\_RAT Q9KX05 rattus norv  
 119 195 5.7 818 1 TRKB\_CHICK Q91987 gallus gall  
 120 194.5 5.7 695 1 FSHR\_SHEEP P35379 ovis aries  
 121 194.5 5.7 835 1 TLR4\_MOUSE Q9UK66 mus musculu  
 122 194 5.6 833 1 TLR4\_PELCA P58727 felis silve  
 123 192 5.6 839 1 TLR4\_HUMAN Q00206 homo sapien  
 124 192 5.6 839 1 TLR4\_PANPA Q9TTNO pan paniscu  
 125 191.5 5.6 692 1 FSHR\_MOUSE P35378 mus musculu  
 126 190.5 5.5 687 1 FSHR\_EQUAS Q95179 equus asinu  
 127 190 5.5 1256 1 FLII\_DROME Q24020 drosophila  
 128 189 5.5 338 1 LUM\_MOUSE P51885 mus musculu  
 129 188.5 5.5 925 1 GLHR\_ATEL P35409 anthropleura  
 130 188 5.5 838 1 TLR4\_CRIGR Q9WV82 cricetus  
 131 188 5.5 1032 1 TLR9\_MOUSE Q9EQU3 mus musculu  
 132 187.5 5.5 338 1 LUM\_RAT P51886 rattus norv  
 133 187.5 5.5 1021 1 PSKR\_DAUCA Q91PBA daucus caro  
 134 187 5.4 793 1 TLR2\_CHICK Q9DD78 gallus gall  
 135 186.5 5.4 692 1 FSHR\_RAT P20395 rattus norv  
 136 185 5.4 257 1 LRR3\_HUMAN Q9BY71 homo sapien  
 137 185 5.4 796 1 TRKA\_HUMAN P04629 homo sapien  
 138 184 5.3 257 1 LRR3\_RAT P59035 rattus norv  
 139 183 5.3 332 1 SD22\_SCHPO P22194 schizosacch  
 140 181 5.3 257 1 LRR3\_MOUSE P59034 mus musculu  
 141 181 5.3 699 1 LSHR\_HUMAN P22888 homo sapien  
 142 181 5.3 784 1 LTR2\_MOUSE Q9GUN7 mus musculu  
 143 180 5.2 701 1 LSHR\_BOVIN Q28005 bos taurus  
 144 179.5 5.2 784 1 TLR2\_HUMAN Q80603 homo sapien  
 145 179 5.2 784 1 TLR2\_BOVIN Q95189 bos taurus  
 146 178 5.2 259 1 LPI5\_HUMAN Q96P88 homo sapien  
 147 178 5.2 259 1 LRI5\_MOUSE Q9VCH9 mus musculu  
 148 178 5.2 1039 1 YR71\_CAEEL Q09564 caenorhabdi  
 149 177.5 5.2 822 1 TRKB\_HUMAN Q16620 homo sapien  
 150 177 5.1 338 1 SD22\_YEAST P36047 saccharomyc

## ALIGNMENTS

RESULT 1  
 GAMP\_HUMAN STANDARD; PRT; 713 AA.  
 AC O75325;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Glioma amplified on chromosome 1 protein precursor.  
 GN GAC1.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Glial tumor;  
 RX MEDLINS=98324709; PubMed=9662332;  
 RA Malfoy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M.,  
 RA Dutrillaux A.-M., Dutrillaux B., Ross D., Hanaah S.;  
 RT "GAC1, a new member of the leucine-rich repeat superfamily on  
 RT chromosome band 1q32.1, is amplified and overexpressed in malignant  
 RT gliomas";  
 RL Oncogene 16:2997-3002(1998).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: OVERAMPLIFIED IN MALIGNANT GLIOMAS.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF030435; AAC39792.1; -.

DR MIM; 605492; -.

DR GO; GO:0004872; P:receptor activity; TAS.

DR GO; GO:0007155; P:cell adhesion; TAS.

DR GO; GO:0007048; P:oncogenesis; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig C2.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR Cterm.

DR InterPro; IPR000372; LRR Nterm.

DR InterPro; IPR003591; LRR\_type.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00560; LRR; 9.

DR Pfam; PF01463; LRRCT; 1.

DR PRINTS; PR00019; LEUCICHRPT.

DR SMART; SM00408; IGC2; 1.

DR SMART; SM00369; LRR\_TYP; 2.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00013; LRRNT; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;

Leucine-rich repeat; Signal.

FT SIGNAL 1 18

FT CHAIN 19 713

FT DOMAIN 19 630

FT TRANSMEM 631 651

FT DOMAIN 652 713

FT REPEAT 92 115

FT REPEAT 116 139

FT REPEAT 140 163

FT REPEAT 164 187

FT REPEAT 188 211

FT REPEAT 212 235

FT REPEAT 236 259

FT REPEAT 261 283

FT REPEAT 309 333

FT REPEAT 334 357

FT REPEAT 358 385

FT REPEAT 422 511

FT DOMAIN 445 497

FT DISULFID 94 94

FT CARBOHYD 381 381

FT CARBOHYD 555 555

FT CARBOHYD 583 583

FT SEQUENCE 713 AA; 78798 MW; EC8BC0FD240C9396 CRC64;

Query Match 11.3%; Score 390; DB 1; Length 713;

Best Local Similarity 24.4%; Pred. NO. 8.4e-20;

Matches 179; Conservative 92; Mismatches 302; Indels 160; Gaps 23;

QY 30 ILCAIAAASAGP-----QNCPSVCSCS-----NQFSKVVCTRGLESEVQGI 73

DB 8 LLANVAGATAAVFVFWVWVPCQACQIRPWTTPRSSYREATTVDCNDLFLAVAPAL 67

QY 74 PNTYLMNMENNIQIADTFRHLHLEVLQLGNSIRQIEVGAFNGLASLITFLFDN 133

DB 68 PACTQTLLIQNSIVRVQDSGLVLANLTDLDSQNSFSDARDQCDFFALPQLLSHLEEN 127

QY 134 WLTVPSGAFAEYLSKRLRLRNPIBSIPYAFNRVPSLMRLDGE----- 180

128 QLTREDSFAGLSQELYNHLYRIAPRAGSLNLLRLHNSLLRAIDRWFEEM 187  
181 LKLEYISEGA-----FEGFLNLYNLMGNCNIXDMPN----- 213  
188 LFNLEILMIGCNKVDAILDNFPLANLSLVLAGNLEISDYALEGLQSLIESLFDYN 247  
214 -----LTPVLGLEELMSGNHPPFIRPGSFHGLSLKLMWNMSO----- 253  
248 QLARVPRALEQVEGKFLDLNKNPLQRPVGFDFANMLHKLGLNMBEELVSIKFAIV 307  
254 -----VSLIERNAPDGLASIVELANLAHNLSSLPDHLFTPLRYLVLEHLH 298  
308 NLBELTKLDTNNPRISFHPHPLPQNEFLMUNNALSALHQOTVBSLENLQEVGLH 367  
299 HNPWNCDDILWL-ANWLR-EYIPTNSTCCGRCHAPMGRGRLVVD--QASFOCSAPP 354  
368 GNPICDCVIRWANATGTRVFTEPQSTLCAE---PPDLQRLPVRVPPREMTDEC-LPL 423  
355 I--WDAPRLNISGRVAELKCR--TPPMSSVKNLLPNCVTLSHASRRPRISVINDGTLN 410  
424 ISPRSPFSLQVAGSGSVLHCSALAPPEFPIYVTPFAGLUTPAHAGRCRCVYPEGTLE 483  
411 FSHVLLSDTGVYTCMTYNVAGNSNAGYLNVSFAEL-----NTSNY----- 451  
484 LREVTAEEAGLYTCVAQNLVGADTKVSVVGRALLQPCRDGSGGLELRVQETHPYHILL 543  
452 SFTTIVVETTESPEDTKRYKXPVTTSTGQPAYTTS--TTVLQTRVPKQVAVPAT 509  
544 SWYTPPTVNTJNT-WSSASSLRGQATALRPLRGTHSYNTLRLLQATEYWACLQVAPA 602  
510 DTTDKMOTSLDEVMKTKIILGCFVA-----VTLLAAALIVFYKLKR---HQQRST 559  
603 DA---HTQLACVWATKEATSCHRALGRDPRGLIALLALAVLLAAGLAHLGTQPRKG 658  
560 VTAARTVEIIQVEDIPATSAATAAPSGVGEAVLPTHTDHNINNYTKPAHGAHT 619  
659 VGGRR-----PLPPAWAFMGWAPSVRVVSAPLVP-----WNP--GRKLP 697  
620 ENSIGNSLHPTVT 632  
698 RSSEGETLPLPLS 710

ESULT 2  
LRI HUMAN STANDARD; PRT; 546 AA.  
C QNZUI; 2003 (Rel. 41, Created)  
T 28-FEB-2003 (Rel. 41, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E Leucine-rich repeat transmembrane protein FLRT1 precursor  
E (Fibronectin-like domain-containing leucine-rich transmembrane protein  
E 1).  
N FLRT1.  
S Homo sapiens (Human).  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
P SEQUENCE FROM N.A. TISSUE SPECIFICITY, AND GLYCOSYLATION.  
X MEDLINE=20112755; PubMed=1084439;  
Lacy S.E., Hornemann C.G., Suzney E.A., Kunkel L.M.;  
T "Identification of FLRT1, FLRT2, and FLRT3: a novel family of  
transmembrane leucine-rich repeat proteins.";  
L Genomics 62:417-426(1999).  
C -!- FUNCTION: May have a function in cell adhesion and/or receptor  
C signaling.  
C -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
C -!- TISSUE SPECIFICITY: Expressed in kidney and brain.  
C -!- PTM: N-glycosylated.  
C -!- SIMILARITY: Contains 1 fibronectin type III domain.  
C -!- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
DR EMBL; AF169675; AAF28459.1; ALT\_INIT.  
DR Genew; HGNC:3760; FLRT1.  
DR MIM; 604806;  
DR GO; GO:0005887; C: integral to plasma membrane; NAS.  
DR GO; GO:0030222; F: adhesive extracellular matrix constituent a...; NAS.  
DR GO; GO:0005057; F: receptor signaling protein activity; NAS.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Cyp.  
DR Pfam; PF06041; fn3; 1.  
DR Pfam; PF00560; LRR; 8.  
DR Pfam; PF01463; LRRCT; 1.  
DR Pfam; PF01462; LRRNT; 1.  
DR SMART; SMO0060; FN3; 1.  
DR SMART; SMO0369; LRR\_TYP; 1.  
DR SMART; SMO0082; LRRCT; 1.  
DR SMART; SMO0013; LRRNT; 1.  
KW Cell adhesion; Repeat; Signal; Transmembrane; Leucine-rich repeat;  
KW Glycoprotein.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 646 LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN  
FT FLRT1.  
FT DOMAIN 21 524 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 525 545 POTENTIAL.  
FT DOMAIN 546 646 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 52 77 LRR 1.  
FT REPEAT 78 98 LRR 2.  
FT REPEAT 99 121 LRR 3.  
FT REPEAT 123 147 LRR 4.  
FT REPEAT 148 169 LRR 5.  
FT REPEAT 170 192 LRR 6.  
FT REPEAT 194 218 LRR 7.  
FT REPEAT 219 241 LRR 8.  
FT REPEAT 242 264 LRR 9.  
FT REPEAT 265 288 LRR 10.  
FT DOMAIN 407 485 FIBRONECTIN TYPE-III.  
FT CARBOHYD 221 221 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 646 AA; 71359 MW; FF2BF5DC3CA13C92 CRC64;  
Query Match 11.3%; Score 389; DB 1; Length 646;  
Best Local Similarity 23.8%; Pred. No. 8.7e-20;  
Matches 166; Conservative 93; Mismatches 270; Indels 168; Gaps 22;  
Qy 29 WI-LCAAIAAAS--AGPNCPSVCSCNQSKVCTRGSLSEVPQGIPSN----- 77  
Db 6 WFLCYGLAFUFTVIDSTTSCVCRCONGF--IYCNDRGLTSIPADIPDDATTLYLQNN 63  
Qy 78 -----RYLNMENNMIQIQADTFRLH 99  
Db 64 QINNAGIPQDLTKVNVYIYENDLDEFFINLPRSLREHLQDNVTRTARDSLRIP 123  
Qy 100 HLEVQLGRNSIR-QIEVGAFNGLASLNTLFLPNWLTVPISGAFYLSKRLRLRN 157  
Db 124 LLEKHLDDNSVTSIEBDAFADSKQLKLLFLSRNHLSSIPSGPLTLELR---LDN 180  
Qy 158 PTESIPSYAPNRPVSLMRLD--GELKKLEYISEGAFGLFKLVNLMGNCNKPNTLP 216  
Db 181 RSTIPLHAFKGLNSLRVLNDGNLANQRIADDTFSRLQNTLSLVRNSLAAP---- 236  
Qy 217 LVGLEELMSGNHFPFIRPGSFHGLSLKLMWNMSQVSLIERNAPDGLASIVELNLAH 276

Db 237 -----LNLPSAH-----LQKLYLQDNALSHIPVNTYLAKEMLERLRLDLSNN 276

Qy 277 NLSLPHLPTPLRYLVYELHHPNCCDILMLAWLREYIPFNCTCGRCHAPWHR 336

Db 277 NLTPLRGLFDLGNLAQLLRNFWFCGNLMLRDWVKARAANVVRGLMCOGPEKVR 336

Qy 337 GRYLVEVDQAFQC--SAPFTMDAPRLNISEGRMAELKCKTTPMSSVYKLLPNGTGLSH 394

Db 337 GWAIKDIITSEDECECTG-----OGGVANAAKTTASNEASATTPOGSLFTL 394

Qy 395 ASRHPRIISVLDGTLNFS-----HV--LLSTGYVTCKWNTVA-----430

Db 395 KAKRPGLR-LPDSNIDYPMATDGAKTALHVKALTADSIKITKATLPASSRFLSLWRL 443

Qy 431 GNSNASAVLNSTAEINTSNY-----SPTFTVTEITSPEDTTRKYKPV--P 477

Db 444 GSPAVGSGTETLVGCKDTEYLLTALPKSTYIICWMTESNAYVADET-----PVCACA 499

Qy 478 TTSYGQFAYTTSITVLQITTRVPKQAVPATDITDMQTSLSLDEVMKTKIIIGCFVAVT 537

Db 500 ETADSYGP-----TTLNQEQNAGPMASLPLAG-----IIGGAVALV 536

Qy 538 LLAAMLVYKLRKHQRQSTVTARTVEILOVDEDPATSAATAAPSGVSGEAVV 597

Db 537 FLFLVGLAICWTV---HQAGELLTTERAYNRGSRKEDYMGSGTKNSILIRGPGLOM 593

Qy 598 LPTIHDHINVTYKPAHGAHWTEISLNSLHPTVTI 634

Db 594 LP-----INPYAKEEYVHTTIPPSGSLCKATHTI 625

RESULT 3

FLR3\_HUMAN

ID FLR3\_HUMAN STANDARD; PRT; 649 AA.

AC QSNZU0; Q96K39; Q96K42; Q96K43; Q9P259;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Leucine-rich repeat transmembrane protein FLRT3 precursor

DE (Fibronectin-like domain-containing leucine-rich transmembrane protein

DE FLRT3 OR KIAA1469)

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

MEDLINE=20112755; PubMed=10644439;

LAZY S.B., Bonnemant C.G., Buzney E.A., Kunkel L.M.;

"Identification of FLRT1, FLRT2, and FLRT3: a novel family of

transmembrane leucine-rich repeat proteins."

Genomics 62:417-426(1999).

[2]

SEQUENCE FROM N.A.

TISSUE=Brain;

MEDLINE=2027482; PubMed=10819331;

Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XVII.

The complete sequences of 100 new cDNA clones from brain which code

for large proteins in vitro."

DNA Res. 7:143-150(2000).

[3]

SEQUENCE FROM N.A.

TISSUE=Embryo, and Teratocarcinoma;

Isoigai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yanamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project."

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

(4)

SEQUENCE FROM N.A.

MEDLINE=21638749; PubMed=11780052;

Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,

Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.S., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.B.,

Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.I., Martin S.L., McConachie I.J., McLeay K., McMurray A.A.,

Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,

Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Beck S.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Rogers J.;

"The DNA sequence and comparative analysis of human chromosome 20.";

Nature 414:865-871(2001).

[5]

SEQUENCE FROM N.A.

TISSUE=Kidney;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullany S.J.,

Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences".

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[1]

FUNCTION: May have a function in cell adhesion and/or receptor

signaling.

[1]

SUBCELLULAR LOCATION: Type I membrane protein (Probable).

[1]

TISSUE SPECIFICITY: Expressed in kidney, brain, pancreas, skeletal

muscle, lung, liver, placenta, and heart.

[1]

SIMILARITY: Contains 1 fibronectin type III domain.

[1]

SIMILARITY: Contains 10 leucine-rich (LRR) repeats.

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EMBL; AF169677; AAF28461.1; -

EMBL; AB040902; BAA95993.1; ALT\_INIT.

[illegible]

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Query Match      11.2%; Score 385; DB 1; Length 649;
Best Local Similarity 24.7%; Pred. No. 1.7e-19;
Matches 167; Conservative 94; Mismatches 270; Indels 146; Gaps 21;

37 AAASAGCNCPSVCSGNSQKSVKCTRRGLSEVPGQIPSN----- 76
b 22 APLSVMAKSPSVCRDAGP--IYCDRFELTSPCTPEDATLYIQNNQINNAGIPSDL 79
iy 77 -----TRYLNMENNIIQIQADTFERLHHLEVLQGRNS 110
b 80 KMLLKVERIYLYHNSLDEFPPTNLPKYVKEUHLQENNRITVDSLSKIPYLELHLDONS 139
iy 111 IR--QIEVGAFNGLASLNTLELFDNMLTVTPSGAFYLSKRLBELMRNNPIESIPSYAFN 168
b 140 VSAVSIIEGAFDSDNYLRLLFLSNLHLSLTPWGLPRTIEBLR--LDDNRISTISSPSLIQ 196
iy 169 RVPGLMRDL-GEUKKLEYISBGAFGLFNLKYLYNIGMNCNIKOMP-NLTPVLGLELEHENS 226
b 197 GLTSLKRLVLDGNLLNNHNGLDKVFNFNLVNLTLSELVRNSLTAAPVNL----- 244

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Qy	227	GNHPEIRPGSPHGLSSILKLLKWNQSVSLIERNAPDGLASLVLAHNHLSLPHDLF	281
Db	245	-----PG-----TNURKLYLQDNHINRVPNAPSYRLQLYLNDNSNNLSNLPGQIF	291
Qy	287	TPRLYLVLHLHHPNCCDILMLAWLREYIPFNSTCCG-RCHAPMHWGRYLVEVDQ	345
Db	292	DLDLNDITQLILRNFPWYCGCKMKVROWLQS-LPVKNVRGLMCOAPEKVRGMAIKDLNA	350
Qy	346	ASFOCSAFPIMDA-----PRDLNISEGRMAELKCTPMPSSVQVLLPNGTVLSHASRH	398
Db	351	ELFDCKCGSIVSTGIQTITAIENVTVPAGQNDAPVTKQPDIKPKLTKDHQTGSPSKT	410
Qy	399	PRISV--LNDGTLPNFHVLSDVTGYTCMTVNTVAGNSNASAYLNVSTAEALNTSNYSFFT	456
Db	411	ITITVKSVTSDTIHISWK-----ALPMTALRLSLKGLCHSPAFGSI	453
Qy	457	VVVFTEIIS-----PEDITRKYPVP-TTSTGQYQAYTTSTTVLIQTVRPKGVAVPA	508
Db	454	ETIVTGERSEYLVLTALPDSYKVCVMPMETSNUY----LPDETVPVCIETETAPLRMYNPT	510
Qy	509	TOTDRQMOTSLDEVNMTTKYI----IIGCFVAVTLAALAMLVFY-----K	549
Db	511	T-TLNREQEK-EPYKPNLPLAALIGGVALVLTIALLVQVHRRNGSLFRNCAYSK	566
Qy	550	LKRHQCRSTVTVAARTVZELIQVEDIPATISAAATAAPSGVSGGAVVLTPIHDHINYNT	609
Db	568	GRRRKDDYAEAGTKKONSILIRE-----TSFQMLPISNRPISKEEFPVHTIPPNGMNL	622
Qy	610	YKPAHGAHWNTENSLGNS 626	
Db	623	YKNNHSESSNFSYRDS 639	

RESULT 4

CHAD MOUSE

ID	CHAD MOUSE	STANDARD	PRT	358 AA.
AC	OS5226;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	18-SEP-2003 (Rel. 42, Last annotation update)			
DE	Chondroadherin precursor (Cartilage leucine-rich protein).			
GN	CHAD			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCB1_TaxID=10090;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=98126439; PubMed=9465299;			
RA	Landgren C., Beier D.R., Faessler R., Heinsegaard D., Sommerlin Y.;			
RT	"The mouse chondroadherin gene: Characterization and chromosomal			
RT	localization."			
RL	Genomics 47:84-91(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=98126439; PubMed=9465299;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			
RA	Bosak S.A., McSwain P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Phaney J., Helton E., Kettman C., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,			

RESULT 4	CHAD_MOUSE	CHAD_MOUSE	STANDARD;	PRT;	358 AA.
ID	_CHAD_MOUSE				
AC	OS5226;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Chondroectodermal precursor (Cartilage leupine-rich protein)				

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1].  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98126439; PubMed=9465299;  
RA Landgren C., Beter D.R., Faessler R., Heinegaard D., Sommarin Y.,  
RT "the mouse chondroadhesin gene: characterization and chromosomal  
ST localization";  
RL Genomics 47:84-91(1998).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=Salivary gland;  
RC TISSUE=22388357; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausnitzer S.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,  
RA Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC !- FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and  
 CC osteoblasts. This binding is mediated (at least for chondrocytes  
 CC and fibroblasts) by the integrin alpha(2)beta(1). May play an  
 CC important role in the regulation of chondrocyte growth and  
 CC proliferation (By similarity).  
 CC !- SUBUNIT: Mostly monomeric. Interacts with collagen type II (By  
 CC similarity).  
 CC !- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By  
 CC similarity).  
 CC !- TISSUE SPECIFICITY: Cartilage.  
 CC !- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SLRP) FAMILY. CLASS IV SUBFAMILY.  
 CC !- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: U96636; AAC39963.1; -;  
 DR EMBL: BC012672; AAH12672.1; -;  
 DR MGD: MGI:1096866; Chad.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00560; LRR; 10.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00369; LRR\_Typ; 5.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 KW Signal; leucine-rich repeat; Repeat; Glycoprotein;  
 KW Extracellular matrix.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 358 CHONDROADHERIN.  
 FT REPEAT 49 72 LRR 1.  
 FT REPEAT 73 96 LRR 2.  
 FT REPEAT 97 120 LRR 3.  
 FT REPEAT 121 144 LRR 4.  
 FT REPEAT 146 168 LRR 5.  
 FT REPEAT 170 192 LRR 6.  
 FT REPEAT 193 216 LRR 7.  
 FT REPEAT 217 240 LRR 8.  
 FT REPEAT 242 265 LRR 9.  
 FT REPEAT 266 290 LRR 10.  
 FT REPEAT 294 317 LRR 11.  
 FT DISULFID 22 37 BY SIMILARITY.  
 FT DISULFID 303 345 BY SIMILARITY.  
 FT DISULFID 305 325 BY SIMILARITY.  
 FT CARBOHYD 143 143 O-LINKED (POTENTIAL).  
 SQ SEQUENCE 358 AA; 40348 MW; 6A062FCEBF84A078 CRC64;  
 Query Match 11.1%; Score 380.5; DB 1; Length 358;  
 Best Local Similarity 29.0%; Pred. No. 1.6e-19;  
 Matches 106; Conservative 65; Mismatches 147; Indels 47; Gaps 10;  
 QY 16 ALLPRLVLTQVWLICAAIAAASAGPNCVSCSNQFQSKVCTRGRLSEVPGQIPS 75  
 DB 4 ALLFSLVFLA-----ILLPALA-----CPQCHCHGDLQHVICDKVGLQKIPK-VSE 50  
 QY 76 NTRYLNMENNTQMTQADTFRLHLHLEVLQGRNSIRQIEVGAFNGLASINLTLELFWNL 135  
 DB 51 TTLLNLRQNNPFLAANSFRTPNVLVSLHLOHCNIREVAAGAFGLKQLLYLSHNDI 110

QY 136 TVIPGAFYLSKRLRLMNNPIESIPYAFNRVPSLRLDLGLKLEYSISGAPEGL 195  
 DB 111 RVLKAGAPDILTETLYLDHKNKVELPGLLSPLVNLFIQLAN-NKIRELRAGAFOGA 169  
 QY 196 FPKYI-----NLGMCNFKMEN-----LTPLVGLLEEMSGNH 229  
 DB 170 KDLRLWLYSENALSSLSQGLSDVDENLAKFLDKNQLSSYFSAALSKLRVVEELKLSNP 229  
 QY 230 FPEIRGSGFHLSS-LKKLWVNSQVSIERNAFDGLASLVELNLAHNNLSLPHDLFTP 288  
 DB 230 LKSIPEINAFQSGRYLETILWLDNTLEKFSDAAPSGVTTLKHVLDNRLNQLPESF--P 287  
 QY 289 LRYLVELHLHHPNWCDCDILWAWLREYPTNSTCCGRCHAPMHMGRVLYVEDVQASP 348  
 DB 288 FDNLETLTITNNPKCTCOLRRLRWLE---AKASRPDATCSSPAKFGQIRDTF-ALR 343  
 QY 349 QCSAP 353  
 DB 344 SCKSP 348  
 RESULT 5  
 CHAD RAT  
 ID CHAD RAT STANDARD; PRT; 358 AA.  
 DT 070210;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DB Chondroaderin precursor (Cartilage leucine-rich protein).  
 GN CHAD.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Chondrosarcoma;  
 RX MEDLINE=98129774; PubMed=9461555;  
 RA Shen Z., Gantcheva S., Maansson B., Heinegaard D., Sommarin Y.;  
 RT "Chondroaderin expression changes in skeletal development.";  
 RL Biochem J 330:549-557(1998).  
 CC !- FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and  
 CC osteoblasts. This binding is mediated (at least for chondrocytes  
 CC and fibroblasts) by the integrin alpha(2)beta(1). May play an  
 CC important role in the regulation of chondrocyte growth and  
 CC proliferation (By similarity).  
 CC !- SUBUNIT: Mostly monomeric (By similarity).  
 CC !- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By  
 CC similarity).  
 CC !- TISSUE SPECIFICITY: Present in femoral head and rib cartilage, as  
 CC well as in tendon. Detected in bone marrow.  
 CC !- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SLRP) FAMILY. CLASS IV SUBFAMILY.  
 CC !- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.  
 CC  
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 CC  
 DR EMBL: AF004953; AAC40060.1; -;  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00560; LRR; 9.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00369; LRR\_Typ; 5.  
 DR SMART: SM00082; LRRCT; 1.





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DB 247 LQRLYLNNHISQLPSPFQMPQLNRLTLFGNSLKLSKLSLGI FGMPNRLRELYDNHIS 306
QY 252 -----SQVSLIERNAPDGLASIVELN----- 272
DB 307 SLDPNVFNLROQLVLIISRNQISFISPCAFNGLTFLRELSLFTNLAQDLQDNGVFRMLAN 366
QY 273 -----LAHNNLSLPHDLFTPLRYLVFLHULHHPWN 303
DB 367 LQNLISLQNNLRQLPCNIFANVNGMLMAIQNNQLENLPLGIFDHLGKLCRLBYDNFWR 426
QY 304 CQCDILNLAWL-----RYIPTNSTCCGRCHAPHHMGRYL-----VEVD 344
DB 427 CQSDILPLNWLNLNQLRGLGTDTPV-----CFSPANVRGQSLIINNNVAVPSVHPV 479
QY 345 QASQPCQSAFFIMDAP 359
DB 480 EYVPSYPTFWYDTP 494

RESULT 7
ID SLIT DROME STANDARD; PRT: 1504 AA.
AC P24014: Q24526; Q9W7F8; Q9V7F9; Q9XV4;
DT 01-MAR-1992 (Rel. 21, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Slit protein precursor.
GN SLI OR CG8355.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=9109665; PubMed=2176636;
RA Rothberg J.M., Jacobs J.R., Goodman C.S., Attavanis-Tsakonas S.;
RT "Slit: an extracellular protein necessary for development of midline
RT glia and extracellular axon pathways contains both EGF and LRR
RT domains.";
RL Genes Dev. 4:2169-2187(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM C).
RX MEDLINE=99200390; PubMed=10102267;
RA Kidd T., Bland K.S., Goodman C.S.;
RT "Slit is the midline repellent for the robo receptor in Drosophila.";
RL Cell 96:785-794(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champs M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Achayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Beeson K.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann M.,
RA Folsler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith I.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RN [4]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RC STRAIN=Berkeley; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE OF 898-1435 FROM N.A.
RC STRAIN=Canton-S; PubMed=3144436;
RX MEDLINE=89077533; PubMed=3144436;
RA Rothberg J.M., Hartley D.A., Walthers Z., Attavanis-Tsakonas S.;
RT "Slit: an EGF-homologous locus of D. melanogaster involved in the
RT development of the embryonic central nervous system.";
RL Cell 55:1047-1059(1988).
CC -|- FUNCTION: A short-range repellent, controlling axon crossing of
CC the midline and a long-range chemorepellent, controlling mesoderm
CC migration and patterning away from the midline. May interact with
CC extracellular matrix molecules.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=C;
CC IsoId=P24014-1; Sequence=Displayed;
CC Name=A;
CC IsoId=P24014-2; Sequence=VSP_001408;
CC Name=B;
CC IsoId=P24014-3; Sequence=VSP_001408, VSP_001409;
CC -|- TISSUE SPECIFICITY: In embryos, highest expression occurs around
CC the midline glia and low expression is observed around CNS axons
CC lateral to the midline.
CC -|- SIMILARITY: Contains 7 EGF-like domains
CC -|- SIMILARITY: Contains 24 leucine-rich (LRR) repeats.
CC -|- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC -|- SIMILARITY: Contains 1 laminin G-like domain.
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CC -----
CC EMBL: X53959; CAA37910.1; -
CC EMBL: AF125450; AAD25567.1; -
CC EMBL: AE003809; AAF58097.1; -
CC EMBL: AE003809; AAF58098.1; -
CC EMBL: AE003809; AAM70966.1; -

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DBL; M23543; AAA72722.1; ALT\_INIT.  
 HSP; P00740; 1EDM.  
 GO; GO:0005576; Extracellular; IEP.  
 GO; GO:0045493; Chemorepellant activity; IMP.  
 GO; GO:0007411; Axon guidance; IGI.  
 GO; GO:0008347; P:Glia cell migration; IMP.  
 GO; GO:0007509; P:mesoderm migration; IMP.  
 GO; GO:0030182; P:neuron differentiation; IMP.  
 GO; GO:0001052; Ax hydroxyl.  
 InterPro; IPR006208; Cys\_knot.  
 InterPro; IPR006207; Cys\_knot\_C.  
 InterPro; IPR00742; EGF\_2.  
 InterPro; IPR001881; EGF\_Like.  
 InterPro; IPR006209; EGF\_Like.  
 InterPro; IPR002049; Laminin\_EGF.  
 InterPro; IPR001791; Laminin\_G.  
 InterPro; IPR001611; LRR.  
 InterPro; IPR000483; LRR\_Cterm.  
 InterPro; IPR000372; LRR\_Nterm.  
 InterPro; IPR003591; LRR\_typ.  
 Pfam; PF00008; EGF; 7.  
 Pfam; PF00054; Laminin\_G; 1.  
 Pfam; PF00560; LRR\_16.  
 Pfam; PF01463; LRRCT; 4.  
 Pfam; PF01462; LRRNT; 4.  
 PRINTS; PR00011; EGF\_LAMININ.  
 PRINTS; PR00019; LEURICHERP.  
 SMART; SM00041; CT; 1.  
 SMART; SM00179; EGF\_CA; 2.  
 SMART; SM00282; LamG; 1.  
 SMART; SM00349; LRR\_TYP; 9.  
 SMART; SM00082; LRRCT; 4.  
 SMART; SM00013; LRRNT; 4.  
 PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 PROSITE; PS01185; CTCK\_1; 1.  
 PROSITE; PS01225; CTCK\_2; 1.  
 PROSITE; PS00022; EGF\_1; 7.  
 PROSITE; PS01186; EGF\_2; 5.  
 PROSITE; PS01187; EGF\_CA; 2.  
 PROSITE; PS00025; LAM\_G\_DOMAIN; 1.  
 Neurogenesis; Glycoprotein; Signal; Alternative splicing;  
 EGF-like domain; Repeat; Leucine-rich repeat.  
 SIGNAL 1 36  
 CHAIN 37 1504 SLIT PROTEIN.  
 CHAIN 37 1135 SLIT PROTEIN N-PRODUCT (BY SIMILARITY).  
 CHAIN 1136 1504 SLIT PROTEIN C-PRODUCT (BY SIMILARITY).  
 SITS 1135 1136 CLEAVAGE (BY SIMILARITY).  
 REPEAT 99 122 LRR 1.  
 REPEAT 123 146 LRR 2.  
 REPEAT 147 170 LRR 3.  
 REPEAT 171 194 LRR 4.  
 REPEAT 195 218 LRR 5.  
 REPEAT 219 242 LRR 6.  
 REPEAT 244 270 LRR 7.  
 REPEAT 270 294 LRR 8.  
 REPEAT 294 318 LRR 9.  
 REPEAT 318 342 LRR 10.  
 REPEAT 342 366 LRR 11.  
 REPEAT 366 390 LRR 12.  
 REPEAT 390 414 LRR 13.  
 REPEAT 414 438 LRR 14.  
 REPEAT 438 462 LRR 15.  
 REPEAT 462 486 LRR 16.  
 REPEAT 486 510 LRR 17.  
 REPEAT 510 534 LRR 18.  
 REPEAT 534 558 LRR 19.  
 REPEAT 558 582 LRR 20.  
 REPEAT 582 606 LRR 21.  
 REPEAT 606 630 LRR 22.  
 REPEAT 630 654 LRR 23.  
 REPEAT 654 678 LRR 24.

FT DOMAIN 931 968 EGF-LIKE 1.  
 FT DOMAIN 970 1007 EGF-LIKE 2.  
 FT DOMAIN 1009 1046 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 Query Match 10.9%; Score 375.5; DB 1; Length 1504;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-18;  
 Matches 111; Conservative 51; Mismatches 141; Indels 103; Gaps 8;  
 QY 46 CPSVCSNQFSKVCTRRGLSEVPGQIPSNTRYLNLMENNMIQIADTPRHHLHLEVLQ 105  
 DB 73 CPRVCSCTG--LNVDCSHRGTSVPRKISADVLELQGNLTVIYETDFQRLKRLMLQ 130  
 QY 106 LGRNSIRQIEVGAFFGLASLNTLFLFONLWLTVPISGAFYLSKLRLWLNRPISPSY 165  
 DB 131 LTDNQIHTIERNSFODLVSLRLR-----LNNRLKAIPEN 166  
 QY 166 AFNRVPSLWRLDLGELKLEVISGAEGLFNKLVNLGMCNIDKMPNLTPLVGLBLEM 225  
 DB 167 FVTSASLRLDI----- 179  
 QY 226 SGNHFEIRPGSFHGLSKLWVNSQVSLIERNADFGLASLVELNLNLSLPHDL 285  
 DB 180 SNNVITVGRVRFKGAQSLRSIQLDNNQITCLDRHAFKGLVELEILTNNNLTSLPHNI 239  
 QY 286 FPLRYLVELHHPNWCDCDILWAWLREYIPTNSTCGRCHAPMHEGRVLYVEVDQ 345  
 DB 240 FGLGLRALRLSDNPFACDCHLSWLSRPLRS--ATRLAPYTCQSPSKLQGNVADLHD 297  
 QY 346 ASFOCS-----APFIMDA---PRDLNISGRMAELKCRTPPMSSVVKWLLPNGTV----- 391  
 DB 298 QEFKCSGLTEHAPMECGAENSCHPFCADG---IVDCREKSLTSVPVTLPPDDITELRL 354  
 QY 392 -----LSHASRHPRIISVNDGTLNPSHVLLSDTGVTTCMV 426  
 DB 355 QNFITELPPKFSFSSFRRLRIDLSNNNISRIADALSGLQLTLV 400  
 RESULT 8  
 CHAD\_BOVIN  
 ID CHAD\_BOVIN STANDARD; PRT; 361 AA.  
 AC Q27972;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chondroadherin precursor (Cartilage leucine-rich protein) (38 kDa bone  
 protein).  
 OS Bos taurus (Bovine).  
 GN CHAD.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_taxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Cartilage;  
 RX MEDLINE=94342341; PubMed=8063792;  
 RA Neame P.J., Sommarin Y., Boynton R.B., Heinigaard D.;  
 RT "The structure of a 38-kDa leucine-rich protein (chondroadherin)  
 isolated from bovine cartilage".  
 RL J. Biol. Chem. 269:21547-21554(1994).  
 RP [2]  
 RP SEQUENCE OF 25-55 AND 77-97.  
 RC TISSUE=Bone;  
 RX MEDLINE=95113864; PubMed=7814406;  
 RA Hu B., Coulson L., Moyer B., Price P.A.;  
 RT "Isolation and molecular cloning of a novel bone phosphoprotein  
 related in sequence to the cystatin family of thiol protease  
 inhibitors".  
 RL J. Biol. Chem. 270:431-436(1995).  
 CC -!- FUNCTION: Promotes attachment of chondrocytes, fibroblasts, and  
 osteoblasts. This binding is mediated (at least for chondrocytes  
 and fibroblasts) by the integrin alpha(2)beta(1). May play an  
 important role in the regulation of chondrocyte growth and

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CC CC proliferation.
CC CC -!- SUBUNIT: Mostly monomeric. Interacts with collagen type II (By
CC CC similarity).
CC CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC CC -!- TISSUE SPECIFICITY: Cartilage.
CC CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC CC (SRP) FAMILY. CLASS IV SUBFAMILY.
CC CC -!- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: U08018; AAA21330.1; -.
CC CC InterPro: IPR001611; LRR.
CC CC InterPro: IPR000483; LRR_Cterm.
CC CC InterPro: IPR000372; LRR_Nterm.
CC CC InterPro: IPR003591; LRR_type.
CC CC Pfam: PF00560; LRR; 10.
CC CC Pfam: PF01463; LRRCT; 1.
CC CC Pfam: PF01462; LRRNT; 1.
CC CC SMART: SM00369; LRR_TYP; 5.
CC CC SMART: SM00082; LRRCT; 1.
CC CC SMART: SM00013; LRRNT; 1.
CC CC Signal: Leucine-rich repeat; Repeat; Glycoprotein;
CC CC Extracellular matrix.
CC CC -----
CC CC SIGNAL 1 24 OR 23 (IN SOME ISOFORM(S)).
CC CC CHAIN 25 361 CHONDROADHERIN.
CC CC CHAIN 25 352 CHONDROADHERIN, MINOR FORM.
CC CC REPEAT 52 75 LRR 1.
CC CC REPEAT 76 99 LRR 2.
CC CC REPEAT 100 123 LRR 3.
CC CC REPEAT 124 147 LRR 4.
CC CC REPEAT 149 171 LRR 5.
CC CC REPEAT 173 195 LRR 6.
CC CC REPEAT 196 219 LRR 7.
CC CC REPEAT 220 243 LRR 8.
CC CC REPEAT 245 268 LRR 9.
CC CC REPEAT 269 292 LRR 10.
CC CC REPEAT 294 319 LRR 11.
CC CC BY SIMILARITY.
CC CC -----
CC CC O-LINKED (POTENTIAL).
CC CC C -> Y (IN REF. 2).
CC CC C -> W (IN REF. 2).
CC CC C -> H (IN REF. 2).
CC CC C -> L (IN REF. 2).
CC CC S -> R (IN REF. 2).
CC CC -----
CC CC QUERY MATCH 10.9%; Score 375; DB 1; Length 361;
CC CC Best Local Similarity 28.3%; Pred. No. 3.9e-19;
CC CC Matches 102; Conservative 66; Mismatches 153; Indels 40; Gaps 9;
CC CC -----
QY 20 PFVYLAQVWILCAIAAASAGPCPCVSCSNQFSAVCTRGELSEVPGQIPSNTRY 79
DB 4 FVLLXLSGLLASLPALAA-----CPQNCCHSDQLQHVICKVGLQKIPK-VSEKTKL 57
QY 80 LNMENNIOIQAOTFRHLHLEVLQGRNSTQIEVGAFNGLASLNTLELFDNWLTVIP 139
DB 58 LNLQRNFFVPLATNSPRAMFNLSLHLCQREVAAGAFGLKQIYLYLSHNDIRVLR 117
QY 140 SGAFVYLSKRLRLNNPISIPSAFNRVPSLMRLDLGELKLEYISEGAFELNKL 199
DB 118 AGAFDDLTETVLYLDHNKVTLEPRGLLSPLVNLFIQLNN-NKIRELSRGAFOGAKDLR 176
QY 200 YNLGLGNCNIK-----DMPN-----LTPVLGLELEMSGNHPEI 233

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DB 177 WLILSENSLSQPGALDDVENLAKFYLDNRQNLSSYPSAALSKLRVVEELKLSHNPISKI 236
QY 234 RPSGFHGLSS-LKKLVWMSQVSLIERNAPDGLASLVEINLAHNNLSLPHDLFTPLRYL 292
DB 237 PDNAFQSGRYLETLWLDNTNLEKPSDGAFLGVTTLKHVLENNRLHQPSNP--PFDSL 294
QY 293 VELHLHNPNWNCDDILWLAWLREYIPNNSCGCHAPMMHMRGYLYVEVDQASFOCSA 352
DB 295 ETTLTNNPWKCTCQLRGLRWLE---AKTSRPDATCASPFRGQHIRDTD-AFRGCKF 350
QY 353 P 353
DB 351 P 351

RESULT 9
RT4R MOUSE
ID RT4R MOUSE STANDARD; PRT; 473 AA.
AC Q99PI8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Reticulon 4 receptor precursor (Nogo receptor) (Nrg) (Nogo-66
DE receptor).
GN RT4R OR NOGOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=Swiss Webster;
RX MEDLINE=21069055; PubMed=11201742;
RA Fournier A.E., Grandpre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration."
RN Nature 409:341-346 (2001).
[2]
RP REVIEW.
RX MEDLINE=21888956; PubMed=11891768;
RA Ng C.B.L., Tang B.L.;
RT "Nogose and the Nogo-66 receptor: factors inhibiting CNS neuron
RT regeneration."
RL J. Neurosci. Res. 67:559-565 (2002).
CC -!- FUNCTION: Receptor for RTN4, OMG and MAG. Mediates axonal growth
CC inhibition and may play a role in regulating axonal regeneration
CC and plasticity in the adult central nervous system (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.
CC -----
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CC -----
CC EMBL: AF283462; AAC53611.1; -.
CC MGD; MGI:2336886; Rtnr.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0007409; P:axogenesis; IDA.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR000372; LRR_Nterm.
CC Pfam: PF00560; LRR; 8.
CC Pfam: PF01463; LRRCT; 1.
CC SMART; SM00369; LRR_TYP; 3.
CC SMART; SM00082; LRRCT; 1.

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DR SMART; SM00013; LRRNT; 1.  
KW Receptor; Signal; GPI-anchor; Repeat; Leucine-rich repeat.  
FT SIGNAL 1 26 POTENTIAL.  
FT CHAIN 27 447  
FT PROPEP 448 473 REMOVED IN MATURE FORM (POTENTIAL).  
FT LIPID 447 447 GPI-ANCHOR (POTENTIAL).  
FT REPEAT 56 79 LRR 1.  
FT REPEAT 81 103 LRR 2.  
FT REPEAT 105 128 LRR 3.  
FT REPEAT 129 152 LRR 4.  
FT REPEAT 153 176 LRR 5.  
FT REPEAT 178 200 LRR 6.  
FT REPEAT 202 224 LRR 7.  
FT REPEAT 225 248 LRR 8.  
FT REPEAT 250 273 LRR 9.  
FT REPEAT 316 339 LRR 10.  
SQ SEQUENCE 473 AA; 50987 MW; 14C5270B5F57E7C CRC64;

Query Match 10.8%; Score 372.5; DB 1; Length 473;  
Best Local Similarity 30.1%; Pred. No. 8.3e-19;  
Matches 126; Conservative 57; Mismatches 154; Indels 81; Gaps 17;

29 WILCAIAAASAGPQNCPSVCSNQFSKV--CTRRLSEVPSQIPSNRYLNLMENN 86  
14 WVLW--LQAWRVATP--CPGACVCYNE-PKVTTSCPGQGLQAVPTGIPASSQRIFLHGNR 68  
87 IQMIOADTFRHLHLEVLQGRNSIROIEVGAFNGLASLNTLLELFDN-WLTVIPSGAFV 145  
69 ISHVPAAFSQCRNLTLINLHNSALADIAAFTGLTLEQLDLSNAQHVVDPPTTFG 128  
146 LSKRLRLRNPIESIPSYAFNRVPSIMRLDLGELKLEIYISGAFGLFNLYLNLM 205  
129 LGHLHTL-----HLDRGLREL---GPGLFRGLAALQYLYLQD 163  
206 NIYKDMNLT--PLVGLLEEMSGNHPEPSPGSLSKLKLWNQSVSLIERNAD 263  
164 NNLQALPDNTRFDLGNLTHLFLHGNRIPSPVPEAFRLGLSLDLHLHQHVARVHPHAFR 223  
264 GLASLVELNLNHNLSLPHDLTPFLRYVELHHLHNPWNCDCDILWLAWLREYIPTNS 323  
224 DLGLMTLYLFANNLSMLPAEVLNPLSLQYLRNDNPNWVCDRCRAPLWNLQKPGSS 283  
324 TCGRCHAPMHMRGYLVEVDQASFO---CSAPP-----INDAPRLN---- 363  
284 EV--PCNLQRLADRLKRLAASDLGCAVASGFPFRPQTSQLTDBELLSPKCCQPDAA 341  
364 -----ISEGRMAE-----LKCRTPMSVKWLLPNGTVLSHSHRPISLVND---GTL 409  
342 DKASVLEPFRPASGNALKGRVPPGDT-----PPGN--GSGPRH-----INDSPFGTL 387  
[1]

RESULT 10  
R15 RAT  
D\_LR15 RAT STANDARD; PRT; 578 AA.  
Q8R5M3;  
15-SEP-2003 (Rel. 42, Created)  
15-SEP-2003 (Rel. 42, last sequence update)  
15-SEP-2003 (Rel. 42, last annotation update)  
Leucine-rich repeat-containing protein 15 precursor (rLib).  
LRRC15 OR L1B.  
Rattus norvegicus (Rat).  
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
C STRAIN=Wistar; TISSUE=Fetal brain;  
X MEDLINE=21645900; PubMed=11785964;  
A Satoh K., Hata M., Yokota H.;  
T "A novel member of the leucine-rich repeat superfamily induced in rat  
L astrocytes by beta-amyloid."  
Biochem. Biophys. Res. Commun. 290:756-762(2002).  
C -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -I- INDUCTION: By beta-amyloid.  
CC -I- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.  
CC  
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CC  
CC EMBL: AB071036; BAB84586.1; --  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR004483; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00560; LRR; 14.  
DR Pfam; PF01463; LRRCT; 1.  
DR SMART; SM00369; LRR\_Typ; 11.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00013; LRRNT; 1.  
KW Repeat; Leucine-rich repeat; Transmembrane; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 578 LEUCINE-RICH REPEAT-CONTAINING PROTEIN  
15.  
FT DOMAIN 22 535 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 536 556 POTENTIAL.  
FT DOMAIN 557 578 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 51 75 LRR 1.  
FT REPEAT 76 99 LRR 2.  
FT REPEAT 100 123 LRR 3.  
FT REPEAT 125 147 LRR 4.  
FT REPEAT 148 171 LRR 5.  
FT REPEAT 173 195 LRR 6.  
FT REPEAT 196 219 LRR 7.  
FT REPEAT 221 243 LRR 8.  
FT REPEAT 244 267 LRR 9.  
FT REPEAT 269 291 LRR 10.  
FT REPEAT 292 315 LRR 11.  
FT REPEAT 316 339 LRR 12.  
FT REPEAT 340 363 LRR 13.  
FT REPEAT 364 387 LRR 14.  
FT REPEAT 389 411 LRR 15.  
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 578 AA; 64127 MW; 991BD057F5912591 CRC64;

Query Match 10.8%; Score 371.5; DB 1; Length 578;  
Best Local Similarity 25.3%; Pred. No. 1.3e-18;  
Matches 118; Conservative 57; Mismatches 131; Indels 161; Gaps 11;

QY 27 QVWILCAIAAASAGPQNCPSVCSNQFSKVCTRRGLSEVPSQIPSNTR----- 78  
DB 14 QAWALGLAY-----YGCPSCTCS-RASQVCECTCARIVAMPTPLPWNAWSLQVVNTH 64  
QY 79 -----YINLM-----ENNIOIADTFRHLHLEVLQGRNSIROIEVGAFNGL 122  
DB 65 ITLPELNLFLNISALIALKMKKEKSELTPGAFNLGSLRYLSLANNKLEMLPIRVFDV 124  
QY 123 ASLNTLELFDNWLTVIPSGAFVYLSKRLRLRNPIESIPSYAFNRVPSLMLDLGELK 182  
DB 125 NNLESLLSNQVLQVQIQPQFSQPSNRLRELQHLGNWLESIPBEAFPHLYGLTYLNLR-N 183  
QY 183 KLEYISGAFGLFNLYLNLMCNKOMP-----NUTP----- 216  
DB 184 SFTHLSPLRFCHLGNLQVLRFLHNRSLSDIPMGFTDALGNLQELALQENQITLSPGLFHN 243  
QY 217 -----LVGLSELEMSGNHFPPIRPGSFHGLSSLKLLWMMN- 251  
DB 244 NRMQLRLYLNHHISQLPGIFMQLPQLNKLTLFGNSLRLESPGVFGPMPNLKELMYNN 303  
QY 252 -----SQVSLIERNADFGLASLVELN----- 272  
[1]

Db 304 HITSADNTFSLNQLVILSHNQLTYSFGAFNGLTNLRLSLTNALQDLSNVFRS 363  
 QY 273 -----LAHNNLSLPHDLFTPLRYLVELLHN 300  
 Db 364 LANLQNISQSNRLRQPSIFANVGLTIOQNNLENLPGLFDHVLNCELRLYDN 423  
 QY 301 PNCDCDILAWLW---REYPTNSTCCGRCHAPMGRGRYLVVD 344  
 Db 424 PNCDCDILPNNWLLNRLRLGDTLPV--CSSPANVRGQSLVIN 468

RESULT 11  
 ID RT4R RAT STANDARD; PRT; 473 AA.  
 AC Q99M75;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Reticulon 4 receptor precursor (Nogo receptor) (Ngr) (Nogo-66 receptor)  
 GN RTN4R OR NOGOR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Jin W.-L., Jia W., Long M., Ju G.;  
 RT "Identification and preparation of polyclonal antibody against rat Nogo receptor";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Certe T., van der Haar M.E., Bandlow C.E., Huber A.B., Simonen M.,  
 RA Schreil L., Broesamle C., Schwab M.E.;  
 RT "Nogo-A: a molecule with two active sites and two membrane topologies";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=2188956; PubMed=11891768;  
 RA Ng C.E.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron regeneration";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 RN [4]  
 RP FUNCTION  
 RX MEDLINE=22033691; PubMed=12037567;  
 RA GrandPre T., Li S., Strittmatter S.M.;  
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration";  
 RL Nature 417:547-551(2002).  
 CC -1- FUNCTION: Receptor for RTN4, OMG and MAG. Mediates axonal growth inhibition and may play a role in regulating axonal regeneration and plasticity in the adult central nervous system (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).  
 CC -1- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.  
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 CC EMBL; AF028438; AA020166.1; -  
 CC EMBL; AY462390; AA046772.1; -  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.

DR InterPro; IPR003591; LRR\_TYP.  
 DR Pfam; PF00560; LRR; 8.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR SMART; SM00369; LRR\_TYP; 3.  
 KW Receptor; Signal; GPI-anchor; Repeat; Leucine-rich repeat.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 447 RETICULON 4 RECEPTOR.  
 FT PROPEP 448 473 REMOVED IN MATURE FORM (POTENTIAL).  
 FT LIPID 447 447 GPI-ANCHOR (POTENTIAL).  
 FT REPEAT 56 79 LRR 1.  
 FT REPEAT 80 103 LRR 2.  
 FT REPEAT 103 128 LRR 3.  
 FT REPEAT 129 152 LRR 4.  
 FT REPEAT 153 176 LRR 5.  
 FT REPEAT 178 200 LRR 6.  
 FT REPEAT 202 224 LRR 7.  
 FT REPEAT 225 248 LRR 8.  
 FT REPEAT 250 273 LRR 9.  
 FT REPEAT 316 339 LRR 10.  
 FT CONFLICT 12 13 FT -> LA (IN REF. 2).  
 FT CONFLICT 43 43 R -> C (IN REF. 2).  
 FT CONFLICT 53 53 A -> T (IN REF. 2).  
 FT CONFLICT 284 284 G -> E (IN REF. 2).  
 FT CONFLICT 287 287 S -> C (IN REF. 2).  
 FT CONFLICT 303 303 T -> A (IN REF. 2).  
 FT CONFLICT 353 355 V -> A (IN REF. 2).  
 SQ SEQUENCE 473 AA; 50858 MW; FF87A6643F3A0A35 CRC64;

Query Match 10.8%; Score 370; DB 1; Length 473;  
 Best Local Similarity 30.0%; Pred. No. 1.2e-18;  
 Matches 130; Conservative 52; Mismatches 152; Indels 100; Gaps 18;

QY 19 LPEVYLTAQVWILCAIAAASAGPQNCPSVCSNPFQKVCVTR--RGLSEVPGQIPSN 76  
 Db 11 LPTWVWLQWLRV-----ATP--CFGACVCVNE--PKVTTSPPQOGLQAVPAGIPAS 58  
 QY 77 TRYLNLMENNIMQIQADTPRHLHLHLVQLGRNSIRQIEVGAFNGLASINTLEFDN-WL 135  
 Db 59 SQRIPLHGKRIISVYTPAASPOSQCNLTILWLSNALAGIDAAAFGLTLLQLDLSNLAQL 118  
 QY 136 TVTPSGAFYELSKLRELWLRNPIESIPSYAFNRVPSLMRLDLGELKKLEVISGAFGL 195  
 Db 119 RYVDPTTFRGLGLHTL-----HLDRCGLQEL-----GPGLFRL 153  
 QY 196 ENLKYLNLMGCMNKMPNLT--PLVGLLEEMSGNHFPFIRPGSPHGLSSLLKLMWVNSQ 253  
 Db 154 AALQVLYLQNNLQALPDNTFRDLGNLTHLFLHGNRIPSVPEHAERGLSLDRLLHQNH 213  
 QY 254 VSLIERNAFDGLASIVELMLAHNNLSLPHDLFTPIRYLVHLHLHNPWNCDCDILWLA 313  
 Db 214 VARVHPHAFRDLGRMLTLYLFANNLSMLPAEVLVPLRSLOVLRNLNDNFVWCDRCARPLWA 273  
 QY 314 WLREY-----IPTNSTCCGRCHAPMGRGRYLVVDQASFO-----CSAPF----- 354  
 Db 274 WLQKFRGSSGVPSN-----LQRLAGRDILKELATSDLEGCAVAGSPFRPTQNTLT 325  
 QY 355 ---IMDAPRLN-----ISEGRMAE---LKCRTFPMSSVVKLLPNGTVLSHARRH 398  
 Db 326 DEELGLPKCCQDAAADKASVLEPGRPASVGNALKGRVPPGDT-----PPGN--GSGPRH 378  
 QY 399 PRISVLND---GTL 409  
 Db 379 -----INDSPFGTL 387

RESULT 12  
 ID RT4R MACFA STANDARD; PRT; 473 AA.  
 AC Q9N0E3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Reticulon 4 receptor precursor (Nogo receptor) (Ngr) (Nogo-66



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305 TCQLGRLRWLEAKASRRDPATCA---SPAKFKGQHIRTD-AFRSCKFP 349

RESULT 14

RT4R HUMAN

ID RT4R HUMAN STANDARD; PRT; 473 AA.

AC Q92R6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Reticulon 4 receptor precursor (Nogo receptor) (Ngr) (Nogo-66 receptor)

GN RTN4R OR NOGOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=21069055; PubMed=11201742;

RA Fournier A.E., GrandPre T., Strittmatter S.M.;

RT "Identification of a receptor mediating Nogo-66 inhibition of axonal regeneration."

RL Nature 409:341-346(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

MEDLINE=20057165; PubMed=10591208;

RA Durham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M., Clapp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Corroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.B., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashregi-Mohammadi M., Matthews L.H., Mccann O.T., McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.I., Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minochima A., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bems G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker A., Wamsley A., Wohlmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanaki J.P., Feyrad M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,

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CC ENBL; U96769; AAC13410.1; --

CC ENBL; U96767; AAC13410.1; JOINED.

CC ENBL; U96768; AAC13410.1; JOINED.

CC ENBL; AF371328; AAK51556.1; --

CC Genew; HGNC:1909; CHAD.

CC MIM: 602178; --

CC GO; GO:0005578; C:extracellular matrix; TAS.

CC GO; GO:0005201; F:extracellular matrix structural constituent; NAS.

CC GO; GO:0001558; P:regulation of cell growth; NAS.

CC InterPro; IPRO01611; LRR.

CC InterPro; IPRO00483; LRR Cterm.

CC InterPro; IPRO00372; LRR Nterm.

CC InterPro; IPRO003591; LRR typ.

CC Pfam; PF00560; LRR; 10.

CC Pfam; PF01463; LRRCT; 1.

CC Pfam; PF01462; LRRNT; 1.

CC SMART; SM00369; LRR\_TVP; 4.

CC SMART; SM00082; LRRCT; 1.

CC SMART; SM00013; LRRNT; 1.

CC Signal; Leucine-rich repeat; Repeat; Glycoprotein;

KW Extracellular matrix

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 359 CHONDRODHERIN.

FT REPEAT 50 73 LRR 1.

FT REPEAT 74 97 LRR 2.

FT REPEAT 99 121 LRR 3.

FT REPEAT 122 145 LRR 4.

FT REPEAT 147 169 LRR 5.

FT REPEAT 171 193 LRR 6.

FT REPEAT 194 217 LRR 7.

FT REPEAT 218 241 LRR 8.

FT REPEAT 243 266 LRR 9.

FT REPEAT 267 290 LRR 10.

FT REPEAT 292 317 LRR 11.

FT DISULFID 23 38 BY SIMILARITY.

FT DISULFID 304 346 BY SIMILARITY.

FT DISULFID 306 326 BY SIMILARITY.

FT CARBOHYD 144 144 O-LINKED (POTENTIAL).

FT CONFLICT 114 114 V -> L (IN REF. 2).

FT CONFLICT 166 166 P -> A (IN REF. 2).

SQ SEQUENCE 359 AA; 40487 MW; 9A318D0A15C157A0 CRC64;

Query Match 10.8%; Score 365.5; DB 1; Length 359;

Best Local Similarity 28.9%; Pred. No. 1.8e-18;

Matches 101; Conservative 62; Mismatches 149; Indels 37; Gaps 9;

QY 31 LCAAIATAASAGPQNCPSVCSNOPSKVCTRRGLSEVPQIPGIPNTRYLMENNIQMI 90

DB 12 LLACGLPALAACPN-----CHCHSDLOHVCDKVGQKIPK-VSEKTLNLRNPPVL 66

QY 91 QADTFRLHHLVQLGRNSIRQIEVGAFNGASLNTLELFDNMTVTPSGAFYSLKL 150

DB 67 AANSFRPNVLSLHLCQIREVAAGPFGKLIYLYSHNDIRVRAGAFDLDLT 126

QY 151 ELWLRNNPTESIPYAFNRVPSLRMLDLGELKLE-----YISE----- 189

DB 127 YLYLHKNKTEPRGLLSPLNLFILQNNKIRLRAGPQCAKDLRWLVLSNLSL 186

QY 190 --GAFGLFNLYLNGMKNIDMPN--LTPVLVGLLEELMSGNHPEIRPGSFGHLS-L 244

DB 187 QPCALDDVENLAKFHVDRNQLNSYFSAALSRLRVVEELKLSHPLKSPIDNAPQSGRYL 246

QY 245 KKLWNNSQVSLIERNAPDGLASLVELNLAHNSLSLPHDLFTPLRYLVELFLHNPNPC 304

DB 247 ETULWNTNLEKPSDGAFLGVTLKGVHLENRLNQLFSNF--PPDSLETALTNPKWC 304

QY 305 DCDILWLAWLREYIPTNSTCCGRCHAPMHRGRYLYVEVDQASFOCSAP 353



UA Tilahun Y., Wright H.;  
 UT "The DNA sequence of human chromosome 22.";  
 LN Nature 402:489-495(1999).  
 LN [4]  
 LN SEQUENCE FROM N.A.  
 IC TISSUE=Lung;  
 IC MEDLINE=22389257; PubMed=12477932;  
 IC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 IC Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 IC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 IC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 IC Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,  
 IC Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 IC Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 IC Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar J.S.,  
 IC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,  
 IC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 IC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 IC Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 IC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 IC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 IC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 IC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 IC Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 IC "Generation and initial analysis of more than 15,000 full-length  
 IC human and mouse cDNA sequences.";  
 IC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 IC [5]  
 IC FUNCTION.  
 IC MEDLINE=22033691; PubMed=12037567;  
 IC Grandpre T., Li S., Strittmatter S.M.;  
 IC "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
 IC Nature 417:547-551(2002).  
 IC [6]  
 IC INTERACTION WITH OMG.  
 IC MEDLINE=22082293; PubMed=12068310;  
 IC Wang X.C., Koprivica V., Kim J.A., Sivasankaran R., Guo Y., Neve R.L.,  
 IC He Z.;  
 IC "Oligodendrocyte-myeelin glycoprotein is a Nogo receptor ligand that  
 IC inhibits neurite outgrowth.";  
 IC Nature 417:941-944(2002).  
 IC [7]  
 IC INTERACTION WITH MAG.  
 IC MEDLINE=22171378; PubMed=12089450;  
 IC Liu B.P., Fournier A., Grandpre T., Strittmatter S.M.;  
 IC "Myelin-associated glycoprotein as a functional ligand for the Nogo-66  
 IC receptor.";  
 IC Science 297:1190-1193(2002).  
 IC [8]  
 IC REVIEW.  
 IC MEDLINE=22171401; PubMed=12183616;  
 IC Woolf C.J., Bloechlinger S.;  
 IC "It takes more than two to Nogo.";  
 IC Science 297:1132-1134(2002).  
 IC [9]  
 IC REVIEW.  
 IC MEDLINE=21889956; PubMed=11891769;  
 IC Ng C.E.L., Tang B.L.;  
 IC "Nogog and the Nogo-66 receptor: factors inhibiting CNS neuron  
 IC regeneration.";  
 IC J. Neurosci. Res. 67:559-565(2002).  
 IC -!- FUNCTION: Receptor for RTN4, OMG and MAG. Mediates axonal growth  
 IC inhibition and may play a role in regulating axonal regeneration  
 IC and plasticity in the adult central nervous system.  
 IC -!- SUBUNIT: Homomultimer.  
 IC -!- SUBCELLULAR LOCATION: Widely distributed in the brain but highest levels in  
 IC the gray matter. Low levels in heart and kidney not expressed in  
 IC oligodendrocytes (white matter).  
 IC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.  
 IC  
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 CC -----  
 CC EMBL; AF283463; AAC53612.1; -;  
 CC EMBL; AL834449; CAD39109.1; -;  
 CC EMBL; AC058790; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL; AC007663; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL; BC011787; AAH11787.1; -;  
 CC Genew; HGNC:18601; RTN4R.  
 CC MIM; 605566; -;  
 CC GO; GO:0016020; C:membrane; NAS.  
 CC GO; GO:0004872; F:receptor activity; NAS.  
 CC GO; GO:0007409; F:axonogenesis; NAS.  
 CC InterPro; IPR001611; LRR.  
 CC InterPro; IPR000483; LRR\_Cterm.  
 CC InterPro; IPR003591; LRR\_type.  
 CC Pfam; PF00560; LRR; 7.  
 CC Pfam; PF01463; LRRCT; 1.  
 CC Receptor; Signal; GPI-anchor; Repeat; Leucine-rich repeat.  
 CC SIGNAL 1 26 POTENTIAL.  
 CC FT CHAIN 27 447 RETICULON 4 RECEPTOR.  
 CC FT PROPEP 448 473 REMOVED IN MATURE FORM (POTENTIAL).  
 CC FT DOMAIN 435 442 POLY-GLY.  
 CC FT LIPID 447 447 GPI-ANCHOR (POTENTIAL).  
 CC FT REPEAT 55 79 LRR 1.  
 CC FT REPEAT 81 103 LRR 2.  
 CC FT REPEAT 104 128 LRR 3.  
 CC FT REPEAT 129 152 LRR 4.  
 CC FT REPEAT 153 176 LRR 5.  
 CC FT REPEAT 178 200 LRR 6.  
 CC FT REPEAT 202 224 LRR 7.  
 CC FT REPEAT 225 248 LRR 8.  
 CC FT REPEAT 250 273 LRR 9.  
 CC SQ SEQUENCE 473 AA; 50707 MW; CA5624B24C584702 CRC64;  
 Query Match 10.6%; Score 364; DB 1; Length 473;  
 Best Local Similarity 30.3%; Pred. No. 3.3e-18;  
 Matches 128; Conservative 49; Mismatches 155; Indels 90; Gaps 16;  
 QY 28 VWILCAIAAASAGPQNCPSVCSNQPSKV--CTTRGLSEVPQIGIPSNTRYLMNEN 85  
 DB 16 LWLOAWQAAP-----CPGACVCYNE-PKVTTSQFQGLQAVPGVIPAASQRIPLHGN 67  
 QY 86 NIQMIQADTFPHLHLEVLQIGRNSIQIEVGAFNGIASLNTLELFDN-WLTVIPSGAFE 144  
 DB 68 RISHVPAASFEACENTILMLHSNVLARIDAAFTGLALLEQLDLSNQAQLRSVDPAFH 127  
 QY 145 YLSKLRSLMLNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAPFGLFNKLYNLG 204  
 DB 128 GLGRHLTL-----HLDRCGLQEL-----GPGLEFGLAALQYLYLQ 162  
 QY 205 MCNIKDMENLT--PLVGLLEEMSGNHFFRIRPGSFHGLSSLLKKLWNNQSVSLIERNAF 262  
 DB 163 DNALQALPDDTFRDLGNLTHLFLGNRISSVPEAFGLSLDRLLLLKQNRVAHVPHAF 222  
 QY 263 DGLASVELNLNHNLSLPHDLFTPLRYLVHLHNNPNCDCDILMLAWNLREYIPTN 322  
 DB 223 RDLGRALTYLFPANNLSALPTEALAPLRLAQYLRLNPNPWCDCRAPLWAWLQKFRGSS 282  
 QY 323 STCCGRCHAPMHMEGRYLVEVDQASFO-----CSAPPI 355  
 DB 283 SEV--PCSLPORLAGRDLKRLAANDLOGCAVATGPHYPIWTGRATDEEPLGLPKCQCP-- 338  
 QY 356 MDAPRDNLNIS-GRMAE-----LKCRTPPMSSVKWLLPNGTVLSHSHRHPRIISVLND---G 407  
 DB 339 -DAADKASVLEPGRPASGNAKGRVPPGDS-----PPGN--GSGPRH-----INDSPFG 385  
 QY 408 TL 409  
 DB 386 TL 387

RESULT 15  
FLR2\_HUMAN STANDARD; PRT; 660 AA.  
AC O43155;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Leucine-rich repeat transmembrane protein FLRT2 precursor  
DE (Fibronectin-like domain-containing leucine-rich transmembrane protein  
DE 2).  
GN FLRT2 OR KIAA0405.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GLYCOSYLATION.  
RP MEDLINE=20112755; PubMed=1064439;  
RA Lacy S.E., Bonnemant C.G., Buzney E.A., Kunkel L.M.;  
RT "Identification of FLRT1, FLRT2, and FLRT3: a novel family of  
RT transmembrane leucine-rich repeat proteins.";  
RL Genomics 62:417-426(1999).  
RN [2]  
SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98116655; PubMed=9455477;  
RA Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. VIII.  
RT 78 new cDNA clones from brain which code for large proteins in  
RT vitro.";  
RL DNA Res. 4:307-313(1997).  
CC -!- FUNCTION: May have a function in cell adhesion and/or receptor  
CC signaling.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: Expressed in pancreas, skeletal muscle, brain,  
CC and heart.  
CC -!- PM: N-glycosylated.  
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
CC -!- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.  
CC  
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CC  
CC -----  
CC EMBL: AF169676; AAF28460.1; --  
CC EMBL: AB007865; BA23701.1; --  
CC Genew: HGNC:3761; FLRT2.  
CC MIM: 604807; --  
CC GO: GO:0005887; C: integral to plasma membrane; NAS.  
CC GO: GO:0030222; F: adhesive extracellular matrix constituent a. . .; NAS.  
CC GO: GO:0005057; F: receptor signaling protein activity; NAS.  
CC InterPro: IPR003961; FN III.  
CC InterPro: IPR016111; LRR.  
CC InterPro: IPR000483; LRR\_Cterm.  
CC InterPro: IPR000372; LRR\_Nterm.  
CC InterPro: IPR003591; LRR\_tyr.  
CC Pfam: PF00041; fn3; 1.  
CC Pfam: PF00560; LRR; 8.  
CC Pfam: PF01463; LRRCT; 1.  
CC Pfam: PF01482; LRRNT; 1.  
CC SMART: SM00060; FN3; 1.  
CC SMART: SM00069; LRR\_TF; 1.  
CC SMART: SM00082; LRRCT; 1.  
CC SMART: SM00013; LRRNT; 1.  
CC Cell adhesion; Repeat; Signal; Transmembrane; Leucine-rich repeat;  
CC Glycoprotein.

FT SIGNAL 1 35  
FT CHAIN 36 660  
FT  
FT POTENTIAL.  
FT LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN  
FT FLRT2.  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT LRR 1.  
FT LRR 2.  
FT LRR 3.  
FT LRR 4.  
FT LRR 5.  
FT LRR 6.  
FT LRR 7.  
FT LRR 8.  
FT LRR 9.  
FT LRR 10.  
FT FIBRONECTIN TYPE-III.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 521 521  
SQ SEQUENCE 660 AA; 74048 MW; 9B15F283B0D5F778 CRC64;  
Query Match 10.4%; Score 356.5; DB 1; Length 660;  
Best Local Similarity 30.1%; Pred. No. 1.7e-17;  
Matches 111; Conservative 38; Mismatches 135; Indels 85; Gaps 10;  
Qy 46 CPSCVCSGKQFQKVTCTRGSLSEVQGI----- 73  
Db 36 CPSCVCRDRNF--VYCNERLSVPLGIDEGVTVIYLNQNNAGFPABLNHVSHTV 93  
Qy 74 -----PNTRYLMNENIOMIQADTFRLHHLHLEVLQLGNSIRQ--IEVG 117  
Db 94 YLYGNQLDEFPNNLPKNVAVLHQQNIQTFISRAALQQLKLEHLDDNSTVGVVDG 153  
Qy 118 AFNGLASLTLELFDNLTIVISGAFYLSKRELWLNPNPIESFYAFNVPVSLRLD 177  
Db 154 AFPEAISLKLFLSKNHLSSVPGV---LPVDLQELRVVDENRAVISCDAFQNTSLERLI 210  
Qy 178 L-GELKKLEYISGAFEGFLNKLMLGMCNKDKPNTLPLVGLLEELMSGHFFPEIRPG 236  
Db 211 VDNGLLTNKGIASTFSLTKLKEFSI-----VRNLSHPDPLPG 251  
Qy 237 SFHGLSLKKLWNNQSVSLIERNAPDGLASLVELNLAHNNLSSLPDLPFLRLVLEHL 296  
Db 252 -----THLIRLYQDNQIHPIPTAFSNLRKLERLDISNNQLRMLTQGVFDNLNKLQT 306  
Qy 297 LHENPNCCDILNLAWLREYIPTNSTCCG-RCHAPMHRGRYLVVDQASFC----- 350  
Db 307 ARNPWFCCSICKVITENLK-YIPSSLVNVRGFWCQCPQVGRGVAVRELNNLLSCPTTTP 365  
Qy 351 SAPPIMDAP 359  
Db 366 GLPLFTTAP 374

RESULT 16  
LGR4\_RAT STANDARD; PRT; 951 AA.  
ID LGR4\_RAT  
AC Q922H4;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucine-rich repeat-containing G protein-coupled receptor 4 precursor.  
GN GPR48 OR LGR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RC MEDLINE=99065210; PubMed=98499958;



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EMBL; Z69594; CAA93440.1; --  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR Cterm.  
DR InterPro; IPR000372; LRR Nterm.  
DR InterPro; IPR003591; LRR typ.  
DR Pfam; PF00560; LRR; 13.  
DR Pfam; PF01463; LRRCT; 1.  
DR PRINTS; PRO00019; LEURICHRPT.  
DR SMART; SM00369; LRR typ; 10.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00013; LRRNT; 1.  
KW Platelet; Transmembrane; Glycoprotein; Blood coagulation;  
Repeat; Leucine-rich repeat; Cell adhesion; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 567  
FT DOMAIN 17 522  
FT TRANSMEM 523 543  
FT DOMAIN 544 567  
FT CYTOPLASMIC (POTENTIAL).  
LRR 1.  
FT REPEAT 97 120  
LRR 2.  
FT REPEAT 122 144  
LRR 3.  
FT REPEAT 145 168  
LRR 4.  
FT REPEAT 169 192  
LRR 5.  
FT REPEAT 194 216  
LRR 6.  
FT REPEAT 217 240  
LRR 7.  
FT REPEAT 241 264  
LRR 8.  
FT REPEAT 266 288  
LRR 9.  
FT REPEAT 289 312  
LRR 10.  
FT REPEAT 314 337  
LRR 11.  
FT REPEAT 338 361  
LRR 12.  
FT REPEAT 362 385  
LRR 13.  
FT REPEAT 387 409  
LRR 14.  
FT CARBOHYD 51 51 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 181 181 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 243 243 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 298 298 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 312 312 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 385 385 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 498 498 (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 567 AA; 63344 MW; CA10708E0D03707F CRC64;

Query Match 9.8%; Score 337; DB 1; Length 567;  
Best Local Similarity 23.7%; Pred. No. 3.3e-16;  
Matches 121; Conservative 56; Mismatches 167; Indels 166; Gaps 14;  
QY 30 ILCAIAAASAGPQNCPSVCSNQSKVCTRGLESEVQ-GIPSNRYLNMENNIQ 88  
DB 5 VLLSAVLSVGAQPPCPKTKCVVR-DAVQCSGSAHIAELGLPTNLTHILLFRMDRG 63  
QY 89 MIQADTFRLHLEVLQGRNRIQIEVCAENGLASLNTLELPNLTVP- 139  
DB 64 VLQSHFSFGVTLQRLMLSDSHSIDPOTFNDLVKLTLELTKNKGSHLPAILDKKVL 123  
QY 140 -----SGAFEYLSKLEMLRNRPNIPESYAFNRPVPSLMELDLG----- 179  
DB 124 LEQFLDHNALRDLDQNLQFQKLLNRLDCLNQNLQSLPANLFSSLGKLVLDLRRNLT 183  
QY 180 -----ELKKLEYISEGAFEGFLN 197  
DB 184 HLPQGLGAGIKLEKLLYSNRLMSLDGLLANLALTELRLNHLRSIAPGAFDSLGN 243  
QY 198 LKYLNGMGNKIDMP-----NLT-----PLVGLBELEMSGNH-- 229  
DB 244 LSTLTLSGNLLSLPPLAFHVSUWLTFLPENPLEELPEVLFGEMAGLRELWNGTLR 303  
QY 230 -----PFPIRPGSHGUSLKKLWVMS----- 252

RESULT 18  
LGR4\_HUMAN

ID LGR4\_HUMAN STANDARD; PRT; 951 AA.  
AC Q9BXB1; Q9NYD1;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucine-rich repeat-containing G protein-coupled receptor 4 precursor  
DE (G protein-coupled receptor 4b).  
DE GPR48 OR LGR4.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=21294803; PubMed=11401528;  
RA Loh B.D., Broussard S.R., Kolakowski L.F. Jr.;  
RT "Molecular characterization of a novel glycoprotein hormone  
RT G-protein-coupled receptor."  
RL Biochem. Biophys. Res. Commun. 282:757-764(2001).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in multiple steroidogenic tissues:  
CC placenta, ovary, testis and adrenal. Expressed also in spinal  
CC cord, thyroid, stomach, trachea, heart, pancreas, kidney, prostate  
CC and spleen.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DB EMBL; AF346711; AAK31153.1;  
DB EMBL; AF346709; AAK31153.1; JOINED.  
DB EMBL; AF346710; AAK31153.1; JOINED.  
DB EMBL; AF257182; AAF68989.1;  
DB Genew; HGNC:13299; GPR48.  
DB MIM; 606666;  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR Nterm.  
DR InterPro; IPR003591; LRR typ.  
DR Pfam; PF00001; 7tm 1; 1.  
DR Pfam; PF00560; LRR; 15.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR PRINTS; PRO00237; GPCR\_Rhodpsn.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR SMART; SM00369; LRR typ; 4.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE\_NEG.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.

G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;

Repeat; Leucine-rich repeat.  
 CHAIN 1 24  
 SIGNAL 25 951  
 DOMAIN 25 544  
 TRANSMEM 545 565  
 DOMAIN 566 575  
 TRANSMEM 576 596  
 DOMAIN 597 620  
 TRANSMEM 621 641  
 DOMAIN 642 661  
 TRANSMEM 662 682  
 DOMAIN 683 703  
 TRANSMEM 704 724  
 DOMAIN 725 756  
 TRANSMEM 757 777  
 DOMAIN 778 783  
 TRANSMEM 784 804  
 DOMAIN 805 951  
 REPEAT 55 79  
 REPEAT 81 103  
 REPEAT 104 127  
 REPEAT 128 151  
 REPEAT 153 175  
 REPEAT 176 199  
 REPEAT 201 223  
 REPEAT 224 247  
 REPEAT 248 270  
 REPEAT 272 294  
 REPEAT 318 341  
 REPEAT 342 366  
 REPEAT 368 387  
 REPEAT 388 411  
 REPEAT 413 435  
 DISULFID 618 693  
 CARBOHYD 68 68  
 CARBOHYD 199 199  
 CARBOHYD 294 294  
 CARBOHYD 314 314  
 CARBOHYD 505 505  
 CONFLICT 292 292  
 CONFLICT 433 433  
 CONFLICT 668 668  
 SEQUENCE 951 AA; 104460 MW; 5E0C2DFCF22CABEB CRC64;  
 Query Match  
 Best Local Similarity 9.7%; Score 334.5; DB 1; Length 951;  
 Matches 107; Conservative 25.8%; Pred. No. 9.8e-16;  
 Mismatches 70; Gaps 13;  
 30 ILC-AATIAAASAGPQ-----CPSCVCSNQPSKVCTRGSLSEVDPQGPSNRYINLM 83  
 7 LCCFALGLGASGFGSAAAPLCAAPCSGDG-RRVDCSGKGLTAVPEGLSAFTQALDIS 65  
 84 ENNTQMIQADTFRH-----LHLEVLQGRNSIRQIEVGAF 119  
 66 MNNTQIPEDAKFPFFLELQAGNDLSFTHPKALSGELKLVLTQNNQLKTVSEAL 125  
 120 NGLASLNTLEFDNLWTVIPGAFYYSKRLRLRN----- 156  
 126 RGLSALQSLRDANHTSVSPDSPEGLVQLRHLMDNLSFVPHPLSNLTQALTLA 185  
 157 -NPITESPYNFAPNVPISMLRDLGELKKLVISGAFEGFLNKKYLMGLMCNKKDMEN-L 214  
 186 LNKISSIPDFAFTLSSLVVLHLHN-NKIRGLSGHGFQDGLDNLDTLDSYNNLGEFPQAI 244  
 215 TPLVGLBLEMSGHNPFEIRPGSPHGLSSLKLLWMSQVSLIERNAFDEL----- 265  
 245 KAPSLKELGPHNSISVIPDGAFGDNPLRTIHLVDNPLSPFVNGSAFHLSDLHSLVIR 304  
 266 -ASLVE-----LNLAHNNLSLPHDLFTPLRLVVLHLHHPNWCDCILWL 311  
 305 GASWVQQPNNLTGTVHLESLLTGLTKTSSIPNNLCQEQKRLTDLISYNN----- 354

QY 312 AMWREYIPTNSTCCGRCHA--PMEMGRYLVVDQASFCQSAFF-IMDAPRDL 362  
 DB 355 ---IRDLSPFNG-----CHALEEISLQRNQIYQIKETFOGLISLRILDSRNL 400  
 RESULT 19  
 LGR5 MOUSE  
 ID LGR5\_MOUSE STANDARD; PRT; 907 AA.  
 AC Q9ZIP4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucine-rich repeat-containing G protein-coupled receptor 5 precursor  
 DE (G protein-coupled receptor 49) (Orphan G protein-coupled receptor  
 DE FEI).  
 GN GPR49 OR LGR5 OR FEI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99121227; PubMed=9920770;  
 RA Hermy G., Methner A., Schaller H.C., Hermans-Borgmeyer I.;  
 RT "Identification of a novel seven-transmembrane receptor with homology  
 RT to glycoprotein receptors and its expression in the adult and  
 RT developing mouse.";  
 RL Biochem. Biophys. Res. Commun. 254:273-279(1999).  
 CC -!- FUNCTION: Orphan receptor. It may be an important receptor for  
 CC signals controlling growth and differentiation of specific  
 CC embryonic tissues.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC and in the brain. In the central nervous system expression is  
 CC restricted to the olfactory bulb. In the adrenal gland detected  
 CC only in the neural-crest derived chromaffin cells of the  
 CC medulla, but not in the cells of the adrenal cortex. In the  
 CC gonads, the expression is high in Graafian follicle, but absent  
 CC from primary and secondary follicles.  
 CC -!- DEVELOPMENTAL STAGE: Expressed from embryonic day 10.5 (E10.5) in  
 CC the developing spinal cord and in the neuroepithelia of the  
 CC myel-, met-, mes-, and diencephalon. Expression is transitory and  
 CC the pattern changed rapidly.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -!- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.  
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 CC  
 CC EMBL; AF110818; AADI4684.1;  
 CC HSP; F23945; LXUN.  
 CC GSD; MGI:1341817; Gpr49.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC InterPro; IPR001611; LRR.  
 CC InterPro; IPR000372; LRR\_Nterm.  
 CC InterPro; IPR003591; LRR\_Typ.  
 CC Pfam; PF00001; 7cm.1; 1.  
 CC Pfam; PF00560; LRR; 14.  
 CC Pfam; PF01462; LRRNT; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PRINTS; PR00019; LEURICHRPT.  
 CC SMART; SM00369; LRR\_TYP; 8.  
 CC SMART; SM00013; LRRNT; 1.  
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; FALSE\_NEG.  
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
 CC G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;  
 KW

Repeat; Leucine-rich repeat.		1	21	POTENTIAL.
FT	SIGNAL	22	907	LEUCINE-RICH REPEAT-CONTAINING G PROTEIN- COUPLED RECEPTOR 5.
FT	CHAIN	22	907	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	22	561	1 (POTENTIAL).
FT	TRANSFEM	562	582	2 (POTENTIAL).
FT	DOMAIN	583	593	3 (POTENTIAL).
FT	TRANSFEM	594	614	4 (POTENTIAL).
FT	DOMAIN	615	638	5 (POTENTIAL).
FT	TRANSFEM	639	659	6 (POTENTIAL).
FT	DOMAIN	660	703	7 (POTENTIAL).
FT	TRANSFEM	704	723	8 (POTENTIAL).
FT	DOMAIN	724	744	9 (POTENTIAL).
FT	TRANSFEM	745	767	10 (POTENTIAL).
FT	DOMAIN	768	788	11 (POTENTIAL).
FT	TRANSFEM	789	802	12 (POTENTIAL).
FT	DOMAIN	803	823	13 (POTENTIAL).
FT	TRANSFEM	824	907	14 (POTENTIAL).
FT	DOMAIN	88	88	15 (POTENTIAL).
FT	REPEAT	89	112	16 (POTENTIAL).
FT	REPEAT	113	136	17 (POTENTIAL).
FT	REPEAT	137	160	18 (POTENTIAL).
FT	REPEAT	162	184	19 (POTENTIAL).
FT	REPEAT	186	208	20 (POTENTIAL).
FT	REPEAT	209	232	21 (POTENTIAL).
FT	REPEAT	233	256	22 (POTENTIAL).
FT	REPEAT	257	279	23 (POTENTIAL).
FT	REPEAT	281	303	24 (POTENTIAL).
FT	REPEAT	304	327	25 (POTENTIAL).
FT	REPEAT	328	350	26 (POTENTIAL).
FT	REPEAT	351	375	27 (POTENTIAL).
FT	REPEAT	377	396	28 (POTENTIAL).
FT	REPEAT	397	420	29 (POTENTIAL).
FT	REPEAT	422	444	30 (POTENTIAL).
FT	REPEAT	444	464	31 (POTENTIAL).
FT	REPEAT	564	585	32 (POTENTIAL).
FT	CARBOHYD	63	63	33 (POTENTIAL).
FT	CARBOHYD	77	77	34 (POTENTIAL).
FT	CARBOHYD	208	208	35 (POTENTIAL).
FT	CARBOHYD	792	792	36 (POTENTIAL).
SQ	SEQUENCE	907 AA; 99681 MW; 553167CGC0AAE253 CRC64;		
Query Match 9.38; Score 321.5; DB 1; Length 907;				
Best Local Similarity 25.28; Pred. No. 7.5e-15; Indels 101; Gaps 10;				
Matches 108; Conservative 64; Mismatches 155;				
Qy	22	VYLTAAQVWILCAATAAASAG----	PQNCPSVCSC----	SNQFSKVCTRGSLSEVPQGP 74
Db	6	VHMLSLALLQVAAGSPGPDAPRGCPDCHCELDGRLMLRVCSDLGSLSPSLNLS	65	
Qy	75	SNTFYINLMENNIOQIOAD-----	TFPHLHLEVLQGRNS	110
Db	66	VFTSYDLSMNISQLPALLRCLFLEURLAGNALTHIPKGAFTGLSLKVLMLQNNQ	125	
Qy	111	IRQEVGAFNGASLNTLEFLDNWLVIPSCAPEYLSKRELMLRNNPIESIPSAFNRV	170	
Db	126	LKRPYBEALQNLRSLSRLDANHSIVPSCFSGLSLHLDNLDNALDTPVQAFSL	185	
Qy	171	PSLMRLDGLKLEUYISEGA-----	FEGLNLYMLGMC	206
Db	186	SALQAMTLA-LNKHIHDIADYAFGNLSLVHLHNNRIHSLGKCKCFDGLSLTDLN	244	
Qy	207	NIKMPN-LTPVGLBLESGNHPFIRPGSFGLSSLLKLMWMSQVSLERNAPD--	263	
Db	245	NLDEFPTAINTLNLKELGFHNNIRSIPEFAFVGNPSLTIHFYDNPQFVGSFAQHL	304	
Qy	264	-----GLASVELMLANNLSLPHDLFTPLRYLVELLHNNPW	302	
Db	305	PELRTLTLNGASHITEFPHLTGTALSLTGAKISSLPQAVCDQLPMLQVLDLSYN--	362	
Qy	303	MCDGDLMLAWREYIPTSTCCGRCHAPMHWGRVYLVEDVQASFCQSAFPTMDAPRL	362	
Db	363	-----LLEDLPFSLSGC--QKIQKIDIAHNEIYIKGTITQ-----	QLFNRLSL	403

Qy	363	NISEGRMA	370	
Db	404	NLAWNKIA	411	
RESULT 20				
GPV_MOUSE		STANDARD;	PRT;	567 AA.
AC	008742;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DB	Platelet glycoprotein V precursor (GPV) (CD42D).			
GN	GP5.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Liver;			
EX	MEDLINE=97275136; PubMed=9129030;			
RA	Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S.,			
RA	Grunert P., Loew D., van Dorsselaer A., Cazenave J.-P., Lanza F.;			
RT	"Gene cloning of rat and mouse platelet glycoprotein V:			
RT	identification of megakaryocyte-specific promoters and demonstration			
RT	of functional thrombin cleavage.";			
RL	Blood 89:3253-3262(1997).			
CC	!- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND			
CC	FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT			
CC	PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO			
CC	INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A			
CC	CRITICAL INITIATING EVENT IN HEMOSTASIS (BY SIMILARITY).			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	!- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.			
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CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; Z69595; CAA93441.1; -			
DR	HSP; P03661; IAN9.			
DR	MGD; MG1:1096363; Gp5.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000483; LRR_Cterm.			
DR	InterPro; IPR003591; LRR_typ.			
DR	Pfam; PF00560; LRR; 13.			
DR	Pfam; PF01463; LRRCT; 1.			
DR	PRINTS; PR00019; LEURICHRPT.			
DR	SMART; SM00082; LRRCT; 1.			
DR	SMART; SM00369; LRR_TYP; 10.			
KW	platelet; Transmembrane; Glycoprotein; Blood coagulation;			
KW	Repeat; Leucine-rich repeat; Cell adhesion; Signal.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	567	PLATELET GLYCOPROTEIN V.
FT	DOMAIN	17	522	EXTRACELLULAR (POTENTIAL).
FT	TRANSFEM	523	543	POTENTIAL.
FT	DOMAIN	544	567	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	73	96	LRR 1.
FT	REPEAT	97	120	LRR 2.
FT	REPEAT	122	144	LRR 3.
FT	REPEAT	145	168	LRR 4.
FT	REPEAT	170	192	LRR 5.
FT	REPEAT	194	216	LRR 6.
FT	REPEAT	217	240	LRR 7.
FT	REPEAT	241	264	LRR 8.
FT	REPEAT	266	288	LRR 9.
FT	REPEAT	289	312	LRR 10.

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., Sakai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann K., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S., Hayashizaki Y.,

Functional annotation of a full-length mouse cDNA collection." ;  
Nature 409:685-690 (2001).

-!- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF CIRCULATING IGFS TO THE TISSUES.

-!- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I OR IGF-II AND IGFBP-3 (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Extracellular.

-!- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.

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EMBL; U66900; AAB17270.1; --  
EMBL; AK004926; BAB23677.1; --  
PIR; JC6128; JC6128.  
MGD; MGI:107973; Igfals.  
InterPro; IPR001611; LRR.  
InterPro; IPR000493; LRR Cterm.  
InterPro; IPR000372; LRR Nterm.  
InterPro; IPR003591; LRR typ.  
Pfam; PF00560; LRR; 19.

PLAM; EF01463; LRRC1; I.  
PRINTS; PR00019; LEURICHRPT.

SMART; SM00369; LRR\_TYP; 9.

```
SMART; SM00082; LRRT; 1.
SMART; SM00013; LRRT; 1.
```

Cell adhesion; Repeat; Signal; Leucine-rich repeat; Glycoprotein.

SIGNAL	1	23	BY SIMILARITY.
CHAIN	24	603	INSITIN-LIKE GROWTH FACTOR BINDING

PROTEIN COMPLEX ACID LABILE CHAIN.

```

REPEAT 52 73 LRR 1.
REPEAT 74 06 LRR 0.

```

REPEAT	74	98	120	120	LRR 2.	LRR 3.
REPEAT	74	98	120	120	LRR 2.	LRR 3.

[illegible]

REPEAT	146	168	LRR 5.
REPEAT	169	192	LRR 6.

REPEAT	194	216	LRR 7.
--------	-----	-----	--------

REPEAT	217	240	LRR 8.
REPEAT	242	264	LRR 9

REPEAT	265	288	LRR 10.
REPEAT	265	288	LRR 10.

REPEAT	289	312	LRR 11.
REPEAT	313	336	1.00 10

REPEAT	338	LRR 12.
REPEAT	360	LRR 13.

REPEAT	361	384	LRR 14.
1	1.00	1.00	1.00
2	1.00	1.00	1.00
3	1.00	1.00	1.00
4	1.00	1.00	1.00
5	1.00	1.00	1.00
6	1.00	1.00	1.00
7	1.00	1.00	1.00
8	1.00	1.00	1.00
9	1.00	1.00	1.00
10	1.00	1.00	1.00
11	1.00	1.00	1.00
12	1.00	1.00	1.00
13	1.00	1.00	1.00
14	1.00	1.00	1.00
15	1.00	1.00	1.00
16	1.00	1.00	1.00
17	1.00	1.00	1.00
18	1.00	1.00	1.00
19	1.00	1.00	1.00
20	1.00	1.00	1.00
21	1.00	1.00	1.00
22	1.00	1.00	1.00
23	1.00	1.00	1.00
24	1.00	1.00	1.00
25	1.00	1.00	1.00
26	1.00	1.00	1.00
27	1.00	1.00	1.00
28	1.00	1.00	1.00
29	1.00	1.00	1.00
30	1.00	1.00	1.00
31	1.00	1.00	1.00
32	1.00	1.00	1.00
33	1.00	1.00	1.00
34	1.00	1.00	1.00
35	1.00	1.00	1.00
36	1.00	1.00	1.00
37	1.00	1.00	1.00
38	1.00	1.00	1.00
39	1.00	1.00	1.00
40	1.00	1.00	1.00
41	1.00	1.00	1.00
42	1.00	1.00	1.00
43	1.00	1.00	1.00
44	1.00	1.00	1.00
45	1.00	1.00	1.00
46	1.00	1.00	1.00
47	1.00	1.00	1.00
48	1.00	1.00	1.00
49	1.00	1.00	1.00
50	1.00	1.00	1.00
51	1.00	1.00	1.00
52	1.00	1.00	1.00
53	1.00	1.00	1.00
54	1.00	1.00	1.00
55	1.00	1.00	1.00
56	1.00	1.00	1.00
57	1.00	1.00	1.00
58	1.00	1.00	1.00
59	1.00	1.00	1.00
60	1.00	1.00	1.00
61	1.00	1.00	1.00
62	1.00	1.00	1.00
63	1.00	1.00	1.00
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65	1.00	1.00	1.00
66	1.00	1.00	1.00
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69	1.00	1.00	1.00
70	1.00	1.00	1.00
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73	1.00	1.00	1.00
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75	1.00	1.00	1.00
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78	1.00	1.00	1.00
79	1.00	1.00	1.00
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81	1.00	1.00	1.00
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83	1.00	1.00	1.00
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86	1.00	1.00	1.00
87	1.00	1.00	1.00
88	1.00	1.00	1.00
89	1.00	1.00	1.00
90	1.00	1.00	1.00

REPEAT 386  
LRR 15. 408  
REPEAT 409  
LRR 16. 432

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REPEAT 433 456 LRR 17.
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REPEAT	458	480	LRR 18.
REPEAT	482	504	LRR 19.

REPEAT	505	529	505	529
REPEAT	505	529	505	529

CARDIOVASC	543	566	LRR 21.	(CONTINUED)
REPEAT				

CARBOHYD	64	N-LINKED (GLCNAC)	64	(POTENTIAL)
CARBOHYD	85	N-LINKED (GLCNAC)	85	(POTENTIAL)





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FT REPEAT 159 180 LRR 5.
FT REPEAT 161 204 LRR 6.
FT REPEAT 205 228 LRR 7.
FT REPEAT 229 252 LRR 8.
FT REPEAT 254 276 LRR 9.
FT REPEAT 277 300 LRR 10.
FT REPEAT 316 338 LRR 11.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 29 36 MISSING (IN CSNB1).
FT VARIANT 31 31 /FTid=VAR_014084.
FT VARIANT 31 31 C -> S (IN XLCNSB).
FT VARIANT 101 101 /FTid=VAR_013867.
FT VARIANT 114 118 MISSING (IN CSNB1).
FT VARIANT 143 143 /FTid=VAR_014086.
FT VARIANT 151 151 /FTid=VAR_013868.
FT VARIANT 155 155 /FTid=VAR_013869.
FT VARIANT 175 175 /FTid=VAR_014087.
FT VARIANT 184 184 /FTid=VAR_013870.
FT VARIANT 187 187 /FTid=VAR_013871.
FT VARIANT 207 207 /FTid=VAR_013872.
FT VARIANT 209 209 /FTid=VAR_014088.
FT VARIANT 213 213 /FTid=VAR_014089.
FT VARIANT 216 216 L -> Q (IN XLCNSB).
FT VARIANT 232 232 /FTid=VAR_013874.
FT VARIANT 243 246 MISSING (IN CSNB1).
FT VARIANT 264 264 N -> K (IN XLCNSB).
FT VARIANT 285 285 L -> P (IN XLCNSB).
FT VARIANT 298 298 /FTid=VAR_013877.
FT VARIANT 307 307 /FTid=VAR_013878.
FT VARIANT 312 312 /FTid=VAR_013879.
FT VARIANT 347 347 /FTid=VAR_013880.
FT VARIANT 370 370 L -> P (IN XLCNSB).
FT SEQUENCE 481 AA; 51999 MW; 77855134DC564515 CRC64;
Query Match 9.38; Score 320; DB 1; Length 481;
Best Local Similarity 25.88; Pred. No. 4.1e-15;
Matches 125; Conservative 66; Mismatches 170; Indels 124; Gaps 18;
34 AIAAAAGPQNCPSVCS-NOFSKVCTRGLEVPQIPSNTRYLMNENNTQ 91
23 AVGACARA---CPAACACSVTGCSCVRDAGLLRVPAELPCEAVSDLDRLGLRFLG 78
92 ADTRHLHLEVLQGRNSIRQTEVGAFNGLASINTLELFDNW-LTVIPSGAFVYLSKLR 150
79 ERAFGTLPISLRNRHNNISFTPGAFKGLPLAELRLAHNGDLRYLHARTFAALSRLR 138

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QY 151 ELWLRRNPISIP-----SVAFNRVPSLMR-----LDLGLKKLE 185
DB 139 RLDLAACLFSVPFELLALPALRELAFAFNLFRVPCALRGLANLTHAHLERG---RIE 195
QY 186 YISGAPEGLNLYNLI-----GMGNI-----KDMF--NLTPVG 219
DB 196 AVASSLQGLRLRLSLSQANRVRAVHAGAGDCVLEHLLNNDNLAELPADAFGLAR 255
QY 220 LEEEMSGNHPEPFRPGSHGLSSKLLWVNSOVSLIERNAPDGLASLVELNHNLS 279
DB 256 LFTMLGNGNLDVARAWFADLALELYLDNLSIAFVEGAFQNLGLLALHNGNRLT 315
QY 280 SLPHDLFTPLRYLVLELHHRHHPWNCDCDILWLAWLREYIPTNSTCCGR-----CHAPMH 334
DB 316 VLAWAFQPGFGLGELFLFRAPWCDCNLEWLRWMEG-----SGRVTDVPCASFGS 367
QY 335 MGRYLVVDQASFOCSAPFIMDAPRLNI---SEGRMAELKCRTPPMSSVKWLLPNGTV 391
DB 368 VAG---LDLSQVTFGRSGDGLCVDPBELNLTTSPPGPSPE-----PAATT 409
QY 392 LSHASR-----HRIISV-----LNDGTLNFHVLLSDTGV-----VTOM 425
DB 410 VSRFSSLSKLLAPRVVVEAANTTGGLANASLSDS---LSSRGVGGAGROPWFLASCL 466
QY 426 VTNVA 430
DB 467 LPSVA 471
RESULT 23
ALS_PAPHA STANDARD; PRT; 605 AA.
AC 002833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Insulin-like growth factor binding protein complex acid labile chain
DE precursor (ALS).
GN IGFALS OR ALS.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN {1}
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97040714; PubMed=8886027;
RA Delhanty P., Baxter R.C.;
RT "The cloning and expression of the baboon acid-labile subunit of the
RT insulin-like growth factor binding protein complex.";
RL Biochem. Biophys. Res. Commun. 227:897-902(1996).
CC -!- FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS THAT RESULT
CC IN PROTEIN COMPLEXES, RECEPTOR-LIGAND BINDING OR CELL ADHESION.
CC -!- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH
CC IGF-I OR IGF-II AND IGFBP-3 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; S83462; AAN86722.1; --
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 19.

```





Db 96 NLSGLFLNQGGQLSLEPQALLGLNCHULHLENRQLRSALGTFHTPALASGLSN 155  
Qy 109 NSIRQIEVGAFNGSLNLTLEFDNLTIPSGAFYLSKIRELMRNPNPIESIPYAFN 168  
Db 156 NLSRLLEDGLFEGGLSLDLNLCWNSLAVLPDAAPRGLGSLAEVLNGLNLAIVLPALFS 215  
Qy 169 RVPSLVRLDGLG-----ELKLL-----EYISEGAFGLFNLKVLNL-- 203  
Db 216 GLAELRELDUSRNALRAIKANVFQPRQKUYLDNRNLAAVAPAGFLGKALRWLDLSH 275  
Qy 204 -----GNCMK-----DMPNLTP-----LVGLELEMGNGHFEIRPGSGFH 239  
Db 276 NRVAIGLEDFTFGLGLGLRVLRLSHNAIASLRPTFKDLHFEELQCHNRIPQLAERSPE 335  
Qy 240 GLASLKKLVWNSQVSLIERNADGLASVELNLAHNNLSLPHDLPTPLRVLVLEHLHH 299  
Db 336 GGLGLEVLTLDDHQLQVQAGAFGLGTVNVAVMNLGKCLNLPFQVFGGLGKLHSLHL-- 393  
Qy 300 NPWNCDDILWLAWLREVIPTNSTCCGCH-----APMHRGRYLVVEVQASFO 349  
Db 394 -----EGSLGRLRHTFTGLSLRLPLKONGLVGIEBQSLW 431  
Qy 350 CSAPFI-MDAPRD-----LNISGRMAELKC-RTPMSSVKML----- 385  
Db 432 GLAELLEDUTSNQLFHLPHRLFQGLGKLEVLNLSRNLAEPLPADALGFLQRAFWDVSH 491  
Qy 386 -----LPNGTVLSHAGSRHPRISVLNDGTNFS 412  
Db 492 NRLEALPN-SLLAPGLRLYLSRNNSLTFT 522

RESULT 26  
GPV\_HUMAN  
ID GPV\_HUMAN STANDARD; PRT; 560 AA.  
AC P40197;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Platelet glycoprotein V precursor (GPV) (CD42D).  
GN GP5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=93391348; PubMed=7690959;  
RA Hickey M.J., Hagen F.S., Yagi M., Roth G.J.,  
RT "Human platelet glycoprotein V: characterization of the polypeptide  
and the related Ib-V-IX receptor system of adhesive, leucine-rich  
glycoproteins";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:8327-8331(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Platelet;  
RX MEDLINE=94012616; PubMed=8407908;  
RA Lanza F., Moraes M., de la Salle C., Cazenave J.-P., Clemetson K.J.,  
RT "Cloning and characterization of the gene encoding the human platelet  
glycoprotein V. A member of the leucine-rich glycoprotein family  
cleaved during thrombin-induced platelet activation";  
RL J. Biol. Chem. 268:20801-20807(1993).  
RN [3]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Platelet;  
RX MEDLINE=90275263; PubMed=2350580;  
RA Shimomura T., Fujimura K., Maehama S., Takemoto M., Oda K.,  
RA Fujimoto T., Oyama R., Suzuki M., Ichiara-Tanaka K., Titani K.,  
RA Kuramoto A.;  
RT "Rapid purification and characterization of human platelet  
glycoprotein V: the amino acid sequence contains leucine-rich

repetitive modules as in glycoprotein Ib.";  
RL Blood 75:2349-2356(1990).  
RN [4]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Platelet;  
RX MEDLINE=90321220; PubMed=2372284;  
RA Roth G.J., Church T.A., McMullen B.A., Williams S.A.;  
RT "Human platelet glycoprotein V: a surface leucine-rich glycoprotein  
related to adhesion";  
RL Biochem. Biophys. Res. Commun. 170:153-161(1990).  
CC -!- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND  
FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT  
PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO  
INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A  
CRITICAL INITIATING EVENT IN HEMOSTASIS.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.  
CC -!- PTM: THE N-TERMINUS IS BLOCKED.  
CC -!- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L11238; AAA03069.1; -;  
CC EMBL; Z23091; CAA90637.1; -;  
CC PIR; A48030; A60164.  
CC HSP; P16473; IXUM.  
CC Genew; HGNC:4443; GP5.  
CC MIM; 173511; -;  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC InterPro; IPR001611; LRR.  
CC InterPro; IPR000483; LRR\_Cterm.  
CC InterPro; IPR000372; LRR\_Nterm.  
CC InterPro; IPR003591; LRR\_Typ.  
CC Pfam; PF00560; LRR; 13.  
CC Pfam; PF01463; LRRCT; 1.  
CC PRINTS; PR00019; LEURICRPT.  
CC SMART; SM00369; LRR\_TYP; 9.  
CC SMART; SM00082; LRRCT; 1.  
CC SMART; SM00013; LRRNT; 1.  
CC Platelet; Transmembrane; Glycoprotein; Blood coagulation;  
KW Repeat; Leucine-rich repeat; Cell adhesion; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 560 PLATELET GLYCOPROTEIN V.  
FT DOMAIN 17 523 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 524 544 POTENTIAL.  
FT DOMAIN 545 560 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 73 96 LRR 1.  
FT REPEAT 97 120 LRR 2.  
FT REPEAT 122 144 LRR 3.  
FT REPEAT 145 168 LRR 4.  
FT REPEAT 169 192 LRR 5.  
FT REPEAT 194 216 LRR 6.  
FT REPEAT 217 240 LRR 7.  
FT REPEAT 241 264 LRR 8.  
FT REPEAT 265 288 LRR 9.  
FT REPEAT 289 312 LRR 10.  
FT REPEAT 314 337 LRR 11.  
FT REPEAT 338 361 LRR 12.  
FT REPEAT 362 385 LRR 13.  
FT REPEAT 386 409 LRR 14.  
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .).

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FT CARBOHYD 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 73 MT -> TK (IN REF. 2).
FT CONFLICT 109 K -> T (IN REF. 2).
FT CONFLICT 130 D -> W (IN REF. 3).
FT CONFLICT 136 GID -> PGG (IN REF. 3).
FT CONFLICT 209 L -> I (IN REF. 2).
FT CONFLICT 267 N -> H (IN REF. 3).
FT CONFLICT 327 L -> I (IN REF. 2).
FT CONFLICT 478 P -> G (IN REF. 2).
FT CONFLICT 509 P -> D (IN REF. 2).
IQ SEQUENCE 560 AA; 60959 MW; BICD804AF8AF7115 CRC64;

Query Match 8.9%; Score 305.5; DB 1; Length 560;
Best Local Similarity 27.6%; Pred. No. 5.3e-14;
Matches 98; Conservative 47; Mismatches 153; Indels 57; Gaps 9;

Y 66 LSEVPOGI---PSNTRYLNLMENNIOIQTDFHHLHVLQLGNSROIIEVGAFNGL 122
Y 182 LTHLPKGLGQAQKLERLLHNSRLVSLDGLNSLGNLTQLFPHNHSIAPGAFDL 241
Y 123 ASLNTLEFDNWLTVIPSGAFYVLSKRLRLNRNPISPIESYAFNRVPSLMELDGLX 182
Y 242 PNLSSLTSLRNHLAFLPSALFLASHNLTLTLTFENPLAELPGLVFGEMGGLQELNLR-T 300
Y 183 KLEVISGAEGLFNLYNLGCMNKMPLTFL-----VGLLELE---MSCNHPEIR 234
Y 301 QRTLPAAAFNLSRLRYLGVTL-----SPRLSALPGQAFQGLGELQVLALHNSGUTALP 355
Y 235 PGSPHGLSSLKXLMNWSQVSLIERNADFGLASIVELNHLNLSLPHDLFTPLVLYS 294
Y 356 DGLRLGLKLRQVSLRRLNRALPRAFLRNLSLLESVQLQHNQLETLPQGVFGLPRLTE 415
Y 295 LHLHNPNKDCDILNLAWMLREVI-----PTNSTCCGRCHAPHHMGRVLYVEVDQAS 347
Y 416 VLLGHNSWRCDGLGPTFLGLRQHLGLVGGEEPP-----RCAGPGAHAGLPLWALPGSD 469
Y 348 FQCSAPPTINDAPRLNTISEGRMAELKCRTPMGSVKWLLPENGTVLGHASHRPRIS 402
Y 470 AECFGP-----RGPPPR-----PAADSSSEAPVHPALA 497

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## RESULT 27

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*GS2 HUMAN
ID PG22 HUMAN STANDARD; PRT: 359 AA.
AC P07585; Q9P020; Q9Y5N8; Q9Y5N9;
JT 01-APR-1988 (Rel. 07, Created)
JT 01-APR-1988 (Rel. 07, Last sequence update)
JT 15-SEP-2003 (Rel. 42, Last annotation update)
YE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
IN DCM.
XS Homo sapiens (Human).
XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX NCBI_TaxID=9606;
IN [1]
IN SEQUENCE FROM N.A.
IX MEDLINE=87017013; PubMed=3484330;
LA Krusius T., Ruoslahti B.;
IT "Primary structure of an extracellular matrix proteoglycan core
IT protein deduced from cloned cDNA.";
IL Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
IN [2]
IN SEQUENCE FROM N.A.
IX TISSUE=Lung;
IX MEDLINE=93162643; PubMed=8432527;
LA Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.;
IT "Human decorin gene: intron-exon junctions and chromosomal
IT localization.";
IL Genomics 15:161-168(1993).
IN [3]
IN SEQUENCE OF 1-70 FROM N.A.
IX MEDLINE=93162642; PubMed=8432526;
LA Danielson K.G., Fazio A., Cohen I.R., Cannizzaro L., Iozzo R.V.;

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```

RT "The human decorin gene: intron-exon organization, discovery of two
RT alternatively spliced exons in the 5' untranslated region, and
RT mapping of the gene to chromosome 12q23.";
RL Genomics 15:146-160(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
RA Cs-Szabo G., Glant T.T.;
RA "Alternative splicing of human decorin.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT MET-268.
RA Kieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.E., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettawan M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 31-50.
RX MEDLINE=90073579; PubMed=2590169;
RA Roughley P.J., White R.J.;
RT "Dermatan sulphate proteoglycans of human articular cartilage. The
RT properties of dermatan sulphate proteoglycans I and II.";
RL Biochem. J. 262:823-827(1989).
RN [8]
RP SEQUENCE OF 31-49.
RX MEDLINE=87250639; PubMed=3597437;
RA Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;
RT "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RT compartment of developing human bone.";
RL J. Biol. Chem. 262:9702-9708(1987).
CC -!- FUNCTION: May affect the rate of fibrils formation.
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=A;
CC IsoId=P07585-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P07585-2; Sequence=VSP_006172;
CC Name=C;
CC IsoId=P07585-3; Sequence=VSP_006173;
CC Name=D;
CC IsoId=P07585-4; Sequence=VSP_006174;
CC Name=E;
CC IsoId=P07585-5; Sequence=VSP_006175; VSP_006176;
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin.

```

CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)  
 CC FAMILY. CLASS 1 SUBFAMILY.  
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
 CC -----  
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 CC -----  
 CC EMBL: M14219; AAB00774.1; ALT SEQ.  
 CC EMBL: L01131; AAB52301.1; ALT SEQ.  
 CC EMBL: L01132; AAB52301.1; JOINED.  
 CC EMBL: L01126; AAB52301.1; JOINED.  
 CC EMBL: L01127; AAB52301.1; JOINED.  
 CC EMBL: L01129; AAB52301.1; JOINED.  
 CC EMBL: L01130; AAB52301.1; JOINED.  
 CC EMBL: M98262; AAB60901.1; --  
 CC EMBL: A1138300; AAD44713.1; --  
 CC EMBL: A1138301; AAF61437.1; --  
 CC EMBL: A1138302; AAD44714.1; --  
 CC EMBL: A1138303; AAF61438.1; --  
 CC EMBL: A1138304; AAD44715.1; --  
 CC EMBL: AF491944; AAL92176.1; --  
 CC EMBL: BC005322; AAO5322.1; --  
 CC PIR: A45016; NBHUC8.  
 CC Genew: HGNC:2705; DCN.  
 CC MIM: 125255; --  
 CC GO: GO:0007397; P.histogenesis and organogenesis; TAS.  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000372; LRR Nterm.  
 CC InterPro: IPR003591; LRR\_TYP.  
 CC Pfam: PF00560; LRR; 8.  
 CC Pfam: PF01452; LRR\_TYP; 1.  
 CC SMART: SM00369; LRR\_TYP; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 CC Leucine-rich repeat; Signal; Signal; Alternative splicing; Polymorphism.  
 CC FT SIGNAL 1 16 POTENTIAL.  
 CC FT PROSEP 17 30  
 CC FT CHAIN 31 359  
 CC FT DOMAIN 54 67  
 CC FT REPEAT 73 93  
 CC FT REPEAT 117 141  
 CC FT REPEAT 118 141  
 CC FT REPEAT 142 162  
 CC FT REPEAT 163 186  
 CC FT REPEAT 187 212  
 CC FT REPEAT 213 233  
 CC FT REPEAT 234 257  
 CC FT REPEAT 258 281  
 CC FT REPEAT 282 304  
 CC FT REPEAT 305 334  
 CC FT REPEAT 335 359  
 CC FT DISULFID 54 67  
 CC FT DISULFID 313 346  
 CC FT CARBOHYD 34 34  
 CC FT CARBOHYD 211 261  
 CC FT CARBOHYD 262 282  
 CC FT CARBOHYD 303 303  
 CC FT VARSPLIC 71 179  
 CC FT VARSPLIC 73 219  
 CC FT VARSPLIC 109 295  
 CC FT VARSPLIC 72 75  
 CC FT VARSPLIC 76 359  
 CC FT VARSPLIC 268 268  
 CC FT VARIANT 268 268  
 CC T -> W.

FT VARIANT 273 273 /FTIQ=VAR\_Q14351.  
 FT FT --> Q (IN DBSNP:1803344).  
 FT CONFLICT 37 37 /FTIQ=VAR\_Q11975.  
 FT CONFLICT 45 45 G -> A (IN REF. 8).  
 FT CONFLICT 45 45 D -> P (IN REF. 8).  
 SQ SEQUENCE 359 AA; 39746 MW; FFS11B871A1A52DD CRC64;  
 Query Match 8.8%; Score 303.5; DB 1; Length 359;  
 Best Local Similarity 31.9%; Pred; No.46-14;  
 Matches 84; Conservative 45; Mismatches 123; Indels 11; Gaps 7;  
 QY 40 SAGPQPCVCSNQFQSKVCTRRGLSEVPQIPGIPNTRYLNLMENNTQMTQADTFRIHL 99  
 DB 49 SLGPV--CPFRQC--HLRVVQCSDLGLDKPKDPDPTLLDLQNNKITEIKDGFKNLK 105  
 QY 100 HLEVLQGRNSIRQIEVGAFNGLASLNTLELPDNWLTWIPSGAFYLSK-LRELWLRNP 158  
 DB 106 NHALILVNNKISKVSPGAPTPVLERLYSKNGLKSLP-----EAPKTYLQELRAHENE 161  
 QY 159 IESIPSYAFNRPVSLMRLDLG-ELKKLEYISGAFGLFNKLYLNLMGNKMDPNLTPL 217  
 DB 162 ITKRVKVTNGLNQMTIVIELGTNELKSSGIENGAFQGMKLSYIRIADTNITSIPQGLP- 220  
 QY 218 VGLRELEMGNGHPPPIRPOSFGLSSLLKLTWPNQSVLSIERNAPDGLASLVELNAENN 277  
 DB 221 PSUTEHLQGNKISRVDAAASLGLANLAKLGLSFSNISAVDNGSLANTPHLRELHLDNNK 280  
 QY 278 LSSLPHDLFTPLRYLWELHNN 300  
 DB 281 LTRVPGGL-AEHKYIQVYVHNN 302  
 RESULT 28  
 LGR5 HUMAN  
 ID LGR5 HUMAN STANDARD; PRT; 907 AA.  
 AC 075473; Q9UP75;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucine-rich repeat-containing G protein-coupled receptor 5 precursor  
 DE (Orphan G protein-coupled receptor HG38) (G protein-coupled receptor  
 DE 49).  
 DE GPR49 OR LGR5 OR GPR67.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RX MEDLINE=98308104; PubMed=9642114;  
 RA McDonald T., Wang R., Bailey W., Xie G., Chen F., Caskey C.T.,  
 RA Liu Q.;  
 RA "Identification and cloning of an orphan G protein-coupled receptor of  
 RA the glycoprotein hormone receptor subfamily.";  
 RA Biochem. Biophys. Res. Commun. 247:266-270(1998).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RN TISSUE=Placenta;  
 RN MEDLINE=99055210; PubMed=9849958;  
 RA Han S.Y., Liang S.-G., Hsueh A.J.W.;  
 RA "Characterization of two LGR genes homologous to gonadotropin and  
 RA thyrotropin receptors with extracellular leucine-rich repeats and a G  
 RA protein-coupled, seven-transmembrane region.";  
 RA Mol. Endocrinol. 12:1830-1845(1998).  
 CC -1- FUNCTION: Orphan receptor. It may be an important receptor for  
 CC signals controlling growth and differentiation of specific  
 CC embryonic tissues (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in skeletal muscle, placenta, spinal  
 CC cord, and various region of brain.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.



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SQ SEQUENCE 907 AA; 99997 MW; 822D5C5E6F0D9092 CRC64;  
Query Match 8.8%; Score 303.5; DB 1; Length 907;  
Best Local Similarity 26.1%; Pred. No. 1.4e-13;  
Matches 111; Conservative 60; Mismatches 156; Indels 99; Gaps 10;  
QY 22 VYLRQWILCAATAAASAGP--QNCPSVCSC---SNQFSKVCTRRGLSEVPGQIPSN 76  
DB 8 VLLSLVLLQATGSSPRSGVLLRGCPCHCKCPDGRMLLRVDCDLGLSELSNLSVF 67  
QY 77 TRYLNLMENNIQ-----MIQADTFR 96  
DB 68 TSYLDLSNNNISQLPPLPSLRLEBLRAGNALTYIPKGAFTGLSLKVLMLQNNQLR 127  
QY 97 H-----LHLEVLQIGRMSIRQIEVGAFNGFGLASNTLELFDNMLTVPSPGAFVYLSK 148  
DB 128 HVPTEALQNLASQSLRDANHSIVPSPSCFGLSLRHLWLDNALTEIPVQAFRSLSA 187  
QY 149 LRELWLRNNPDESIPSVAFNPVPSIMRLDGLGELKLEIVISGAPEGLFNKLYNLGMCNI 208  
DB 188 LQAMTLALNKIHHPDYAFGNLSSLVVLHLHN-NRIHSLGKKCFDGLHSLLETLDLNNL 246  
QY 209 KDMPN-LTFLVGLLELEMSGNHFPPIRPGSPHGLSSKCLWVWNSQVSLIERNAFD--- 263  
DB 247 DEFPATIRTLNKLGLPHSNIRSIPEKAFVGNPSLTIHFYDNPQFVGRSAFQHLPE 306  
QY 264 -----GLASIVELNLAHNNLSLPHDLFTPLRYLVELHLHNPANC 304  
DB 307 LATFLNGASQITEPDLTGANLESITLTAQISSLFQVTCNQLNLQVLDLSYN--- 362  
QY 305 DCDILWALWLRREYPTNSTCCGRCHAPMHRGRLVVEVDQASQCSAFPIMDAPRLNI 364  
DB 363 -----LLELPSFSVC--QKLQXIDLRHNEIYKVDTFQ-----QLLSLSLSNL 405  
QY 365 SEGRMA 370  
DB 406 AWNKIA 411

RESULT 29  
PGS2\_HORSE  
ID PGS2\_HORSE STANDARD; PRT; 360 AA.  
AC O46542;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (Dermatan sulfate proteoglycan II) (DS-PGII).  
GN DCM.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Richardson D.W., Dodge G.R.;  
RT "Effects of interleukin-1 beta and tumor necrosis factor-alpha on the expression of matrix related genes in cultured equine articular chondrocytes";  
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RL -!- FUNCTION: May affect the rate of fibrils formation (By similarity).  
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).  
CC -!- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.  
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC FT DOMAIN 1 561  
CC FT TRANSMEM 562 582  
CC FT DOMAIN 583 593  
CC FT TRANSMEM 594 614  
CC FT DOMAIN 615 638  
CC FT TRANSMEM 639 659  
CC FT DOMAIN 660 682  
CC FT TRANSMEM 683 703  
CC FT DOMAIN 704 722  
CC FT TRANSMEM 723 743  
CC FT DOMAIN 744 767  
CC FT TRANSMEM 768 788  
CC FT DOMAIN 789 802  
CC FT TRANSMEM 803 823  
CC FT DOMAIN 824 907  
CC FT REPEAT 64 88  
CC FT REPEAT 89 112  
CC FT REPEAT 114 136  
CC FT REPEAT 137 160  
CC FT REPEAT 162 184  
CC FT REPEAT 185 208  
CC FT REPEAT 209 232  
CC FT REPEAT 233 256  
CC FT REPEAT 257 279  
CC FT REPEAT 281 303  
CC FT REPEAT 304 327  
CC FT REPEAT 328 350  
CC FT REPEAT 351 375  
CC FT REPEAT 377 396  
CC FT REPEAT 397 420  
CC FT REPEAT 422 444  
CC FT REPEAT 444 464  
CC FT REPEAT 464 563  
CC FT CARBOHYD 63 63  
CC FT CARBOHYD 77 77  
CC FT CARBOHYD 208 208  
CC FT CARBOHYD 500 500  
CC FT CARBOHYD 792 792  
CC FT CARBOHYD 90 90  
CC FT CONFLICT 90 212  
CC FT CONFLICT 212 212  
L -> W (IN REF. 21).  
R -> H (IN REF. 21).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
R -> H (IN REF. 21).  
L -> W (IN REF. 21).  
LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-  
COUPLED RECEPTOR 5.  
EXTRACELLULAR (POTENTIAL).  
1 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
2 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
3 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
4 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
5 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
6 (POTENTIAL).  
EXTRACELLULAR (POTENTIAL).  
7 (POTENTIAL).  
CYTOPLASMIC (POTENTIAL).  
LRR 1.  
LRR 2.  
LRR 3.  
LRR 4.  
LRR 5.  
LRR 6.  
LRR 7.  
LRR 8.  
LRR 9.  
LRR 10.  
LRR 11.  
LRR 12.  
LRR 13.  
LRR 14.  
LRR 15.  
LRR 16.  
LRR 17.  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
R -> H (IN REF. 21).  
L -> W (IN REF. 21).  
GO; GO:0005887; C: integral to plasma membrane; TAS.  
GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; TAS.  
InterPro: IPR000276; GPCR\_Rhodpsn.  
InterPro: IPR001611; LRR.  
InterPro: IPR000372; LRR\_Nterm.  
InterPro: IPR003591; LRR\_Typ.  
Pfam: PF00001; 7tm\_1; 1.  
Pfam: PF00560; LRR; 14.  
Pfam: PF01462; LRRNT; 1.  
PRINTS: PR00237; GPCR\_Rhodopsn.  
PRINTS: PR00019; LEURICHPRT.  
SMART: SM00369; LRR\_TYP; 8.  
SMART: SM00013; LRRNT; 1.  
PROSITE: PS00237; G-PROTEIN RECP F1\_1; FALSE\_NEG.  
PROSITE: PS0262; G-PROTEIN RECP F1\_2; 1.  
KW G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;  
Repeat; Leucine-rich repeat.  
SIGNAL 1 21  
CHAIN 22 907

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CC -----
DR EMBL; AF038127; AAB92652.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SMO0013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 314 347
FT CARBOHYD 34
FT CARBOHYD 190
FT CARBOHYD 212
FT CARBOHYD 263
FT CARBOHYD 304
SQ SEQUENCE 360 AA; 39939 MW; 2DAB97CDE16F7C45 CRC64;
Query Match 8.8%; Score 302; DB 1; Length 360;
Best Local Similarity 30.7%; Pred. No. 5.2e-14;
Matches 86; Conservative 49; Mismatches 120; Indels 26; Gaps 8;
Oy 38 AASAGPON-----CPSCVSCSNQPSKVCTRRGLSEVPQGPISNTRYLNLM 83
Db 33 ASGIGPEDRIHEVDLEPLGVCVFFRCOC--HLRVVQCSDLGLDKVPKDLPPDTLLDLQ 90
Oy 84 ENNIQMTQADTFHLLHLEVLQGRNSIRQIEVGAFNGLASINTLELPFNWLTVIPSGAF 143
Db 91 NNKITEIKDGFKNLXHALIWNKKISKISPGFTPLVKLERLYLSKNHLKELP---- 146
Oy 144 EYLSK-LRELWLRNPIESTPSVAFKRVPSLMDLGL-ELKLELYISEGAFGLFNLYL 201
Db 147 EKPKTKQLSRVHENEITKRVKAVFNGLNQIMVLTGTPFKSSGLENGAFQMKKLSYI 206
Oy 202 NLGMCNKIDM-PMLTPIVGLLEHLEMSGNHFPETIRPGSFGLSSEKKLWMNYSQVSLIERN 260
Db 207 RIADTNTITTPGGLPP--SLTELHLDSNKTKTVDAAASLRGLANLAKLGLSPNSISAVDNG 264
Oy 261 AFDGLASIVELINLAHNNLSLPHDLTPPLRYLYVELLHN 300
Db 265 SLANTPHLEHLDDNNKLKIKVPGGL-ADHKYIQVYVLHNN 303
RESULT 30
PGS2_PIG
ID PGS2_PIG STANDARD; PRT; 360 AA.

```

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AC O9XSD9; O9XGH4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DCM.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Yorkshire;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Cloning of the porcine decorin gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RV Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RW [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Yorkshire; TISSUE=Aorta;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Alternatively spliced version of the porcine decorin gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O9XSD9-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O9XSD9-2; Sequence=VSP_006177;
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)
CC FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125537; AAD23578.1; -.
DR EMBL; AF140270; AAD33862.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SMO0369; LRR_Typ; 2.
DR SMART; SMO0013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 314 347
FT CARBOHYD 34
FT CARBOHYD 190
FT CARBOHYD 212
FT CARBOHYD 263
FT CARBOHYD 304
SQ SEQUENCE 360 AA; 39939 MW; 2DAB97CDE16F7C45 CRC64;

```



Db 147 EKPKYLOELRVHNEITKVRKSVFNGLNQMIWVGLGNTNPLKSSGIENGAPQGMKKLSYI 206

Qy 202 NLGMCNIKOMPNTPLVGLLEEMSGNHFFPEIRPGSEHGLSKLKLWVMSOVSLIERN 261

Db 207 RIADTNTTTPQGLP-PSLTELHLDGKTKITKDDAASLKLGLNNLAKLGLSFSISAVDNGS 265

Qy 262 FDGLASIVELNAHNNLSLPHDLFTPLRYVVELHLHN 300

Db 266 LANTPHRLHLNNKLAKVPGGV-ADHKYIQVYVYHLHN 303

RESULT 32

PGS2 SHEEP STANDARD; PRT; 360 AA.

AC QRTT2; 2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).

GN DCN.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Myometrium.

XX MEDLINE=20113292; PubMed=10644528;

RA Wu W.X., Zhang Q., Unno N., Derks J.B., Nathanielsz P.W.;

RT "Characterization of decorin mRNA in pregnant intrauterine tissues of

RT the ewe and regulation by steroids."

RL Am. J. Physiol. 278:C199-C206(2000).

CC -i- FUNCTION: May affect the rate of fibrils formation (By

CC similarity).

CC -i- SUBUNIT: Binds to type I and type II collagen, to fibronectin and

CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By

CC similarity).

CC -i- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By

CC similarity).

CC -i- PTM: The attached glycosaminoglycan chain can be either

CC chondroitin sulfate or dermatan sulfate depending upon the tissue

CC of origin (By similarity).

CC -i- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN

CC (SLRP) FAMILY. CLASS I SUBFAMILY.

CC -i- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC

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CC

DR EMBL; AF125041; AF00585.1; --

DR HSSP; P09661; IAGN.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR003372; LRR\_Nterm.

DR InterPro; IPR003591; LRR\_Typ.

DR Pfam; PF00560; LRR; 9.

DR SMART; PF01462; LRRNT; 1.

DR SMART; SN00369; LRR\_TVP; 2.

DR SMART; SN00013; LRRNT; 1.

KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;

KW Leucine-rich repeat; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT PROPEP 17 30 BY SIMILARITY.

FT CHAIN 31 360 DECORIN.

FT DOMAIN 55 68 CYS-RICH.

FT REPEAT 74 94 LRR-S 1.

FT REPEAT 95 118 LRR-T 1.

FT REPEAT 119 142 LRR-T 2.

FT REPEAT 143 163 LRR-S 2.

FT REPEAT 164 187 LRR-T 3.

FT REPEAT 188 213 LRR-T 4.

FT REPEAT 214 234 LRR-S 3.

FT REPEAT 235 258 LRR-T 5.

FT REPEAT 259 282 LRR-T 6.

FT REPEAT 283 305 LRR-S 4.

FT REPEAT 306 335 LRR-T 7.

FT REPEAT 336 360 LRR-T 8.

FT DISULFID 55 68 BY SIMILARITY.

FT DISULFID 314 347 BY SIMILARITY.

FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY

FT CARBOHYD 212 212 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 304 304 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 360 AA; 39972 MW; 0095D0DFDAB88624 CRC64;

Query Match 8.7%; Score 298; DB 1; Length 360;

Best Local Similarity 30.5%; Pred. No. 9.9e-14;

Matches 85; Conservative 47; Mismatches 123; Indels 24; Gaps 7;

Qy 38 AASAGQN-----CPSCVCSNPFKVVCTRGSLSEVPQGISNTYINLM 83

Db 33 ASGIGPEERFHEVPELEPMPVPCFQCQ--HLRVVQCSDLGLEKYPKDLPPDPTALLDLQ 90

Qy 84 ENNIQIQADTFRHLHLHLVQLGRNSIRQIEVGAFNGLASLNTLEFDNMLTVIPSGAF 143

Db 91 NNKITEIKGDFKGLKNLHTLILNNKISKISPGAFAPLVKLERLYLSKNQLKEP---- 146

Qy 144 EYLSK-LRELNRNNDIESPYANRVPSLMRLDGL-ELKLELVISGAFGLNLYL 201

Db 147 EKMPKTLQELRVHNEITKVRKSVFNGLNQMIWVGLGNTNPLKSSGIENGAPQGMKKLSYI 206

Qy 202 NLGMCNIKOMPNTPLVGLLEEMSGNHFFPEIRPGSEHGLSKLKLWVMSOVSLIERN 261

Db 207 RIADTNTTTPQGLP-PSLTELHLDGKTKITKDDAASLKLGLNNLAKLGLSFSISAVDNGS 265

Qy 262 FDGLASIVELNAHNNLSLPHDLFTPLRYVVELHLHN 300

Db 266 LANTPHRLHLNNKLAKVPGGL-ADHKYIQVYVYHLHN 303

RESULT 33

PGS2 CANFA STANDARD; PRT; 360 AA.

AC Q29393;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Decorin precursor (Bone proteoglycan II) (PG-S2).

GN DCN OR DCNIC.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Giant T.T.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 244-259 FROM N.A.

RA Vanta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

CC -i- FUNCTION: May affect the rate of fibrils formation (By

CC similarity).

CC -i- SUBUNIT: Binds to type I and type II collagen, to fibronectin and

CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By

CC similarity).

CC -i- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By

CC similarity).

CC -i- PTM: The attached glycosaminoglycan chain can be either

CC chondroitin sulfate or dermatan sulfate depending upon the tissue

```

CC of origin (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -|- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83141; AB51245.1; -
CC EMBL; L77684; AA98062.1; -
CC InterPro; IPR001611; LRR_Nterm.
CC InterPro; IPR003372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 8.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00369; LRR_Typ; 1.
CC SMART; SM00013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat; Signal.
CC SIGNAL 1 16
CC PROPEP 17 30
CC CHAIN 31 360
CC DOMAIN 55 68
CC REPEAT 74 94
CC REPEAT 95 118
CC REPEAT 119 142
CC REPEAT 143 163
CC REPEAT 164 187
CC REPEAT 188 213
CC REPEAT 214 234
CC REPEAT 235 258
CC REPEAT 259 282
CC REPEAT 283 305
CC REPEAT 306 335
CC REPEAT 336 360
CC DISULFID 55 68
CC BY SIMILARITY.
CC DISULFID 314 347
CC CARBOHYD 34 34
CC -----
CC CARBOHYD 212 212
CC CARBOHYD 263 263
CC CARBOHYD 304 304
CC SEQUENCE 360 AA; 39980 MW; 99BE311A9C812906 CRC64;
CC -----
Query Match 8.6%; Score 297; DB 1; Length 360;
Best Local Similarity 30.5%; Pred. No. 1.2e-13;
Matches 85; Conservative 46; Mismatches 124; Indels 24; Gaps 7;
CC -----
CC 38 AASAGPQK-----CPVSCSNQFSKVCTRGSLSEVPQGIPTNRYLNLM 83
CC 33 ASGIGPEDRADPMDLLELGPVCFRCQ--HLVQCSDGLDKVPKLPDPTLLDLQ 90
CC 84 ENNTQMTQDTPRLHLEVLQIGRNIROIEVCAFNGLASLTLEFDNWLTVPSGAP 143
CC 91 NNKITEIKDGFKNLKNLHTLILVNNKISKISPGAFPLKLRLLYLSKNHLKELP---- 146
CC 144 EYLSK-LRELWLRNNTPESTPSVAFNPVPSLMRLDLQ-ELKLEVTSEGAFLFKYL 201
CC 147 EKMPKTCLELAHENEITKVKAVFNGNLQNMIVELGTNPLKSGIENGAFQGMKLSVI 206
CC 202 NLGMCNKDKNLPLVGLSELENGSNHFPPIRPGSPHGLSSLKXKLWVMSQVSLIERNA 261
CC 207 RIADNTNTTTPQGLP-PSLTHELHGKNIKVDASLSKGLNLIKGLSPNSISAVDNGT 265
CC 262 FDGLASIVELNLAHNNLSPLPHDLFTPLRLYLVELHLHNN 300
CC 266 LANTPHRLHLDNKNLIRVPGGL-AEHKTIQVYLHNN 303

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RESULT 34
PGS2 RABIT
ID PGS2 RABIT STANDARD; PRT; 360 AA.
AC Q28888; Q28608;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DCN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea;
RX MEDLINE=95122319; PubMed=7822148;
RA Zhan Q., Burrows R., Cintron C.;
RT "Cloning and in situ hybridization of rabbit decorin in corneal
RT tissues.";
RL Invest. Ophthalmol. Vis. Sci. 36:206-215(1995).
RN [2]
RP SEQUENCE OF 38-358 FROM N.A.
RC TISSUE=Cartilage;
RA Hering T.M., Kollar J.;
RT "The primary structure of rabbit chondrocyte decorin deduced from
RT nucleotide sequence.";
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -|- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -|- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -|- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC -----
CC EMBL; S76584; AB33083.1; -
CC EMBL; U03394; AAC04315.1; -
CC PIR; I47020; I47020.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 8.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00369; LRR_Typ; 1.
CC SMART; SM00013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat; Signal.
CC SIGNAL 1 16
CC PROPEP 17 30
CC CHAIN 31 360
CC DOMAIN 55 68
CC REPEAT 74 94
CC REPEAT 95 118
CC REPEAT 119 142
CC REPEAT 143 163
CC REPEAT 164 187
CC REPEAT 188 213

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PT REPEAT 214 234 LRR-S 3.
FT REPEAT 235 258 LRR-T 5.
FT REPEAT 259 282 LRR-T 6.
FT REPEAT 283 305 LRR-S 4.
FT REPEAT 306 335 LRR-T 7.
FT REPEAT 336 360 LRR-T 8.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 314 347 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 360 AA; 33989 MW; 0B50C6756FE02369 CRC64;

Query Match 8.5%; Score 293.5; DB 1; Length 360;
Best Local Similarity 32.2%; Pred. No. 28-13;
Matches 84; Conservative 44; Mismatches 122; Indels 11; Gaps 7;

QY 42 GPQNCPSVCSNQFSKVVCTRGLEVPQGIPTSNTRYLNLMENNIOIQAOTPRHLHL 101
Db 52 GPV-CFPRCC--HLAVVQSDGLGDKVPKDPDPDTLLDLQNNKITEIKGDFNKLNL 108
QY 102 EVLQGRNSIRQIEVGAFNGLASINLTLFQDNLTVIPSGAFYLSK-LRELWLRNPNIE 160
Db 109 HALILVNNKISKISPGAFTPLVKLERLYLSKHLKELP----EKMPKSLQELRAHENEIT 164
QY 161 SIFSAPNRPVSLMRDLG-ELKLEYISEGAFGLFNKLYNLGMCNKKMPNLTPLVG 219
Db 165 KVKSVFSGNQMIVIELGNTNPKSSGIENGAFQGMKLSYRIADNTITTPQGLP-PS 223
QY 220 LEELEMSGNHPPFIRPGSPHGLSSKLKLVWMSQVSLIERNAPFDGLASIVELNLAHNLS 279
Db 224 LTELHLDGKNITKIDASSLGLNKLAKLGLSFNDISAVDNGSLANAPHRELHLHNNKLI 283
QY 280 SLPHDLFTPLRYVELHLHNN 300
Db 284 RVFPGGL-ADHKYIQVYVLENN 303

RESULT 35
PGS2 CHICK STANDARD; PRT; 357 AA.
ID PGS2_CHICK
AC P28675;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=White leghorn; TISSUE=Cornua;
RX MEDLINE=32296795; PubMed=1605630;
RA Li W., Vergnes J.-P., Cornuet P.K., Hassell J.R.;
RT "cDNA clone to chick corneal chondroitin/dermatan sulfate
RT proteoglycan reveals identity to decorin."
RL Arch. Biochem. Biophys. 296:190-197(1992).
CC -1- FUNCTION: May affect the rate of fibrils formation (By similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and SLN (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.

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CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X63797; CAA45318.1; -.
CC PIR; S24317; S24317.
CC InterPro; IPR001611; LRR
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 10.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00369; LRR_TVP; 2.
CC SMART; SM0013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 357 DECORIN.
FT DOMAIN 52 65 CYS-RICH.
FT REPEAT 71 91 LRR-S 1.
FT REPEAT 92 115 LRR-T 1.
FT REPEAT 116 139 LRR-T 2.
FT REPEAT 140 160 LRR-S 2.
FT REPEAT 161 184 LRR-T 3.
FT REPEAT 185 210 LRR-T 4.
FT REPEAT 211 231 LRR-S 3.
FT REPEAT 232 255 LRR-T 5.
FT REPEAT 256 279 LRR-T 6.
FT REPEAT 280 302 LRR-S 4.
FT REPEAT 303 332 LRR-T 7.
FT REPEAT 333 357 LRR-T 8.
FT DISULFID 52 65 BY SIMILARITY.
FT DISULFID 311 344 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 357 AA; 39687 MW; 31B104C7C3CD711D CRC64;

Query Match 8.4%; Score 287.5; DB 1; Length 357;
Best Local Similarity 32.2%; Pred. No. 5.3e-13;
Matches 84; Conservative 43; Mismatches 123; Indels 11; Gaps 7;

QY 42 GPQNCPSVCSNQFSKVVCTRGLEVPQGIPTSNTRYLNLMENNIOIQAOTPRHLHL 101
Db 49 GPV-CFPRCC--HLRVQSDGLGDERVPKDPDPDTLLDLQNNKITEIKGDFNKLNL 105
QY 102 EVLQGRNSIRQIEVGAFNGLASINLTLFQDNLTVIPSGAFYLSK-LRELWLRNPNIE 160
Db 106 HALILVNNKISKISPAAPAPLKKLERLYLSKHLKELP----ENMPKSLQELRAHENEIS 161
QY 161 SIFSAPNRPVSLMRDLG-ELKLEYISEGAFGLFNKLYNLGMCNKKMPNLTPLVG 219
Db 162 KLRKAVFNGLNQIVLELGTNPLKSSGIENGAFQGMKLSYRIADNTITTPQGLP-PS 220
QY 220 LEELEMSGNHPPFIRPGSPHGLSSKLKLVWMSQVSLIERNAPFDGLASIVELNLAHNLS 279
Db 221 LTELHLDGKNISKIDAGLSGLTNLAKLGLSFNSISVNGSLANVPHRELHLHNNELV 280
QY 280 SLPHDLFTPLRYVELHLHNN 300
Db 281 RVPSGL-GEHKYIQVYVLENN 300

RESULT 36
PGS2_RAT STANDARD; PRT; 354 AA.
ID PGS2_RAT

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AC Q01129;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40) (Dermatan  
 DE sulfate proteoglycan-II) (DSPG).  
 EN DCN.  
 JS Rattus norvegicus (Rat).  
 DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 DX NCBI\_TaxID=10116;  
 ZN [1]  
 ZN [2]  
 ZN [3]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley; TISSUE=Uterus;  
 RX MEDLINE=93003331; PubMed=1390895;  
 RA Abramson S.R., Woessner J.F.;  
 RT "cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).";  
 RL Biochim. Biophys. Acta 1132:225-227(1992).  
 ZN [2]  
 RP SEQUENCE OF 11-354 FROM N.A.  
 RP MEDLINE=93154359; PubMed=1493796;  
 RA Asundi V.K., Dreher K.L.;  
 RT "Molecular characterization of vascular smooth muscle decorin:  
 RT deduced core protein structure and regulation of gene expression.";  
 RL Eur. J. Cell Biol. 59:314-321(1992).  
 ZN [3]  
 RP SEQUENCE OF 31-48 AND 171-191.  
 RP STRAIN=Sprague-Dawley; TISSUE=Uterus;  
 RX MEDLINE=89350825; PubMed=2764879;  
 RA Kokenyesi R., Woessner J.F.;  
 RT "Purification and characterization of a small dermatan sulphate  
 RT proteoglycan implicated in the dilatation of the rat uterine  
 RT cervix.";  
 RL Biochem. J. 260:413-419(1989).  
 ZN [3]  
 XC -!- FUNCTION: May affect the rate of fibrils formation (By  
 XC similarity). May be implicated in the dilatation of the rat  
 XC cervix.  
 XC  
 XC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and  
 XC TGF-beta. Forms a ternary complex with MPAP2 and ELN (By  
 XC similarity).  
 XC  
 XC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 XC  
 XC -!- DEVELOPMENTAL STAGE: The amount of DSPG per cervix increases 4-  
 XC fold during pregnancy, then falls precipitously within 1 day post  
 XC partum.  
 XC  
 XC -!- PTM: The attached glycosaminoglycan chain can be either  
 XC chondroitin sulfate or dermatan sulfate depending upon the tissue  
 XC of origin (By similarity).  
 XC  
 XC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 XC (SLRP) FAMILY. CLASS I SUBFAMILY.  
 XC  
 XC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
 XC  
 XC  
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 XC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 XC  
 XC  
 XC EMBL; 212298; CAA78170.1; -;  
 XC EMBL; X59859; CAA42519.1; -;  
 XC F01; S29145; S29145.  
 XC InterPro; IPR001611; LRR.  
 XC InterPro; IPR003372; LRR\_Nterm.  
 XC InterPro; IPR003591; LRR\_Typ.  
 XC Pfam; PF00560; LRR; 9.  
 XC Pfam; PF01462; LRRNT; 1.  
 XC SMART; SM00369; LRR\_Typ; 2.  
 XC SMART; SM00013; LRRNT; 1.  
 XC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 CW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 16  
 FT PROPEP 17 30  
 FT POTENTIAL.

FT CHAIN 31 354  
 FT DOMAIN 49 62  
 FT REPEAT 68 88  
 FT REPEAT 89 112  
 FT REPEAT 113 136  
 FT REPEAT 137 157  
 FT REPEAT 158 181  
 FT REPEAT 182 207  
 FT REPEAT 208 228  
 FT REPEAT 229 252  
 FT REPEAT 253 276  
 FT REPEAT 277 299  
 FT REPEAT 300 329  
 FT REPEAT 330 354  
 FT DISULFID 49 62  
 FT DISULFID 308 341  
 FT CARBOHYD 34 34  
 FT CARBOHYD 184 184  
 FT CARBOHYD 206 206  
 FT CARBOHYD 241 241  
 FT CARBOHYD 257 257  
 FT CARBOHYD 298 298  
 FT SEQUENCE 354 AA; 39805 MW; 152D92F42D9F5A5B CRC64;  
 SQ  
 Query Match 8.3%; Score 286.5; DB 1; Length 354;  
 Best Local Similarity 31.3%; Pred. No. 6.2e-13;  
 Matches 83; Conservative 44; Mismatches 123; Indels 15; Gaps 7;  
 QY 43 PQN-----CPSCVCSNQFSKVCTRRGLSEVPQIGIPSNTRYLNLMENNIQIADTFRH 97  
 DB 41 PDNPLSMCPCYRCQC--HLRVVQCSDLGLDKVPWFPPDTLLDLQNNKLTKEKSAFKN 98  
 QY 98 LHHLEVLQGNLSIRQIEVGAFNGLASLNTLELPDNMLTVIPSGAFYLSK-LRELWLRN 156  
 DB 99 LKDLHTLILVNNKISKISPEAFKLVKLERLYLSKNELKELP-----EKLKTLQBLELHD 154  
 QY 157 NPISIPSYAFNRVPSLWRLLDL-CELKKEIVISBGAPEGLFNLYNLMGNKMDMENLT 215  
 DB 155 NEITYLKKSVEVNGLRNMIIVIELGONPLKNSGIENGALQGNKGLGYIRISDTNITAIQGL 214  
 QY 216 PLVGLLELEMSGNHFFPIRPGSPHGLSSKLKLMWMSQVSLIERNAPDGLASIVELNLAH 275  
 DB 215 P-TSTSELHLDGNKIADKVAASLXGMSNLKSLGFSNLSITVWVNGSLANVPHRLRLHLDN 273  
 QY 276 NNLSSLPHDLFTPLRYLVELLELHN 300  
 DB 274 NKLRLVPAGL-AQHKYVQVVYVLEHN 297  
 RESULT 37  
 PGS2\_COTJA  
 ID PGS2\_COTJA STANDARD; PRT; 356 AA.  
 AC Q9D568;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Decorin precursor (Bone proteoglycan II) (PG-S2).  
 EN DCN.  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OC NCBI\_TaxID=93934;  
 RN [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea and Sclera;  
 RX MEDLINE=20556471; PubMed=11102759;  
 RA Corpe L.M., Duniev J.R., Hassell J.R., Conrad A.H., Conrad G.W.;  
 RT "Molecular cloning and relative tissue expression of decorin and  
 RT lumican in embryonic quail cornea";  
 RL Matrix Biol. 19:699-704(2000).



CC -!- FUNCTION: May affect the rate of fibrils formation (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and  
 CC TGF-beta. Forms a ternary complex with MAP2 and SLN (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By  
 CC similarity).  
 CC -!- PTM: The attached glycosaminoglycan chain can be either  
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue  
 CC of origin (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
 CC  
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 CC  
 CC ENBL: AF125250; AAG48154.1; --  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR00372; LRR Nterm.  
 CC InterPro: IPR003591; LRR\_Typ.  
 CC Pfam: PF00560; LRR; 10.  
 CC SMART: PF01462; LRRNT; 1.  
 CC SMART: SM00369; LRR\_Typ; 2.  
 CC SMART: SM00013; LRRNT; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC GlycoProtein: Extracellular matrix; Proteoglycan; Repeat;  
 CC Leucine-rich repeat; Signal.  
 CC  
 CC SIGNAL 1 15 POTENTIAL.  
 CC FT PROPEP 16 29 BY SIMILARITY.  
 CC FT CHAIN 30 356 DECORIN.  
 CC FT DOMAIN 51 64 CYS-RICH.  
 CC FT REPEAT 70 90 LRR-S 1.  
 CC FT REPEAT 91 114 LRR-T 1.  
 CC FT REPEAT 115 138 LRR-T 2.  
 CC FT REPEAT 139 159 LRR-S 2.  
 CC FT REPEAT 160 183 LRR-T 3.  
 CC FT REPEAT 184 209 LRR-T 4.  
 CC FT REPEAT 210 230 LRR-S 3.  
 CC FT REPEAT 231 254 LRR-T 5.  
 CC FT REPEAT 255 278 LRR-T 6.  
 CC FT REPEAT 279 301 LRR-S 4.  
 CC FT REPEAT 302 331 LRR-T 7.  
 CC FT REPEAT 332 356 LRR-T 8.  
 CC FT DISULFID 51 64 BY SIMILARITY.  
 CC FT CARBOHYD 310 343 O-LINKED (GLYCOSAMINOGLYCAN) (BY  
 CC CARBOHYD 33 33 SIMILARITY).  
 CC FT CARBOHYD 208 208 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC FT CARBOHYD 259 259 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC SQ SEQUENCE 356 AA; 39571 MW; BE9583CGARD7DB26 CRC64;  
 CC  
 CC Query Match 8.3%; Score 284.5; DB 1; Length 356;  
 CC Best Local Similarity 32.2%; Pred. No. 8.6e-13;  
 CC Matches 84; Conservative 43; Mismatches 123; Indels 11; Gaps 7;  
 CC  
 CC 42 GPONCPVCSGCSQFQSVKVTGRGLSEVPGIPSNTRYLNLMENNTQMIOADTFPHLHL 101  
 CC 48 GPV-CPPRCQC--HLRVVQCSGLERVPKDPDPTLLDLQNNKITEIRDGDFKNLKNL 104  
 CC  
 CC 102 EVLQGLGNSIRQTEVGAFNGLASLNTLEFDNNMLTVIPSGAFYLSK-LRELWLRNNPIE 160  
 CC 105 HALLIVNKKISKISPOFAPEKLERLYLSKNNKELP-----ENMPKSLQETRAHENEIS 160  
 CC 161 SIPSYAFNRVPSNRDLG-ELKKLEYISGAEGLFNKLYNLGMCNKIDPNLTPLVG 219  
 CC 161 KLRKAVENGINQVTLVBLGTNPLKSSGIENGAFQGMKRLSYIRIADTNTISPKGLP-PS 219  
 CC 220 LEELEMSGNHFFPFRPGSFHGLSLKGLWMVNSQVSLIERNAPDGLASLVELNLAHNLS 279

Db 220 LTELHLGDKISKIDAGSLGSLTNLAKGLSFNSISSVSGSLNNVPHLRHLNANNELV 279  
 Qy 280 SLPHDLFTPLRLYLVELLHKN 300  
 Db 280 RVPSGL-GEHKYIQVYLENN 299  
 RESULT 38  
 TLR7 MOUSE  
 ID TLR7\_MOUSE STANDARD; PRT; 1050 AA.  
 AC P5681; Q92311;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Toll-like receptor 7 precursor.  
 GN TLR7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Macrophage;  
 RA Heil F.J., Lipford G.B., Wagner H., Bauer S.M.;  
 RT "Molecular cloning of murine Toll-like-Receptor 7."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Participates in the innate immune response to microbial  
 CC agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B  
 CC activation, cytokine secretion and the inflammatory response (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds MyD88 via their respective TIR domains (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 TIR domain.  
 CC -!- SIMILARITY: Contains 28 leucine-rich (LRR) repeats.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC ENBL: AY035889; AAK62676.1; --  
 CC MGD; MGI:2176882; Tlr7.  
 CC InterPro: IPR004075; ILL\_receptor1.  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000483; LRR\_Nterm.  
 CC InterPro: IPR000372; LRR\_Nterm.  
 CC InterPro: IPR003591; LRR\_Typ.  
 CC InterPro: IPR000157; TIR\_domain.  
 CC Pfam: PF00560; LRR; 11.  
 CC Pfam: PF01463; LRRCT; 1.  
 CC Pfam: PF01582; TIR; 1.  
 CC PRINTS: PR01537; INTRLNRLRP.  
 CC PRINTS: PR00019; LEURICHRPT.  
 CC SMART: SM00369; LRR\_Typ; 3.  
 CC SMART: SM00082; LRRCT; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC PROSITE: PS0104; TIR; 1.  
 CC Receptor; Immune response; Inflammatory response; Signal;  
 CC Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.  
 CC SIGNAL 1 26 POTENTIAL.  
 CC FT CHAIN 27 1050 TOLL-LIKE RECEPTOR 7.  
 CC FT DOMAIN 27 837 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 838 858 POTENTIAL.  
 CC FT DOMAIN 859 1050 CYTOPLASMIC (POTENTIAL).  
 CC FT REPEAT 42 64 LRR 1.  
 CC FT REPEAT 65 87 LRR 2.  
 CC FT REPEAT 89 111 LRR 3.

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PT REPEAT 126 149 LRR 4.
PT REPEAT 151 170 LRR 5.
PT REPEAT 171 195 LRR 6.
PT REPEAT 203 226 LRR 7.
PT REPEAT 228 247 LRR 8.
PT REPEAT 248 273 LRR 9.
PT REPEAT 275 289 LRR 10.
PT REPEAT 290 312 LRR 11.
PT REPEAT 314 337 LRR 12.
PT REPEAT 339 364 LRR 13.
PT REPEAT 369 392 LRR 14.
PT REPEAT 396 419 LRR 15.
PT REPEAT 421 443 LRR 16.
PT REPEAT 493 516 LRR 17.
PT REPEAT 517 542 LRR 18.
PT REPEAT 543 565 LRR 19.
PT REPEAT 567 589 LRR 20.
PT REPEAT 596 619 LRR 21.
PT REPEAT 620 645 LRR 22.
PT REPEAT 650 673 LRR 23.
PT REPEAT 675 698 LRR 24.
PT REPEAT 699 722 LRR 25.
PT REPEAT 724 746 LRR 26.
PT REPEAT 747 770 LRR 27.
PT REPEAT 773 796 LRR 28.
PT DOMAIN 890 1037 TIR.
PT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 524 524 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 535 535 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 591 591 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 680 680 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 721 721 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 800 800 N-LINKED (GLCNAC. .) (POTENTIAL).
PT SEQUENCE 1050 AA; 495B75DEEB49D8E CRC64;
SQ
Query Match
Best Local Similarity 8.2%; Score 281.5; DB 1; Length 1050;
Matches 121; Conservative 60; Mismatches 169; Indels 125; Gaps 14;
2Y 59 VCTRGLSEVPOGIPSTRVYLNWENNQMIDTRHLLHVLVLGNSI----- 111
3Y 49 VDCDRLTEPEIGPTNTTLTTHINPSIDSPSRRLHLEEDERCNCVPLGSK 108
4Y 112 -----RQIEVGAFNGLASLNTLEFDNWLTVPSGAFVLSKLRLRNPNPIESIP 164
5Y 109 ANVCTKRLQIRPGSFGSLDKALYDGNQLLEIPQ---DLPSLHLLSLEANNIPSI 165
6Y 165 YAFNRVPSLMRLDGE-----LKKLEY-ISEGAFGLFNKYNLGNKCNKDMPLTPL 217
7Y 166 ENLTAVNIETLYLQNCYVYENPCNVSYSEKDAFLVWRNLKVLSDKNNVTAVPTLP- 224
8Y 218 VGLRELSGNGHPEIRPGSPHGLSSLCKKLVW-----NSQVSLIERN 260
9Y 225 PNLLEYLYNNIIKKIQENDFNNLQVLDLQNSCPRCVNVYPCPCENNSPLQIHND 284
10Y 261 AFDGLASIVELNLAHNNLSLPHDLFTPLRYLVBLHLHHPNWCDCDILMLAWLREYIP 320
11Y 285 AFNSITELKVLRLHNSLQHPVPTWFKMNNLQELDLQN----- 324
12Y 321 TNSCCGCECHAPMURGHYIV-EVDQASFOCSAPFMDAPDLNISEGRMAELKCRPT-- 377
13Y 325 -----YLARETEBAKFLHFLPNLVELDFSNY-ELQVTHASITLPHS 365
14Y 378 --PMSSVKWLLPNGTV-----LSHASRHPRISSLVNDGLTFNPSHVLSDTGWTGWT 427
15Y 366 LSSLENKILVKGVYFKELKNSLSVLHKLPRLEVLDLGT-NE----- 408
16Y 428 NVAGNSNASVLYNSTAEIANT-SNYSPTTIVTVETTEISSDTRTKYKVPVTTST 481

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Db 409 -----IKIADLNIFKHFENKLDLSVWKISPSSESREVGFCEPNAQT 450
RESULT 39
PGS2 MOUSE
ID PGS2 MOUSE STANDARD; PRT; 354 AA.
AC P28654;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
RA Naitoh Y., Suzuki S.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RW [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95050610; PubMed=7961765;
RA Scholzen T., Solursh M., Suzuki S., Reiter R., Morgan J.L.,
RA Buchberg A.M., Siracusa L.D., Iozzo R.V.;
RT "The murine decorin. Complete cDNA cloning, genomic organization,
RT chromosomal assignment, and expression during organogenesis and
RT tissue differentiation.";
RL J. Biol. Chem. 269:28270-28281(1994).
CC -!- FUNCTION: May affect the rate of fibrils formation.
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MPAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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CC -----
CC EMBL; X53929; CAA37876.1; -.
CC PIR; A55454; A55454.
CC HSSP; P23945; 1XUN.
CC MGD; MGI:94872; Dcn.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_type.
CC Pfam; PF00560; LRR; 9.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SM00369; LRR_TYP; 2.
CC SMART; SM00013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat; Signal.
CC SIGNAL 1 16
CC PROPEP 17 30
CC CHAIN 31 354
CC DOMAIN 49 62
CC REPEAT 68 88
CC REPEAT 89 112
CC REPEAT 113 136
CC REPEAT 137 157
CC REPEAT 158 181

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FT REPEAT 182 207 LRR-T 4.
FT REPEAT 208 228 LRR-S 3.
FT REPEAT 229 252 LRR-T 5.
FT REPEAT 253 276 LRR-T 6.
FT REPEAT 277 299 LRR-S 4.
FT REPEAT 300 329 LRR-T 7.
FT REPEAT 330 354 LRR-T 8.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 308 341 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 354 AA; 33809 MW; F05B5CC08DCABF6F CRC64;

Query Match 8.1%; Score 279.5; DB 1; Length 354;
Best Local Similarity 30.7%; Pred. No. 1.9e-12;
Matches 41; Conservative 45; Mismatches 125; Indels 13; Gaps 6;

QY 43 PQN-----CPSCVCSNQSKVCTRGLESEVPEQIPSNTRYLMNENNIQMIQADTFRH 97
DB 41 PENPLISMCPYRCQC--HLRVVQCSDGLGDKVPWPPDPTLLDQNNKITEIKGAFKN 98
QY 98 LHLEVLQGRNSIRQIEVGAFNGLASLNTLEFDMNLTVPISGAFVLSKLRRLMLRN 157
DB 99 LKDLHTLLLVNKKISKISEAKPLVKLRLLXKNQKELPE---KMPRTLOELRVHEN 155
QY 158 PISIPSYAFNRVPSLMRLDL-GELKKLEYISEGAFGLFNKYNLGMNCKMKNPNTLP 216
DB 156 EITKLRKSPFNGLNVLVIELOGNPLKNSIENGAFQGLKLSYIRISDTNITAIPOGLP 215
QY 217 LVGLELEKSGNHFPRIKPSFHGLSSKLKLVMSQVSLIERNAPDGLASLVELNLAHN 276
DB 216 -TSLTEVHLGDKNITKVDAPSLKGLNLKSLGSLNSIIVMNGSLANVPHLRHLN 274
QY 277 NLSSLPDLFTPLRYLVVELLHNN 300
DB 275 KLLRVPAGL-AQHKYIQVVVLHNN 297

RESULT 40
Y918_HUMAN STANDARD; PRT; 966 AA.
ID Y918_HUMAN
AC Q94931;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein KIAA0918 (Fragment).
GN KIAA0918.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 5:355-364 (1998).
CC -1- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
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CC EMEL; AB020725; BAA74941.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00580; LRR; 8.
DR Pfam; PF01463; LRRCT; 2.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 4.
DR SMART; SM00082; LRRCT; 2.
DR SMART; SM00013; LRRNT; 1.
KW Hypothetical protein; Repeat; Leucine-rich repeat.
FT NON_TER 1 1
FT REPEAT 88 111 LRR 1.
FT REPEAT 112 135 LRR 2.
FT REPEAT 136 159 LRR 3.
FT REPEAT 161 183 LRR 4.
FT REPEAT 184 207 LRR 5.
FT REPEAT 209 231 LRR 6.
FT REPEAT 240 263 LRR 7.
FT REPEAT 264 287 LRR 8.
FT REPEAT 288 311 LRR 9.
FT REPEAT 312 335 LRR 10.
FT REPEAT 336 359 LRR 11.
SQ SEQUENCE 966 AA; 108296 MW; AID236413E2B27DF CRC64;

Query Match 8.1%; Score 277; DB 1; Length 966;
Best Local Similarity 20.3%; Pred. No. 1.1e-11;
Matches 130; Conservative 78; Mismatches 173; Indels 260; Gaps 22;

QY 43 PQMCPVCSNQSKVCTRGLESEVPEQIPSNTRYLMNENNIQMIQADTFRH 96
DB 379 PLRCPTACSCNQLQISDLGLNVCQERKESIAELQPKYPNPKMYLTENYIAVVRTDFL 438
QY 97 HLHLVLQGRNSIRQIEVGAFNGLASLNTLEFDMNLTVPISGAFVLSKLRRLMLRN 156
DB 439 EATGLDLHLGNRISMIQDRAFGD-----LTLNRLRYLNG 474
QY 157 NPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFGLFNKYNLGMNCKMKNPNTLP 216
DB 475 N-----RIERLSPFLFYGLQSLQYLFL----- 496
QY 217 LVGLELEKSGNHFPRIKPSFHGLSSKLKLVMSQVSLIERNAPDGLASLVELNLAHN 276
DB 497 -----QYNLIRIEIQSGTDPVPENLQLLFLNNLLQAMPQSGVFSGL-TLLRLNLRSN 546
QY 277 NLSSLP-HDLFTPLRYLVVELLHNNPNCDCDILAWLWLRVYIPNTSTCCORCHAPHNM 335
DB 547 HFTSLPVSGLDQLKELIQIDLHDPNDCDCTDIVGKLVWVQL----- 589
QY 336 RGRYLVEVDQASFQCSAPPFMDAPRDLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHA 395
DB 590 --KGVLYLDEVI--CKAP-----KKFAETDKRSIK----- 615
QY 396 SRHPRISVLNDGTLNFSVLLSDTGYYTCMTNVCNAGSNASAYLNVSIAELNYSYFT 455
DB 616 -----SELLCPD-----YS 624
QY 456 TVTVETTESIPDTRTKKYPVTTGTGVPAYTTSTT-VLIQTTTRVPKQV-----AV 506
DB 625 DVVVSF-----TPPSIQVPARTSAVTPAVRLNSTGAPASLACGAGGASSV 669
QY 507 PATDTTDMKQTSIDVEMTKKIIIGCFVAVTLAAAMLIVFKLRKQOQSTVTVAATV 566
DB 670 PLS-----VLISLLLV--FIMSVEFAAGLFLVWKRKKKQSDHTSTNNSDV 715
QY 567 ELIQVDEDIPAAATAAPSGVSGEAVLPTIHDHINYN-----TYK 611
DB 716 SSFNQYSV-----YGGGGGTGG----HFAHVRHGRPALPKVKTYPAGHVYVI 760
QY 612 PAHGAHWHTENSL-----GNS-----LHPTVTVTISEPVIQ 641
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FT	DISULFID	322	355	BY SIMILARITY.
SEQ	SEQUENCE	369 AA;	41566 MW;	8C919E922D6377B6 CRC64;
	Query Match	8.0%;	Score 275.5;	DB 1; Length 369;
	Best Local Similarity	32.7%;	Pred. No. 3.9e-12;	Indels 11; Gaps 7;
	Matches	84;	Conservative	40; Mismatches 122;
Qy	46	CPVCSNPSKVVCTRRGLSEVPOGIPENTRYLNLMMENIOMIQADTFRHLHLEVLQ	105	
Db	64	CPFGCHC-HLRVVQCSDLGKAVPKBISPD'TMLDLQNNDISLRADDPKGLHLYALV	121	
Qy	106	LCGRNSIRQIEVGAFENGLASNTLELFDNWLTVPSGAFEVLSKRLRLWRNPTESIPSY	165	
Db	122	LWNKISKIHEKAPSPURKQKLYISKNHVLEIPP---NLPSLVELRIHDNRIRKVPKG	178	
Qy	166	AFNRVPSIMKLDLGLKXLEY--ISGAFEGFLFNLYLNLMCKNIKOMPMLTPIVGLLEL	223	
Db	179	VFGSLRNMCNIEGG-NPLENSGFEPGAFDGL-KLNYLRISBAKLTGIPKOLPET-LNEL	235	
Qy	224	EMSGNHFPETRPQSGFCHLSLKLGKLVNWSQVSLIERNAFDGLASLVELNLAHNLSLPH	283	
Db	236	HLDHINKIQALEBDLARYSKLYELGLGHQIRMIENGSSUSFUTPLRELHLDDNKLGRVPS	295	
Qy	284	DLFTPLRYLVELHLHN	300	
Db	296	GL-PDLKLLQVVVLTN	311	
RESULT	42			
TLR3	MOUSE			
ID	TLR3 MOUSE	STANDARD;	PRT;	905 AA.
AC	Q99MB1; Q912M4;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Toll-like receptor 3 precursor.			
GN	TLR3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
FN	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=129/SV;			
RC	MEDLINE=21519099; PubMed=11607032;			
RA	Alexopoulos L., Holt A.C., Medzhitov R., Flavell R.A.;			
RT	"Recognition of double-stranded RNA and activation of NF-kappaB by			
RT	Toll-like receptor 3.";			
RL	Nature 413:732-738 (2001).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c x NIH; TISSUE=Macrophage;			
RC	Applquist S.E., Ljunggren H.G.;			
RA	"Molecular cloning of mouse Toll-like receptor 3 cDNA.";			
RT	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Participates in the innate immune response to microbial			
CC	agents. May be involved in the recognition of ds-RNA. Acts via			
CC	MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine			
CC	secretion and the inflammatory response (By similarity).			
CC	-!- SUBUNIT: Binds MyD88 via their respective TIR domains (By			
CC	similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-!- TISSUE SPECIFICITY: Highly expressed in lung. After			
CC	intra-peritoneal injection of lipopolysaccharide, highly expressed			
CC	in brain, heart, kidney, liver, lung and spleen.			
CC	-!- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.			
CC	-!- SIMILARITY: Contains 1 TIR domain.			
CC	-!- SIMILARITY: Contains 22 leucine-rich (LRR) repeats.			
CC	-----			
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CC DR EMBL; AF420279; AAL27007.1; -  
 CC DR EMBL; AF355152; AAX26117.1; -  
 CC DR MGD; MGI:2156367; TIR3.  
 CC DR GO; GO:0003793; F:defense/immunity protein activity; ISS.  
 CC DR GO; GO:0003725; F:double-stranded RNA binding activity; ISS.  
 CC DR GO; GO:0004888; F:transmembrane receptor activity; ISS.  
 CC DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.  
 CC DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.  
 CC DR GO; GO:0005957; P:perception of viruses; ISS.  
 CC DR GO; GO:0045359; P:positive regulation of interferon-beta bios. . .; ISS.  
 CC DR InterPro; IPR001611; LRR.  
 CC DR InterPro; IPR000483; LRR\_Cterm.  
 CC DR InterPro; IPR003591; LRR\_Typ.  
 CC DR InterPro; IPR000157; TIR\_domain.  
 CC DR Pfam; PF00560; LRR; 12.  
 CC DR Pfam; PF01463; LRRCT; 1.  
 CC DR Pfam; PF01582; TIR; 1.  
 CC DR PRINTS; PR00019; LEURICHRPT.  
 CC DR SMART; SM00369; LRR\_TYP; 4.  
 CC DR SMART; SM00082; LRRCT; 1.  
 CC DR SMART; PS00255; TIR; 1.  
 CC DR PROSITE; PS00104; TIR; 1.  
 CC KW Receptor; Immune response; Inflammatory response; Signal;  
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.  
 CC FT SIGNAL 1 25 POTENTIAL.  
 CC FT CHAIN 26 905 TOLL-LIKE RECEPTOR 3.  
 CC FT DOMAIN 26 705 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 706 726 POTENTIAL.  
 CC FT DOMAIN 727 905 CYTOPLASMIC (POTENTIAL).  
 CC FT REPEAT 51 74 LRR 1.  
 CC FT REPEAT 76 98 LRR 2.  
 CC FT REPEAT 99 122 LRR 3.  
 CC FT REPEAT 124 146 LRR 4.  
 CC FT REPEAT 148 170 LRR 5.  
 CC FT REPEAT 171 194 LRR 6.  
 CC FT REPEAT 197 220 LRR 7.  
 CC FT REPEAT 248 271 LRR 8.  
 CC FT REPEAT 274 297 LRR 9.  
 CC FT REPEAT 298 321 LRR 10.  
 CC FT REPEAT 355 378 LRR 11.  
 CC FT REPEAT 380 404 LRR 12.  
 CC FT REPEAT 407 430 LRR 13.  
 CC FT REPEAT 432 455 LRR 14.  
 CC FT REPEAT 456 479 LRR 15.  
 CC FT REPEAT 481 505 LRR 16.  
 CC FT REPEAT 506 529 LRR 17.  
 CC FT REPEAT 531 553 LRR 18.  
 CC FT REPEAT 562 585 LRR 19.  
 CC FT REPEAT 587 609 LRR 20.  
 CC FT REPEAT 610 633 LRR 21.  
 CC FT REPEAT 635 660 LRR 22.  
 CC FT DOMAIN 755 897 TIR.  
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 670 670 S -> P (IN REF. 2).  
 CC FT SEQUENCE 905 AA; 103670 NW; 8EA6DBA981E14B4 CRC64;

Query Match 7.8%; Score 268; DB 1; Length 905;  
 Best Local Similarity 28.6%; Pred. No. 4.3e-11;  
 Matches 99; Conservative 46; Mismatches 129; Indels 72; Gaps 10;  
 QY 79 YINLNNIOMIQADTRHLLHLEVLQGR--NSIRQIEVGAENGLA--SLNTLELFDNW 134  
 DB 360 YLNDDNNIPSTKSTNTFTGLVSLKYLSTKFTSLQTLTNETVSLAHSPLLTINLTQKH 419  
 QY 135 LTVIPSGAFVYLSKLR-----ELWLNKNPIESIPSYAFNR 169  
 DB 420 ISKIANTFTFWGLQRLDILGLNEIRQKLSGQWRGLRNIFEIYLSVNYQLQSTSSFAL 479  
 QY 170 VPSLMRDLGE--LKKLEYISGAFGLFVLKYLNLGKMKNIKMPMLTPIVLGLEELF--- 224  
 DB 480 VPSLQRLMLARVALKNVD--ISPSFFRPLRLNTLIDLSNNNIANI--NEDLLEGLENLEILD 537  
 QY 225 -----MSGNHFFPIRPGSFHGLSSLKLVWMS 252  
 DB 538 FQHNVLARLWKRANPGPVNFKLGLSHLHILNLSGLDEIPVGVFNLFELKSLNGLN 597  
 QY 253 QVSLIERNAPDGLASIVELMAHNNLSLPHDLF--TPLRYLVELHLLHNPWNCDD--ILW 310  
 DB 598 NLNKLPEFIQDQTSRLSLMLQKLNITSVEKQVFGPPFQNLNSLDRFPNPFDCETCSISW 657  
 QY 311 LAWLREYIPTNSTCCGR--CHAPMHRGRIYLVEDVQASPOCSAPP 354  
 DB 658 FVWINGTHNISLSTHYLCNTPHHYGYFPLKLFDTSSCKOSAPP 703  
 RESULT 43  
 PRLP\_BOVIN  
 ID PRLP\_BOVIN STANDARD; PRT; 381 AA.  
 AC QSGKN8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein).  
 GN PRELP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Articular cartilage;  
 RX MEDLINE=20576219; PubMed=11007795;  
 RA Bengtsson B., Aspegberg A., Heinegaard D., Sommarin Y., Spillmann D.;  
 RT "The amino-terminal part of PRELP binds to heparin and heparan sulfate.";  
 RL J. Biol. Chem. 275:40695-40702(2000).  
 RN [2]  
 RP FUNCTION  
 RX MEDLINE=21964083; PubMed=11847210;  
 RA Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D., Aspegberg A.;  
 RT "The leucine-rich repeat protein PRELP binds perlecan and collagens and may function as a basement membrane anchor.";  
 RL J. Biol. Chem. 277:15061-15068(2002).  
 CC -!- FUNCTION: May anchor basement membranes to the underlying connective tissue.  
 CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain.  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.  
 CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AF163568; AAG23723.1; --  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR Nterm.  
 DR InterPro; IPR003591; LRR typ.  
 DR Pfam; PF00560; LRR; 9.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00013; LRRNT; 1.  
 KW Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;  
 KW Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 381 PROLAGIN.  
 FT DOMAIN 72 88 CYS-RICH.  
 FT REPEAT 94 113 LRR-S 1.  
 FT REPEAT 114 137 LRR-T 1.  
 FT REPEAT 138 161 LRR-T 2.  
 FT REPEAT 162 182 LRR-S 2.  
 FT REPEAT 183 206 LRR-T 3.  
 FT REPEAT 207 232 LRR-T 4.  
 FT REPEAT 233 253 LRR-S 3.  
 FT REPEAT 254 277 LRR-T 5.  
 FT REPEAT 278 302 LRR-T 6.  
 FT REPEAT 303 322 LRR-S 4.  
 FT REPEAT 323 361 LRR-T 7.  
 FT REPEAT 362 381 LRR-T 8.  
 FT DOMAIN 196 201 POLY-LEU.  
 FT DISULFID 331 372 BY SIMILARITY.  
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 381 AA; 43682 MW; 23DA99C01B8772A0 CRC64;

Query Match 7.8%; Score 267; DB 1; Length 381;  
 Best Local Similarity 32.1%; Pred. No. 1.6e-11;  
 Matches 79; Conservative 45; Mismatches 104; Indels 18; Gaps 8;  
 QY 45 NCPSCVCSNQF-SKVVTRGLSVQPGIPSNRYLNMENNQMIOADTFRLHLELV 103  
 DB 71 DCPRECYCPFPFPPSALYCDSENLRKVPV-IPSRHYLYLQNNFTPLVPSFKVATGLRW 129  
 QY 104 LQLGNSIRQIEVGAFNGLASLNTLELFDNNLTVIPSGAFYLSKLRELMLRNNPIESIP 163  
 DB 130 INLDNNRIRKVDQVLEKLPVLFVLEKQLEEVPAALPNRLQLR---LSQNCISRIIP 186  
 QY 164 SFANFVPSLMLDLGELKLEYISEG-----AFGLFNLKYLNLGWCNIKDMNLTPLV 218  
 DB 187 PGVFSKLENLLLDLQHNK----LSDGVKEDPTFGGLRNLQMLNLAUNLRKPPKVP-S 241  
 QY 219 GLEELMSGNFPPEIRPGSFHGLSSKLKLVWNSQVS--LIERNAFDGLASLVVELMLAHN 276  
 DB 242 AIHQVLYDSNRIEAPSCVPGFNPFLAIRLNYNQLSDRGLPKNSFN-ISNLLVHLHSHN 300  
 QY 277 NLSLIP 282  
 DB 301 RISSVP 306  
 RESULT 44  
 CBP8\_HUMAN  
 ID CBP8\_HUMAN STANDARD; PRT; 536 AA.  
 AC P22792;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carboxypeptidase N 83 kDa chain (Carboxypeptidase N regulatory

DE subunit) (Fragment).  
 GN CPN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90094386; PubMed=2378615;  
 RA Tan F., Weerasinghe D.K., Skidgel R.A., Tamei H., Kaul R.K.,  
 RA Roninson I.B., Schilling J.W., Erdoes E.G.;  
 RT "The deduced protein sequence of the human carboxypeptidase N high  
 RT molecular weight subunit reveals the presence of leucine-rich tandem  
 RT repeats.";  
 RL J. Biol. Chem. 265:13-19(1990).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE=88309120; PubMed=3408501;  
 RA Skidgel R.A., Bennett C.D., Schilling J.W., Tan F., Weerasinghe D.K.,  
 RA Erdoes E.G.;  
 RT "Amino acid sequence of the N-terminus and selected tryptic peptides  
 RT of the active subunit of human plasma carboxypeptidase N: comparison  
 RT with other carboxypeptidases.";  
 RL Biochem. Biophys. Res. Commun. 154:1323-1329(1988).  
 CC -1- FUNCTION; THE 83 kDa SUBUNIT BINDS AND STABILIZES THE CATALYTIC  
 CC SUBUNIT AT 37 DEGREES CELSIUS AND KEEPS IT IN CIRCULATION. UNDER  
 CC SOME CIRCUMSTANCES IT MAY BE AN ALLOSTERIC MODIFIER OF THE  
 CC CATALYTIC SUBUNIT.  
 CC -1- SUBUNIT: Tetramer of two catalytic chains and two glycosylated  
 CC INACTIVE CHAINS.  
 CC -1- SUBCELLULAR LOCATION: Secreted  
 CC -1- PTM: O-GLYCOSYLATED IN THE SER/THR-RICH REGION (POTENTIAL).  
 CC BONDS IS UNKNOWN, BUT THEY DO NOT FORM INTERCHAIN DISULFIDE BONDS  
 CC WITH THE 50 kDa CATALYTIC SUBUNIT.  
 CC -1- DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CONSIDERED TO BE  
 CC COMPATIBLE WITH LIFE.  
 CC -1- SIMILARITY: Contains 13 leucine-rich (LRR) repeats.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; J05158; AAAS1921.1; --  
 DR PIR; A34901; A34901.  
 DR Genew; HGNC:2313; CPN2.  
 DR MIM; 603104; --  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003234; F:enzyme regulator activity; NAS.  
 DR GO; GO:0017028; F:protein stabilization activity; NAS.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR Nterm.  
 DR InterPro; IPR003591; LRR typ.  
 DR Pfam; PF00560; LRR; 11.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00369; LRR typ; 10.  
 DR SMART; SM00013; LRRNT; 1.  
 KW Repeat; Leucine-rich repeat; Glycoprotein.  
 FT NON TER 1 1  
 FT REPEAT 51 74 LRR 1.  
 FT REPEAT 75 98 LRR 2.  
 FT REPEAT 99 122 LRR 3.  
 FT REPEAT 123 146 LRR 4.  
 FT REPEAT 148 170 LRR 5.  
 FT REPEAT 171 194 LRR 6.  
 FT REPEAT 196 218 LRR 7.  
 FT REPEAT 220 242 LRR 8.  
 FT REPEAT 243 266 LRR 9.

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FT REPEAT 268 290 LRR 10.
FT REPEAT 291 314 LRR 11.
FT REPEAT 316 338 LRR 12.
FT REPEAT 339 362 LRR 13.
FT DOMAIN 359 379 SER/THR-RICH.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 536 AA; 58649 MW; D524011243C9B2A6 CRC64;

Query Match 7.8; Score 267; DB 1; Length 536;
Best Local Similarity 27.7; Pred. No. 2.5e-11;
Matches 104; Conservative 60; Mismatches 145; Indels 66; Gaps 14;

66 LSEVPOGIPSN--TRYLNLMENNMIQADTRHLHLHLEVLQGRNSIRQTEVGAFNGL 122
112 LEALPEGLFOHLAALESHLQOQLQALPRELPQPLTHLKTLMAGNLQAQPEELFHEL 171
123 ASLMTLEFDNLWLVIPSGAFYLSKLRLELWLRNPIESIPYAFNRPVPSLMRLDGLK 182
172 TSLQTKLSNNALSGLPQGVFGKLSGLQELFSDNNISBELPPQVPSQLFCLERLWL-QRN 230
183 KLEVISGAEGLFNLYNLGNLGNKIDPE---NLTP-LVGLLEELMSGNHFFPIRQS 237
231 AITHPLSIFASGNLTFLSQWMLRVLPAGLFAHTPCLVG---LSLTHNQLETVTGT 287
238 FHGLSSLKLVWVNSQVSLIERNAFQGLASVLELNLARNLSLPHDLTPRLYLVVHLL 297
288 FAHLSNLSRLSMLSYNAITHLPGAFIDLEELVLYLGSNNLTALHPALFQNLKLELSL 347
298 HNN-----PNCDCDILWLAWVREVIPYNTSTCCG-----RCHAP 332
348 SKNQLATLPEASPTTTCSTWCTVTPGSATAPGLPLQAAVAHRSAPHEPDLRLC--P 405
333 MNRVG-----RYLVEV--DQASFOCSAFFIMDAPR-----DLNISBGRMAELKCRTP 377
406 AYLKGQVTHALNEKQLVSVTRDHLHGQVTPW---DESKAGGWDLAQVB-RAARSQC--- 458
378 PMSVSKWLLNGTVL 392
459 -----TYSNPEGTWV 468

RESULT 45
TIR3_HUMAN STANDARD; PRT; 904 AA.
AC 015455;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DE 28-FEB-2003 (Rel. 41, Last annotation update);
GN Toll-like receptor 3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=98118556; PubMed=9435236;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
Toll.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593 (1998).
CC -I- FUNCTION: Participates in the innate immune response to microbial
agents. May be involved in the recognition of ds-RNA. Acts via
MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine
secretion and the inflammatory response (By similarity).
CC -I- SUBUNIT: Binds MyD88 via their respective TIR domains (By
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similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- TISSUE SPECIFICITY: Expressed at high level in placenta and
pancreas. Also detected in CD11c+ immature dendritic cells.
CC Only expressed in dendritic cells and not in other leukocytes,
including monocyte precursors.
CC -I- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -I- SIMILARITY: Contains 1 TIR domain.
CC -I- SIMILARITY: Contains 22 leucine-rich (LRR) repeats.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; U88879; AAC34134.1; --
CC Genew: HGNC:11849; TLR3.
CC MIM; 603029; --
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0003797; F:antibacterial peptide activity; TAS.
CC GO; GO:0003793; F:defense/immunity protein activity; NAS.
CC GO; GO:0003725; F:double-stranded RNA binding activity; NAS.
CC GO; GO:0004888; F:transmembrane receptor activity; NAS.
CC GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0045671; P:negative regulation of osteoclast different. . . ; NAS.
CC GO; GO:0009597; P:perception of viruses; NAS.
CC GO; GO:0045359; P:positive regulation of interferon-beta bios. . . ; IMP.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_Cterm.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC InterPro; IPR000157; TIR_domain.
CC Pfam; PF00560; LRR; 15.
CC Pfam; PF01463; LRRCT; 1.
CC PRINTS; PR00019; LEURICRPT.
CC SMART; SM00369; LRR_Typ; 2.
CC SMART; SM00082; LRRCT; 1.
CC SMART; SM00013; LRRNT; 1.
CC SMART; SM00255; TIR; 1.
CC PROSITE; PS01014; TIR; 1.
KW Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
PT SIGNAL 1 21 POTENTIAL.
PT CHAIN 22 904 TOLL-LIKE RECEPTOR 3.
PT DOMAIN 22 704 EXTRACELLULAR (POTENTIAL).
PT TRANSMEM 705 725 POTENTIAL.
PT DOMAIN 726 904 CYTOPLASMIC (POTENTIAL).
PT REPEAT 50 73 LRR 1.
PT REPEAT 75 97 LRR 2.
PT REPEAT 98 121 LRR 3.
PT REPEAT 123 145 LRR 4.
PT REPEAT 147 169 LRR 5.
PT REPEAT 170 193 LRR 6.
PT REPEAT 196 219 LRR 7.
PT REPEAT 247 270 LRR 8.
PT REPEAT 273 296 LRR 9.
PT REPEAT 298 320 LRR 10.
PT REPEAT 354 377 LRR 11.
PT REPEAT 379 403 LRR 12.
PT REPEAT 406 429 LRR 13.
PT REPEAT 431 454 LRR 14.
PT REPEAT 455 478 LRR 15.
PT REPEAT 480 504 LRR 16.
PT REPEAT 505 528 LRR 17.
PT REPEAT 530 552 LRR 18.
PT REPEAT 561 584 LRR 19.
PT REPEAT 586 608 LRR 20.
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FT REPEAT 610 632 LRR 21.
FT REPEAT 634 659 LRR 22.
FT DOMAIN 754 896 TIR.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 662 662 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 904 AA; 103828 MW; 034E05ECA7A4D2F7 CRC64;

Query Match 7.8%; Score 267; DB 1; Length 904;
Best Local Similarity 30.9%; Pred. No. 5e-11;
Matches 101; Conservative 48; Mismatches 146; Indels 32; Gaps 12;

ZY 51 SCSNQPSKVC-----TRGLSEVPQIGPSNTRYLNMENNQMIOADTFRLHLHLVLQL 106
DB 385 SLNSFTSLRLTNETFVSLAHSPLRI-----LNLTKNKISKIESDAFSLGHLVLDL 438
ZY 107 GRNSIRQIEVG-AFNGLASLNTLELFONLTVIPSGAFYLSKLRLWLN-----NPISL 162
DB 439 GLNIGELTQEWRLGLENIPFVLSYKYLQLTRNSFALVPSLQRLMLRLRVALKNDVSS 498
ZY 163 PSYAFNRVPSLRDLGLKLEKLYISEGAFEGFLNLYMLGMCNFKDM-----PN---- 213
DB 499 PS-PFQPLRLNLTLDLSN-NNIANINDMDLEGLKLBILDQNNLRLARWKHPGPIY 556
ZY 214 -LTELVLGLELEMSGNHPPHPIRPGSGFLGSLKLLKWLWNQSVLSIERNAPDGLASVELN 272
DB 557 FLKGLSHLHLNLSNGFDEIPVVFVKDLPELKIIDLGLANLNTLPASVFNQVSLKSLN 616
ZY 273 LAHNNLSLPHDLFTPL-LRYLVELLHLHNPNWDCD-ILALWKLRE---YIPNSTCCG 327
DB 617 LQKNLITSVEKKVGPAPRNLTLDLRFNPFDCESIANFVWVWINTHINIPELSHY- 675
ZY 328 RCHAPMGRGYLVEVVOQASQCQAPF 354
DB 676 LCNTPPHYHGFVRLFTSTSCCKDSAPF 702

RESULT 46
XD_OMD_RAT STANDARD; PRT; 423 AA.
AC Q92LS7;
YT 28-FEB-2003 (Rel. 41, Created)
YT 28-FEB-2003 (Rel. 41, Last sequence update)
YT 28-FEB-2003 (Rel. 41, Last annotation update)
YE Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate
YE proteoglycan osteomodulin) (RSPG osteomodulin).
FN OMD.
YS Rattus norvegicus (Rat).
YC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
YC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
YX NCBI TaxID=10116;
YN [1]
YQ SEQUENCE FROM N.A.
YC TISSUE=Calvaria;
YX MEDLINE=20076689; PubMed=10607915;
YA Shen Z., Gantcheva S., Sommarin Y., Heinigaard D.;
YT "Tissue distribution of a novel cell binding protein, osteoadherin, in
YT the rat.";
YL Matrix Biol. 18:533-542(1999).
YC -!- FUNCTION: May be implicated in biomineralization processes. Has a
YC function in binding of osteoblasts via the alpha(V)beta(3)-

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integrin.
CC -!- SUBUNIT: Binds the alpha(V)beta(3)-integrin.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Osteoblast and odontoblast. Expressed in
CC femoral bone and calvaria tissues. Detected in femoral head, rib,
CC tendon and bone marrow.
CC -!- DEVELOPMENTAL STAGE: In developing molars, it was first detected
CC in alveolar bone in 19-day-old embryos. In more mature teeth
CC (newborn and 2-day-old rats), the expression starts in the
CC polarized odontoblasts and increases in the secretory and mature
CC odontoblasts.
CC -!- PTM: Binds keratan sulfate chains.
CC -!- PTM: Sulfated on tyrosine residue(s) (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SRP) FAMILY. CLASS II SUBFAMILY.
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC
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CC
CC EMBL; AP104362; AAD04570.1; -.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR003772; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 9.
CC SMART; SM0013; LRRNT; 1.
CC Cell adhesion; Glycoprotein; Extracellular matrix; Proteoglycan;
CC Repeat; Leucine-rich repeat; Signal; Sulfation.
CC SIGNAL.
CC CHAIN 1 20
CC REPEAT 21 423
CC LRR-S 1.
CC REPEAT 84 103
CC LRR-T 1.
CC REPEAT 104 127
CC LRR-T 2.
CC REPEAT 128 153
CC LRR-S 2.
CC REPEAT 154 174
CC LRR-T 3.
CC REPEAT 175 198
CC LRR-T 4.
CC REPEAT 199 224
CC REPEAT 225 245
CC LRR-S 3.
CC REPEAT 246 269
CC LRR-T 5.
CC REPEAT 270 292
CC LRR-T 6.
CC REPEAT 293 312
CC LRR-S 4.
CC REPEAT 313 342
CC LRR-T 7.
CC REPEAT 343 367
CC LRR-T 8.
CC ASP/GLU-RICH (ACIDIC).
CC BY SIMILARITY.
CC Sulfation (POTENTIAL).
CC Sulfation (POTENTIAL).
CC Sulfation (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 423 AA; 49783 MW; 587D679FD9482B9F CRC64;

Query Match 7.7%; Score 263.5; DB 1; Length 423;
Best Local Similarity 28.9%; Pred. No. 3.2e-11;
Matches 83; Conservative 47; Mismatches 100; Indels 57; Gaps 12;

QY 46 CPVSCSNQF-SKVVCTRGSLSEVPQIGPSNTRYLNMENNQMIOADTFRLHLHLVL 104
DB 62 CAKCEPCTNPTPTSKYCDNRKLTIPD-IPWHIQQLNQFNDEAVTADSFNATHLKEI 120
QY 105 QLGNSIR--QIEVGAFNGLASLNTLELFONLTVIPSGAFYLSKLRLWLNPNPISI 162
DB 121 NLSHNKIKSQIDYGVFAKLSNQQQLHLDHNNLEFPF---FPLPKSLERLLGNYEISTL 177

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QY 166 AFNRVPSLRMLDLGELKKLEY--ISEGAFEGFLNLYNLGNKCNKMPNLTPLVGLBEL 223  
 DB 179 VPSGLRNMCIEGG-NPLENSGFGPAGDGL-KLYLRISAKLTGPKDLPET-LNEL 235  
 QY 224 ENSGNHFPPIRPGSFHGLSSKLLKWMNSQVSLIERNADFGLASIVELNLAHNNLSLPH 283  
 DB 236 HLDHNKIQAIIELEDLRYSKLYRLGHLGHQIRMIENGSLFPLTRELHLDNNKLSRVA 295  
 QY 284 DLFTPLRYLYVELLHHN 300  
 DB 296 GL-PDLKLLQVYVLSN 311

RESULT 48  
 PGS1\_RAT STANDARD; PRT; 369 AA.  
 AC P47853;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SI).  
 GN BGN.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Vascular smooth muscle;  
 RX MEDLINE=91184222; PubMed=2081545;  
 RA Dreher K.L., Asundi V.K., Matzura D., Cowan K.;  
 RT "Vascular smooth muscle biglycan represents a highly conserved  
 proteoglycan within the arterial wall.";  
 RL Eur. J. Cell Biol. 53:295-304(1990).  
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By  
 similarity).  
 CC -!- SUBUNIT: Forms a ternary complex with WFAP2 and BLN (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By  
 similarity).  
 CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially  
 in articular cartilages.  
 CC -!- PTM: The two attached glycosaminoglycan chains can be either  
 chondroitin sulfate or dermatan sulfate (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 (SLRP) FAMILY. CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC  
 CC EMBL: U17834; AAA58797.1; --  
 DR PIR: S32793; S32793.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000372; LRR Nterm.  
 DR InterPro: IPR003591; LRR typ.  
 DR Pfam: PF00560; LRR; 9.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT PROPEP 20 37  
 FT CHAIN 38 369 BIGLYCAN.  
 FT DOMAIN 64 77 CIS-RICH.  
 FT REPEAT 83 103 LRR-S 1.  
 FT REPEAT 104 127 LRR-T 1.  
 FT

FT REPEAT 128 151 LRR-T 2.  
 FT REPEAT 152 172 LRR-S 2.  
 FT REPEAT 173 196 LRR-T 3.  
 FT REPEAT 197 221 LRR-T 4.  
 FT REPEAT 222 242 LRR-S 3.  
 FT REPEAT 243 266 LRR-T 5.  
 FT REPEAT 267 290 LRR-T 6.  
 FT REPEAT 291 313 LRR-S 4.  
 FT REPEAT 314 343 LRR-T 7.  
 FT REPEAT 344 369 LRR-T 8.  
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY  
 SIMILARITY).  
 FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY  
 SIMILARITY).  
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 64 77 BY SIMILARITY.  
 FT DISULFID 322 355 BY SIMILARITY.  
 SQ SEQUENCE 369 AA; 41706 MW; 319DC15117F2C604 CRC64;  
 Query Match 7.6%; Score 262.5; DB 1; Length 369;  
 Best Local Similarity 31.9%; Pred. No. 3.2e-11;  
 Matches 82; Conservative 40; Mismatches 124; Indels 11; Gaps 7;  
 QY 46 CPSVCSNQFSKVVCTRGSEVPGGIPSNTRYLNLMNNIQQADTFRLHLEVLQ 105  
 DB 64 CPGGCHC--HLRVQCSDLGLKTVPKBISPDITLDLQNNDISELRKDDFKGLQHLVALV 121  
 QY 106 LGRNSIROIEVCAFNGLASLNTLELFDNMLTVIPSGAFYLSKLPRLWLRNPNIESIPSY 165  
 DB 122 LVNNKISKIHEKAFSPRLKQKLYISKHNLVEIPP---NLFSVELLHIDNRIRKKVPG 178  
 QY 166 AFNRVPSLRMLDLGELKKLEY--ISEGAFEGFLNLYNLGNKCNKMPNLTPLVGLBEL 223  
 DB 179 VPSGLRNMCIEGG-NPLENSGFGPAGDGL-KLYLRISAKLTGPKDLPET-LNEL 235  
 QY 224 ENSGNHFPPIRPGSFHGLSSKLLKWMNSQVSLIERNADFGLASIVELNLAHNNLSLPH 283  
 DB 236 HLDHNKIQAIIELEDLRYSKLYRLGHLGHQIRMIENGSLFPLTRELHLDNNKLSRVA 295  
 QY 284 DLFTPLRYLYVELLHHN 300  
 DB 296 GL-PDLKLLQVYVLSN 311

RESULT 49  
 TLR7\_HUMAN STANDARD; PRT; 1049 AA.  
 ID TLR7\_HUMAN  
 AC Q9NYK1; Q9NYR98;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Toll-like receptor 7 precursor.  
 GN TLR7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Placenta;  
 RX MEDLINE=20477806; PubMed=11022119;  
 RA Du X., Poltorak A., Wei Y., Beutler B.;  
 RT "Three novel mammalian Toll-like receptors: gene structure,  
 expression, and evolution.";  
 RL Eur. Cytokine Netw. 11:362-371(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Placenta;  
 RX MEDLINE=20477807; PubMed=11022120;  
 RA Chuang T.-H., Ulevitch R.J.;  
 RT "Cloning and characterization of a sub-family of human Toll-like  
 receptors: hTLR7, hTLR8 and hTLR9.";

RL Eur. Cytokine Netw. 11:372-378(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Participates in the innate immune response to microbial  
 agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B  
 activation, cytokine secretion and the inflammatory response (By  
 similarity).  
 CC -!- SUBUNIT: Binds MyD88 via their respective TIR domains (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- TISSUE SPECIFICITY: Detected in brain, placenta, spleen, stomach,  
 small intestine, lung and in plasmacytoid pre-dendritic cells.  
 CC -!- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 TIR domain.  
 CC -!- SIMILARITY: Contains 27 leucine-rich (LRR) repeats.  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC  
 CC EMBL: AF240457; AAF60188.1; -  
 CC EMBL: AF245702; AAF78035.1; -  
 CC EMBL: BC033651; AAH33651.1; -  
 CC HSPSP: O60603; IPIW.  
 CC Genew: HGNC:15631; TLR7.  
 CC MIM: 300365; -  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000483; LRR Cterm.  
 CC InterPro: IPR000372; LRR Nterm.  
 CC InterPro: IPR003591; LRR typ.  
 CC InterPro: IPR000157; TIR\_domain.  
 CC Pfam: PF00560; LRR; 10.  
 CC Pfam: PF01463; LRRCT; 1.  
 CC Pfam: PF01582; TIR; 1.  
 CC PRINTS: PRO0019; LEURICHRPT.  
 CC SMART: SM00369; LRR TYP; 3.  
 CC SMART: SM00082; LRRCT; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC PROSITE: PS0104; TIR; 1.  
 KW Receptor; Immune response; Inflammatory response; Signal;  
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.  
 FT SIGNAL 1 26  
 FT CHAIN 27 1049  
 FT DOMAIN 27 839 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 840 860 POTENTIAL.  
 FT DOMAIN 861 1049 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 43 64 LRR 1.

FT REPEAT 65 87  
 FT REPEAT 110 126 LRR 2.  
 FT REPEAT 127 149 LRR 3.  
 FT REPEAT 151 170 LRR 4.  
 FT REPEAT 171 195 LRR 5.  
 FT REPEAT 203 226 LRR 6.  
 FT REPEAT 228 247 LRR 7.  
 FT REPEAT 248 275 LRR 8.  
 FT REPEAT 289 312 LRR 9.  
 FT REPEAT 314 337 LRR 10.  
 FT REPEAT 339 368 LRR 11.  
 FT REPEAT 369 392 LRR 12.  
 FT REPEAT 396 419 LRR 13.  
 FT REPEAT 421 443 LRR 14.  
 FT REPEAT 492 515 LRR 15.  
 FT REPEAT 516 540 LRR 16.  
 FT REPEAT 541 564 LRR 17.  
 FT REPEAT 566 588 LRR 18.  
 FT REPEAT 595 618 LRR 19.  
 FT REPEAT 619 644 LRR 20.  
 FT REPEAT 649 672 LRR 21.  
 FT REPEAT 674 697 LRR 22.  
 FT REPEAT 698 721 LRR 23.  
 FT REPEAT 723 745 LRR 24.  
 FT REPEAT 746 769 LRR 25.  
 FT REPEAT 772 795 LRR 26.  
 FT REPEAT 889 1036 LRR 27.  
 FT DOMAIN TIR.  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 488 488 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 590 590 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 679 679 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 720 720 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 799 799 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 725 725 L -> H (IN REF. 2).  
 FT CONFLICT 738 738 L -> P (IN REF. 2).  
 SQ SEQUENCE 1049 AA; 120921 MW; 8C701E9E437F2721 CRC64;  
 Query Match 7.6%; Score 262; DB 1; Length 1049;  
 Best Local Similarity 23.7%; Pred. No. 1.4e-10;  
 Matches 117; Conservative 66; Mismatches 151; Indels 160; Gaps 19;  
 QY 80 LNLMMNNIOMIQADTFRHLHLHLVQLGRNSRQIEVGA-FNGLASINTLELPDNMLTVI 138  
 DB 498 LDISKNSIPFVKSSDFQHLKFLKCNLSGNTLSQTLNGSEFQPLAELRYLDFSNRLDLL 557  
 QY 139 PSGAPEYLSK-----LRELNRNFI-----159  
 DB 558 HSTAFELHKLVLVDISSNSHYFQSGITHMLNPTNKLVLQKLMWMDISSISRTME 617  
 QY 160 -ESIPSYAP-----NRVPSLMR--LDLGL-----KKLEYTSEGAFGL-FML 198  
 DB 618 SESLRTLEFEGNHLVDLWREGNRYQLQFLNKLKLELDISKNSLSFLPSGVFDGMPNL 677  
 QY 199 KYNLGMCNIKOM--FNLPVLGLELWSEVGNHFFRIPGSPFGLSSLKLWMSQVSL 256  
 DB 678 KNLSLAKNGLKSPSKWKLOCLKNLETLDLHSHQLTVTPERLNCRSRLKNLILKNQIRS 737  
 QY 257 IERNAFDGLASLVELNAHNNL-----SSLPHDLFTPLRYLVLELHNNHPWCDCDILWL 311  
 DB 738 LTKYFLQDAFQRLYDLSSNKKIQMKTSFFPENLVNNAKMLL-----LHNRPLCTDAVNF 794  
 QY 312 AWWLRE-----YIPNTSCCECHAPMEWRGRLVVEVDQASFO-----349  
 DB 795 VWWNVNTEVTIPYLATDVTVCV-----FGAHRGQSVISEDLTYCELDLTLILFSLISVS 850

QY 350 -----CSAPFMDAPDRLNISEGRMA 370  
 DB 851 LFLVMYMTASHLYFDWVWYIYHFCCKAKIYGYORLISPDCCYDADIVYDTKOPAVTEWVLA 910  
 QY 371 EL--KCRTPP-----MSSVKWLEPNTVLSHRSRPRIS-----VLND---GTLNPF-- 411  
 DB 911 ELVAKLEDPREKHFNLCLERDQ-LPGQVLENLSQISQISKTVFWYDKYAKTENFKI 969  
 QY 412 ----SHVLISDTGV 421  
 DB 970 AFYLSHORLMDKV 983  
 RESULT 50  
 PGSI\_HUMAN  
 ID PGSI\_HUMAN STANDARD; PRT; 368 AA.  
 AC 21810; P13247;  
 XT 01-JAN-1990 (Rel. 13, Created)  
 YT 01-APR-1993 (Rel. 25, Last sequence update)  
 XT 15-SEP-2003 (Rel. 42, Last annotation update)  
 XE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).  
 XN BGN.  
 XS Homo sapiens (Human).  
 XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 XC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX NCBI\_taxID=9606;  
 XP SEQUENCE FROM N.A.  
 XC TISSUE=Bone;  
 XA MEDLINE=99174714; PubMed=2647739;  
 XA Fisher L.W., Termine J.D., Young M.F.;  
 XT "Deduced protein sequence of bone small proteoglycan I (biglycan)  
 XT shows homology with proteoglycan II (decorin) and several  
 XT nonconnective tissue proteins in a variety of species.";  
 UL J. Biol. Chem. 264:4571-4576(1989).  
 XN SEQUENCE FROM N.A.  
 XP MEDLINE=91317791; PubMed=1860845;  
 XA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,  
 XA Termine J.D., Young M.F.;  
 XT "Human biglycan gene. Putative promoter, intron-exon junctions, and  
 XT chromosomal localization.";  
 UL J. Biol. Chem. 266:14371-14377(1991).  
 XN SEQUENCE FROM N.A.  
 XP MEDLINE=20314869; PubMed=10854409;  
 XA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,  
 XA Nordstrek G., Stevens M.A., Kioschis P., Dangei A., Cunningham D.,  
 XA Straw K., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,  
 XA Kerry G., Greystron J.S., Clark D., Goerdes M., Blechechmidt K.,  
 XA Rump A., Hinzmann S., Mundy C.R., Miller W., Poustka A., Herman G.E.,  
 XA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;  
 XT "Comparative genome sequence analysis of the Bpa/Str region in mouse  
 XT and man.";  
 TL Genome Res. 10:758-775(2000).  
 LN SEQUENCE FROM N.A.  
 XP TISSUE=Brain;  
 XA MEDLINE=22388257; PubMed=12477932;  
 XA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 XA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 XA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,  
 XA Diatchenko L., Marusik A., Kioschis P., Dangei A., Rubin G.M., Hong L.,  
 XA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 XA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 XA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 XA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 XA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 XA Feany J., Heiton M., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 XA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 XA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 38-57.  
 RX MEDLINE=90073579; PubMed=2590169;  
 RA Roughley P.J., White R.J.;  
 RT "Dermatan sulphate proteoglycans of human articular cartilage. The  
 RT properties of dermatan sulphate proteoglycans I and II.";  
 RL Biochem. J. 262:823-827(1989).  
 RN [6]  
 RP SEQUENCE OF 38-66.  
 RX MEDLINE=87250639; PubMed=3597437;  
 RA Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;  
 RT "Purification and partial characterization of small proteoglycans I  
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 RL J. Biol. Chem. 262:9702-9708(1987).  
 RN [7]  
 RP SEQUENCE OF 361-368 FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=95187185; PubMed=7881444;  
 RA Just W., Rau W., Muller R., Geerkens C., Vogel W.;  
 RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)  
 RT locus.";  
 RL Hum. Mol. Genet. 3:2268-2268(1994).  
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By  
 CC similarity).  
 CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially  
 CC in articular cartilages.  
 CC -!- PTM: The two attached glycosaminoglycan chains can be either  
 CC chondroitin sulfate or dermatan sulfate (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN  
 CC (SRP) FAMILY. CLASS I SUBFAMILY.  
 CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
 CC -----  
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 CC -----  
 DR EMBL; J04599; AAA36009.1; -;  
 DR EMBL; M65153; AAA52287.1; ALT SEQ.  
 DR EMBL; M65152; AAA52287.1; JOINED.  
 DR EMBL; U82695; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; BC002416; AAH02416.1; -;  
 DR EMBL; BC004244; AAH04244.1; -;  
 DR EMBL; U11636; AAC50117.1; -;  
 DR FIR; A40757; BGHUN.  
 DR Genew; HGNC:1044; BGN.  
 DR MIM; 301870; -;  
 DR GO; GO:0005778; C:extracellular matrix; NAS.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_type.  
 DR Pfam; PF00560; LRR; 9  
 DR Pfam; PF01482; LRRNT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR GlycoProtein; Extracellular matrix; Proteoglycan; Repeat;  
 KW Leucine-rich repeat; Signal.  
 FT SIGNAL 1 19  
 FT PROPEP 20 37  
 FT POTENTIAL.

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FT CHAIN 38 368 BIGLYCAN.
FT DOMAIN 63 76 CYS-RICH.
FT REPEAT 82 102 LRR-S 1.
FT REPEAT 103 126 LRR-T 1.
FT REPEAT 127 150 LRR-T 2.
FT REPEAT 151 171 LRR-S 2.
FT REPEAT 172 195 LRR-T 3.
FT REPEAT 196 220 LRR-T 4.
FT REPEAT 221 241 LRR-S 3.
FT REPEAT 242 265 LRR-T 5.
FT REPEAT 266 289 LRR-T 6.
FT REPEAT 290 312 LRR-S 4.
FT REPEAT 313 342 LRR-T 7.
FT REPEAT 343 368 LRR-T 8.
FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN).
FT CARBOHYD 47 47 O-LINKED (GLYCOSAMINOGLYCAN).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 63 76 BY SIMILARITY.
FT DISULFID 321 354 BY SIMILARITY.
FT CONFLICT 139 140 KL -> NV (IN REF. 1).
FT CONFLICT 163 164 EL -> DV (IN REF. 1).
SQ SEQUENCE 368 AA; 41654 MW; BF16F304C5CD3B3E CRC64;

Query Match 7.6%; Score 261.5; DB 1; Length 368;
Best Local Similarity 31.5%; Pred. No. 3.7e-11;
Matches 31; Conservative 41; Mismatches 124; Indels 11; Gaps 7;

QY 46 CPSCVCSNQFSKVCTRRGLSEVPQGISNTRYLMNENNIQADTFRHLHLEVLQ 105
Db ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
63 CPGCHC--HLRVQCSDLGKSVKPEISPDFTLLDQNNDISELRKDDFKGLQLYALV 120
QY 106 LGENSIROIEVGAFNGLASLITLLEFDNLTWIPSGAFYLSKLRMLRNPIESIPSY 165
Db ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
121 LVNKKISKEHKAFSPRLKQKYISKHLVEIPP---NLPSSLVELRIHDNRIRKVPKG 177
QY 166 AFNRVPSLRDLGLKXLEY--ISEGAFEGFLNKLKYNLGMCNIKDMPNLTPLVGLREL 223
Db ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
178 VFGSLRNWNCIENG-G-NPLENSGFEPGADGL-KNYLRISAKLTGIPKDLPET-LNEL 234
QY 224 EMSGNHPPPIRPGSFHGLSSLKLYWMSQVSLIERNAPDGLASLVELNLAHNLSLPH 283
Db : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
235 HLDHNKIQAIELEDLRLYSLKLYGLGHQIRMIENGSLSLFTLRELHLDNNKLARVPS 294
QY 284 DLFTPLRYLVELLHNN 300
Db | : : : |||
295 GL-PDLKLLQVYLNEN 310

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